STIC Search Report
Biotech-Chem Library

USPTO

To: Sarvamangala Devi
Location: CM1/7E15
Art Unit: 1645
Thursday, December 18, 2003

Case Serial Number: 09/428122

From: Beverly Shears
Location: Biotech-Chem Library
CM1-1E05
Phone: 308-4994

beverly.shears@uspto.gov

Search Notes

Shears, Beverly

110600

From:	Devi, Sarvamangala
Sent:	Tuesday, December 16, 2003 10:17 AM
To:	Shears, Beverly
Subject:	09/428,122

Beverly:

   Would you please perform a sequence and an interference search for SEQ ID NO: 1 and SEQ ID NO: 2 in application 09/428,122? Please also run SEQ ID NO: 1 against the amino acid sequence.

Thanks.

S. DEVI, Ph.D.
AU 1645
CM1-7E15

SEARCH REQUEST FORM

Requestor's
Name: _____

Serial
Number: _____

Date: _____   Phone: _____   Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevent citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevent claim(s).

STAFF USE ONLY

Date completed: 12-17-03   **Search Site**   Vendor

SEARCH REQUEST FORM

7449 5

Requestor's
Name: _Devi_

Serial
Number: _09/428,122_

Date: _12/3_   Phone: _308-9347_   Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevent citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevent claim(s).

A Seq 1 vs A81735

Seq 1

MUST BE

SCANNED.

75.8

100

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: December 16, 2003, 12:14:27 ; Search time 10698 Seconds
(without alignments)
11472.133 Million cell updates/sec

Title: US-09-428-122-1
Perfect score: 3000
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Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0
Searched: 2888711 seqs, 2045481386 residues
Total number of hits satisfying chosen parameters: 5777422
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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       2: gb_htg:*
       3: gb_in:*
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      13: gb_un:*
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      41: em_htgo_other:*

SUMMARIES

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	2988	99.6	26920	1	CPN133035	AJ133035 Chlamydia
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	4	2986.4	99.5	299650	1	AP002545	AP002545 Chlamydop
	5	2975.4	99.2	110000	6	AR310754_00	AR310754 Sequence
	6	2775.8	92.5	2787	6	A81835	A81835 Sequence 9
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	9	546.6	18.2	2781	6	AX662119	AX662119 Sequence
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	11	546.6	18.2	4926	6	CPU72499	U72499 Chlamydophi
	12	531.8	17.7	12676	1	AE002192	AE002192 Chlamydop
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c	14	531.2	17.7	10757	1	AE001628	AE001628 Chlamydia
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ALIGNMENTS

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DEFINITION Chlamydia pneumoniae section 3 of 103 of the complete genome.
ACCESSION   AE001587 AE001363
VERSION   AE001587.1 GI:4376271
KEYWORDS   .
SOURCE   Chlamydophila pneumoniae CWL029
  ORGANISM Chlamydophila pneumoniae CWL029
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
REFERENCE   1 (bases 1 to 16448)
  AUTHORS   Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Hyman,R.W.,
            Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S.
  TITLE   Comparative genomes of Chlamydia pneumoniae and C. trachomatis
  JOURNAL   Nat. Genet. 21 (4), 385-389 (1999)

Pred. No. is the number of results predicted by chance to have a

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MEDLINE    99206606
PUBMED     10192388
REFERENCE  2  (bases 1 to 16448)
AUTHORS    Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Olinger,L.,
           Grimwood,J., Davis,R.W. and Stephens,R.S.
TITLE      Direct Submission
JOURNAL    Submitted (01-DEC-1998) Program in Infectious Diseases, University
           of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA
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ORIGIN

Query Match     99.6%;  Score 2988;  DB 1;  Length 16448;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 2999;   Conservative   0;  Mismatches   0;  Indels   1;  Gaps   1;

Qy      1 CGCTCTTACCTAGTAGAGGTTGAGTGAATTCCTGACTTGTTCTCCTATTGGTGTATCT   60
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Db     72 CGCTCTTACCTAGTAGAGGTTGAGTGAATTCCTGACTTGTTCTCCTATTGGTGTATCT   131

Qy     61 CTTAAAATATTAAATTCAAAATCAAAGTATATATTTTACAATGAGAAGTCTTCTTCCCAA  120
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Nucleotide sequence alignment (Query "Qy" vs. Database "Db"), with flanking residue position numbers:

Db 132 / Qy 121 / Db 192 ... Qy 181 / Db 252 ... Db 1201 / Qy 1271 ...

(The page consists of a two-sequence nucleotide alignment displayed in stacked Qy/Db blocks with match bars between them; residue position numbers run from 121/132 through approximately 2291/2350.)

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Qy   2281  TTGTTCGTTGTCTTATGTCCTACAGAGATTCCTGTTCCTCTTTTCAGGAAACCTTAGCTA  2340
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Qy   2341  CACCCATACGGATAACGATCTGAAAACCAAGTATACAACATATCCTACTGTTAAAGGAAG  2400
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Qy   2521  GGAAGGTTTAAAGAACAGGGAACAGAAGCTCGTGAATTGGAAGTAGCCGTCTTGTGAA  2580
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Qy   2941  ATTTCTTCTGAAGGCTCTTTTCGATTTCGATTTCCATTTTAGTGTTTTGCTAAAACACTTTC  3000
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Query Match     99.6%;     Score 2988;    DB 1;    Length 26920;
Best Local Similarity 100.0%;    Pred. No. 0;
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Qy        1 CGCTCTTACCTAGTAGAGGTTGAGTGAATTCTTGACTTGTTTCTCCTATTGGTGTATCT 60
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Qy       61 CTTAAAATATTAAAATCAAAGTATATATTTTACAATGAAGTCTTCTTTCCCCAA 120
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Qy      421 TGTTAACAGCAGCCGTGGTAGATAAATCTACCACCGTTTATAGGGTTTCTTCGCTATCTTT 480
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BASE COUNT     3532 a   2722 c   2431 g   3441 t     1 others
ORIGIN
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Qy      241  GGAAGATGCTGGAACTACCTACCTATTTAAGGGAATAAAAATGTCACTCTTAGAAAATATTCCTGG  300
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Qy      301  AACAGGCACAGCAATCACAAAAAGCTGTTTTAACAACACTAGTGTTTGACTTCAC  360
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Db  7831  AGAGACAGAGGCCGCAGATTCTCAAAAATCTTACTTGAAGCTACTACAGCCTGTAACTCT  7772
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Qy  1441  TTCAGGAGGTACTCTATCTTTAAAAACATGGAGTGACTTCTGCGAGCATTCACTCA  1500
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COMMENT   (E-mail:mshirai@po.cc.yamaguchi-u.ac.jp, Tel:81-836-22-2227,
            Fax:81-836-22-2415)
            On or before Aug 31, 2000 this sequence version replaced
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RESULT 4
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REFERENCE   1
  AUTHORS   Shirai,M., Hirakawa,H., Ouchi,K., Tabuchi,M., Kishi,F., Kimoto,M.,
            Takeuchi,A., Nishida,J., Shibata,K., Fujinaga,R., Yoneda,H.,
            Matsushima,H., Tanaka,C., Furukawa,S., Miura,K., Nakazawa,A.,
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  TITLE   Comparison of outer membrane protein genes omp and pmp in the whole
            genome sequences of Chlamydia pneumoniae isolates from Japan and
            the United States
  JOURNAL   J. Infect. Dis. 181 Suppl 3, S524-S527 (2000)
   MEDLINE   20298986
   PUBMED   10839753
REFERENCE   2
  AUTHORS   Shirai,M., Hirakawa,H., Kimoto,M., Tabuchi,M., Kishi,F., Ouchi,K.,
            Shiba,T., Ishii,K., Hattori,M., Kuhara,S. and Nakazawa,T.
  TITLE   Comparison of whole genome sequences of Chlamydia pneumoniae J138
            from Japan and CWL029 from USA
  JOURNAL   Nucleic Acids Res. 28 (12), 2311-2314 (2000)
   MEDLINE   20330349
   PUBMED   10871362
REFERENCE   3 (bases 1 to 299650)
  AUTHORS   Shirai,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (04-JUL-2000) Mutsunori Shirai, Yamaguchi University
            School of Medicine, Department of Microbiology; 1-1-1
            Minamikogushi, Ube, Yamaguchi 755-8505, Japan

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Db  21749  AATTTTTACAGAAGAGCCTCGGTGACTATTCTAATAATGCTAAATAATGACAA  21808

Qy    841  TAAGGTCACGAGGAGCGAGCCTCCTCAACAACGGGGATATGTCAGGAGTGTGCTATCTGTGC  900
           |||||||||| |||||||||||||||||||| || ||||||||||||||||||||||||||||
Db  21809  TAAGGTCACAGGAGCGAGCCTCCTCAACACACGGGGATATGTCAGGAGTGTGCTATCTGTGC  21868

Qy    901  TTATAAAACTAGTACAGATACTAAGGTCACCCCTCACTGGAAATCAGAGTTACTCTTCAG  960
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Db  21869  TTATAAAACTAGTACAGATACTAAGGTCACCCCTCACTGGAAATCAGAGTTACTCTTCAG  21928

Qy    961  CAACAATAACATCGACAACACGCGGGAGGAGCTATCTATGTGAAAAAGCTGAACTGGCTTC  1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  21929  CAACAATAACATCGACAACACGCGGGAGGAGCTATCTATGTGAAAAAGCTGAACTGGCTTC  21988

Qy   1021  CGGAGGACTTACCCCATTCCAGTAGAAATAGTGTCAATGGAGGTACAGCTTCCTAAAGGTGG  1080
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Db  21989  CGGAGGACTTACCCCATTCCAGTAGAAATAGTGTCAATGGAGGTACAGCTTCCTAAAGGTGG  22048

Qy   1081  AGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGT  1140
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Db  22049  AGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGT  22108

Qy   1141  CTTTTTAGGGAATACAGTCACTTCTACTACTCCTGGGACGAATAGAAGTAGTATCGACTT  1200
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Db  22109  CTTTTTAGGGAATACAGTCACTTCTACTACTCCTGGGACGAATAGAAGTAGTATCGACTT  22168

Qy   1201  AGGAACGAGTGCAAAGATGACAGCTTGCGTTTCTGCGTTTGCTGCTGGTGTAGCCATCACTACTTCTA  1260
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Db  22169  AGGAACGAGTGCAAAGATGACAGCTTGCGTTTCTGCGTTTGCTGCTGGTGTAGCCATCACTACTTCTA  22228

Qy   1261  TGATCCCATAACTACTACAGATCATCCACAACAGTTACAGATGTCTTAAAGTTAATGAGAC  1320
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Db  22229  TGATCCCCATAACTACTACAGATCATCCACAACAGTTACAGATGTCTTAAAGTTAATGAGAC  22288

Qy   1321  TCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAGAGGAAAGTTATC  1380
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Db  22289  TCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAGAGGAAAGTTATC  22348

Qy   1381  AGAGACAGAGGCCGCAGATTCTAAAAAATCTAAAAATCTTGAAGCTACTACAGCCTAACTCT  1440
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Db  22349  AGAGACAGAGGCCGCAGATTCTAAAAAATCTAAAAATCTTGAAGCTACTACAGCCTAACTCT  22408

Qy   1441  TTCAGGAGGTACTCTATCTTTAAAACATGGACTCTGCAGACTCAGGCATTCACTCA  1500
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Db  22409  TTCAGGAGGTACTCTATCTTTAAAACATGGACTCTGCAGACTCAGGCATTCACTCCA  22468

Qy   1501  ACAGGCAGATTCTCGTCTCGAAATGGACGTAGGACTACTTGCTAGAACCTGCTGATACTAG  1560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22469  ACAGGCAGATTCTCGTCTCGAAATGGACGTAGGACTACTTGCTAGAACCTGCTGATACTAG  22528

Qy   1561  CACCATAAACAAATTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGAAGGCAAAAAT  1620
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22529  CACCATAAACAAATTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGAAGGCAAAAAT  22588

Qy   1621  AGAAACCAAAGCTACGTCAAAATTCTGACTTTATCTGAAACCATCACTTATTGGACCC  1680
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22589  AGAAACCAAAGCTACGTCAAAATTCTGACTTTATCTGAAACCATCACTTATTGGACCC  22648

Qy   1681  GACGGGCACGTTTTATGAAAATCATAGTTAAGAAATCCTCAGTCCTACGACATCTTAGA  1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22649  GACGGGCACGTTTTATGAAAATCATAGTTAAGAAATCCTCAGTCCTACGACATCTTAGA  22708

Qy   1741  GCTCAAAGCTTCTTGGAACTGTAACAAGCACCGCAGTGTAACAGATCCTATATAAATGGGTGA  1800
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Db  22709  GCTCAAAGCTTCTTGGAACTGTAACAAGCACCGCAGTGTAACAGATCCTATATAAATGGGTGA  22768

Qy   1801  GAAATTCCATTACGGCTATCAGGGAACTTGGGGCCCAATTGTTTGGGGGACCAGGGGCTTC  1860
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Db  22769  GAAATTCCATTACGGCTATCAGGGAACTTGGGGCCCAATTGTTTGGGGGACAGGGGCTTC  22828

Qy   1861  TACGACTGCAACCTTCAACTGGACTAAAACTGGCTATATTCCTAATCCTCCATTATCGG  1920
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Db  22829  TACGACTGCAACCTTCAACTGGACTAAAACTGGCTATATTCCTAATCCTCCATTATCGG  22888

Qy   1921  CTCTTTAGTCCCTAATAGCTTATGGAATGCATTTATAGATATTAGCTCTCCATTATCT  1980
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Db  22889  CTCTTTAGTCCCTAATAGCTTATGGAATGCATTTATAGATATTAGCTCTCCATTATCT  22948

Qy   1981  TATGGAGACTGCAAACGAAGGGTTGCAGGGGAGACCGTGCTTTTGGTGTGCTGGATTATC  2040
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Db  22949  TATGGAGACTGCAAACGAAGGGTTGCAGGGGAGACCGTGCTTTTGGTGTGCTGGATTATC  23008

Qy   2041  TAACTTCTTCATAAGGATAGTACAAAAACACGACGCGGGGTTCGCCATTGAGTGCGCGG  2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23009  TAACTTCTTCATAAGGATAGTACAAAAACACGACGCGGGGTTCGCCATTGAGTGCGCGG  23068

Qy   2101  TTATGTCATAGGAGGAAAACTACATACTGTTCAGATAAGAATTCTTAGTGCTGCATTTTG  2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23069  TTATGTCATAGGAGGAAAACTACATACTGTTCAGATAAGAATTCTTAGTGCTGCATTTTG  23128

Qy   2161  TCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAATCAAGGTACAGTCTACGG  2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23129  TCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAATCAAGGTACAGTCTACGG  23188

Qy   2221  AGGAACTCTCTATTACCAGCACAACGAAACCTATATCTCTTCCTTCCTGCAAACTACGGCC  2280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23189  AGGAACTCTCTATTACCAGCACAACGAAACCTATATCTCTTCCTTCCTGCAAACTACGGCC  23248

Qy   2281  TTGTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTCTTCTTTCAGGAAACCTTAGCTA  2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23249  TTGTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTCTTCTTTCAGGAAACCTTAGCTA  23308

Qy   2341  CACCCATACGGATAACGATCTGAAAACCAAGTATACAACAAGTATCAACATATCCTACTG  2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23309  CACCCATACGGATAACGATCTGAAAACCAAGTATACAACAAGTATCAACATATCCTACTG  23368

Qy   2401  CTGGGGAATGATAGTTCGGCTTTAGAATTCGGTGGAAGAGCTCCGATTTGCTTAGATGA  2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23369  CTGGGGAATGATAGTTCGGCTTTAGAATTCGGTGGAAGAGCTCCGATTTGCTTAGATGA  23428

Qy   2461  AAGTGCTCTATTTGAGCAGTACATGCCCTCATGAAATTGTCTCATGCACATCA  2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23429  AAGTGCTCTATTTGAGCAGTACATGCCCTCATGAAATTGTCTCATGCACATCA  23488

Qy   2521  GGAAGGTTTAAAGAACAGGGAACAGAGAGCTCGTGAATTTGGAAGTAGCCGTCTTGTGAA  2580
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23489  GGAAGGTTTTAAAGAACAGGGAACAGAGAGCTCGTGAATTTGGAAGTAGCCGTCTTGTGAA  23548

Qy   2581  TCTTGCCTTACCTATCGGAGATCCGATTGATAAGGAATCAGTTGATAAGGAACAACGTA  2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23549  TCTTGCCTTACCTATCGGAGATCCGATTGATAAGGAATCAGTTGATAAGGAACAACGTA  23608

Qy   2641  CAATCTAACTCTTGGTATACTGTTCGTCATGCTGTTATACTGGATCGTGGATCTTGTGGATCTTGTCGTACGACAAC  2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23609  CAATCTAACTCTTGGTATACTGTTCGTCATGCTGTTATACTGGATCGTGGATCTTGTGGATCTTGTCGTACGACAAC  23668

Qy   2701  ACTGCGAATTAGCGGTGATTCTTCGGAAAACCTTCGGTACGAAGACAAGCTTT  2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23669  ACTGCGAATTAGCGGTGATTCTTCGGAAAACCTTCGGTACGAAGACAAGCTTT  23728

Qy   2761  AGTCCTTCGTGCAGGGAACCATTTTTGCTTTAACTCAAATTTTGAAGCCTTTAGCCCAATT  2820
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Db  23729  AGTCCTTCGTGCAGGGAACCATTTTTGCTTTAACTCAAATTTTGAAGCCTTTAGCCCAATT  23788

Qy   2821  TTCTTTTGAATTGCGTGGGTCATCTGCAATGTGTAAATGTACAATTACAAATACCA  2880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23789  TTCTTTTGAATTGCGTGGGTCATCTGCAATGTGTAAATGTACAATTACAAATACCA  23848

Qy   2881  ATTCTAATGCGTTAGCTTTGGTAAAGAGCTGAAGGGAAAAGAGCTTTTAAG  2940
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23849  ATTCTAATGCGTTAGCTTTGGTAAAGAGCTGAAGGGAAAAGAGCTTTTAAG  23908

Qy   2941  ATTTCTTGAAGGCTCTTTTCGATTTCGATTTCCATTTTAGTGTTTTGCTAAAACACTTTC  3000
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Db  23909 ATTTCTTGAAGGCTCTTTTCGATTTCGATTCCATTTTAGTGTTTTGCTAAAACACTTTC 23968
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RESULT 5
AR310754_00
WPCOMMENT
Sequence split into 13 fragments    LOCUS AR310754
Fragment Name        Begin        End
AR310754_00              1     110000
AR310754_01         100001     210000
AR310754_02         200001     310000
AR310754_03         300001     410000
AR310754_04         400001     510000
AR310754_05         500001     610000
AR310754_06         600001     710000
AR310754_07         700001     810000
AR310754_08         800001     910000
AR310754_09         900001    1010000
AR310754_10        1000001    1110000
AR310754_11        1100001    1210000
AR310754_12        1200001    1230025

LOCUS       AR310754     1230025 bp    DNA     linear    PAT 12-JUN-2003
DEFINITION  Sequence 1 from patent US 6559294.
ACCESSION   AR310754
VERSION     AR310754.1    GI:31704180
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1230025)
AUTHORS     Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
TITLE       Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL     Patent: US 6559294-A 1 06-MAY-2003;
FEATURES    Location/Qualifiers
   source   1..1230025
            /organism="unknown"
BASE COUNT  367211 a   249831 c   249019 g   363587 t    .377 others
ORIGIN

Query Match          99.2%;    Score 2975.4;    DB 6;   Length 110000;
Best Local Similarity 99.9%;   Pred. No. 0;
Matches 2998;    Conservative 0;    Mismatches 0;    Indels 2;    Gaps 2;

Qy      1 CGCTCTTACCTAGTAGAGGTTGAGTGAATTCTTGACTTGTTCTCCTATTGGTGTATCT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  31658 CGCTCTTACCTAGTAGAGGTTGAGTGAATTCTTGACTTGTTCTCCTATTGGTGTATCT 31717

Qy     61 CTTAAAATATTAAATTCAAAATCAAAGTATATATTTTACAAGTCTTCTTTCCCCAA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  31718 CTTAAAATATTAAATTCAAAATCAAAGTATATATTTTACAAGTCTTCTTTCCCCAA 31777

Qy    121 GTTTGTATTTTCTACATTTGCTATTTTGTCTATTTTGTCCCTTTGTCTATGATGATGTCTACCGAGACAGTTTT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  31778 GTTTGTATTTTCTACATTTTGCTATTTTGTCTATTTTCCCTTTGTCTATGATGATGTCTACCGAGACAGTTTT 31837

Qy    181 GGATTCAAGTGCGAGTTTCGATGGGAATAAAAATGGTAATTTTCAGTTCGTGAGAGTCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  31838 GGATTCAAGTGCGAGTTTCGATGGGAATAAAAATGGTAATTTTCAGTTCGTGAGAGTCA 31897

Qy    241 GGAAGATGCTGGAACTACCTATTTAAGGGAAATGTCACTCTAGAAAATATTCCTGG 300
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Db  31898 GGAAGATGCTGGAACTACCTATTTAAGGGAAATGTCACTCTAGAAAATATTCCTGG 31957

Qy    301 AACAGGCACCAGCAATCACAAAAAGCTGTTTTAACAACACGTGTTTTAACAACACTGTTTTAACAACACTGTTTTGACTTTCAC 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  31958 AACAGGCACCAGCAATCACAAAAAGCTGTTTTAACAACACGTGTTTTAACAACACTGTTTTGACTTTCAC 32017

Qy    361 AGGTAACGGGAACTTCTATTGTTCCAAACGGTCGATGCAGGGACTGTAGCAGGGGCTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  32018 AGGTAACGGGAACTTCTATTGTTCCAAACGGTCGATGCAGGGACTGTAGCAGGGGCTGC 32077

Qy    421 TGTTAACAGCAGCGTGGTAGATAAATCACCACGTTTATAGGTTTCTCGCTATCTTT 480
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Db  32078 TGTTAACAGCAGCGTGGTAGATAAATCACCACGTTTATAGGTTTCTCGCTATCTTT 32137

Qy    481 TATTGCGTCTCCTGGAAGTTGATAACTACCACCGGCAAAGGAGCCGTTAGCTGCTCTACGGG 540
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Db  32138 TATTGCGTCTCCTGGAAGTTGATAACTACCACCGGCAAAGGAGCCGTTAGCTGCTCTACGGG 32197

Qy    541 TAGCTTGAGTTGACAAAAAATGTCAGTTGCTCTTCAGCAAAAACTTTCAACGGATAA 600
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db  32198 TAGCTTGAGTTGAC-AAAAATGTCAGTTGCTCTTCAGCAAAAACTTTCAACGGATAA 32256

Qy    601 TGGCGGTGCTATCACCGCAAAAACTCTTTCATTAACAGGGACTACAATGTCAGCTCTGTT 660
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Db  32257 TGGCGGTGCTATCACCGCAAAAACTCTTTCATTAACAGGGACTACAATGTCAGCTCTGTT 32316

Qy    661 TTCTGAAAATACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTACCAT 720
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Db  32317 TTCTGAAAATACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTACCAT 32376

Qy    721 TACTGGAAACCAAGGGAAGTCTCTTTTTCTGACAATACTTCTTCGGATTCTCGGAGCTGC 780
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Db  32377 TACTGGAAACCAAGGGAAGTCTCTTTTTCTGACAATACTTCTTCGGATTCTCGGAGCTGC 32436

Qy    781 AATTTTTACAGAAGCCCTCGGTGACTATTCTAATAATGCTAAAGTTCCTTTATTGACAA 840
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Db  32437 AATTTTTACAGAAGCCCTCGGTGACTATTCTAATAATGCTAAAGTTTCCTTTATTGACAA 32496

Qy    841 TAAGGTCACAGGAGCGGAGCTCCTCAACAACGGGGATATGTCAGGAGGTGCTATCGTGTGC 900
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Db  32497 TAAGGTCACAGGAGCGGAGCTCCTCAACAACGGGGATATGTCAGGAGGTGCTATCGTGTGC 32556

Qy    901 TTATAAAACTAGTACAGATACTAAGGTCACCCTCACTGAAATCAGATGTTACTCTTCAG 960
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Db  32557 TTATAAAACTAGTACAGATACTAAGGTCACCCTCACTGAAATCAGATGTTACTCTTCAG 32616

Qy    961 CAACAATACATCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTGAACTGGCTTC 1020
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Db  32617 CAACAATACATCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTGAACTGGCTTC 32676

Qy   1021 CGGAGGAGACTTACCCTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCTAAAGGTGG 1080
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Db  32677 CGGAGGAGACTTACCCTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCTAAAGGTGG 32736

Qy   1081 AGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGT 1140
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Db  32737 AGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGT 32796

Qy   1141 CTTTTTAGGGAATACAGTCACTTCTACTACTCCTGGGACAGAATAGAAGTAGTATCGACTT 1200
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Db  32797 CTTTTTAGGGAATACAGTCACTTCTACTACTCCTGGGACAGAATAGAAGTAGTATCGACTT 32856

Qy   1201 AGGAACGAGTGCAAAGATGACAGCTTTGCCGTTCTGGTTCTGCGTGCTGGTAGAGCCATCATCTACTTCTA 1260
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Db  32857 AGGAACGAGTGCAAAGATGACAGCTTTGCCGTTCTGGTTCTGCGTGCTGGTAGAGCCATCATCTACTTCTA 32916

Qy   1261 TGATCCCATAACTACAGGAGATCATCCAACACAGTACAGCTACTACAGTTAATGAGAC 1320
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Db  32917 TGATCCCATAACTACAGGAGATCATCCAACACAGTACAGCTACTACAGTTAATGAGAC 32976

Qy   1321 TCCGCAGAATTCTGCCACTACCAATATACAGGAACATCATCTTCACGGAGAAAGTTATC 1380
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Db  32977 TCCGCAGAATTCTGCCACTACCAATATACAGGAACATCATCTTCACGGAGAAAGTTATC 33036

Qy   1381 AGAGACAGGAGGCCGCGAGATTCTAAAAATCTTAAAAAATCTTGAGCTACTACAGCCTGTAACTCT 1440
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Qy   1441 TTCAGGAGTGTACTTCTTATCTTATCTTTAAAAACACTGAGTGAGACTCTGCGACTCTGCGAGCATTCAGGACTCACTCA 1500
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Db  33097 TTCAGGAGTACTTCTTATCTTTTAAAAACACTGAGTGAGACTCTGCGACTCTGCGAGCATTCAGGACTCACTCA 33156

Qy   1501 ACAGGCAGATTCTGTCTGAAATGGACGGTAGGAACTACTCTAGAACCTGCTGATACTAG 1560
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Db  33157  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1561  CACCATAAACAATTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGAAGGCAAAAAT   1620
Db  33217  CACCATAAACAATTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGAAGGCAAAAAT  33276

Qy   1621  AGAAACCAAAGCTACGTCAAAAAATCTGACTTATCTGGAACCATCACTTTATTGGACCC   1680
Db  33277  AGAAACCAAAGCTACGTCAAAAAATCTGACTTATCTGGAACCATCACTTTATTGGACCC  33336

Qy   1681  GACGGGCACGTTTTATGAAAAATCATAGTTTAAGAAATCCTCAGTCCTACACATCTTAGA   1740
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Qy   1741  GCTCAAAGCTTCTGGAACTGTAACAAGCACCGCAGTGACTCCAGATCCTATAATGGGTGA   1800
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Qy   1801  GAAATTCCATTACGGCTATCAGGGAACTTGGGGCCCCAATTGTTTGGGGACAGGGGCTTC   1860
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Qy   1861  TACGACTGCAACCTTCAACTGGACTAAAACTGGCTATATTCCTAATCCCGAGCGTATCGG   1920
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Qy   1921  CTCTTTAGTCCCTAATAGCTTATGGAATGCATTTATAGATATTAGAGATATTCCCATTATCT   1980
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Qy   1981  TATGGAGACTGCAAACGAAGGGTTGCAGGGAGACCGTGCTTTTTGGTGTGTCTGGATTATC   2040
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Qy   2041  TAACTTCTTCCATAGGAGATAGTACAAAAAACACGACGCGGGTTCGCATTTGAGTGGCGG   2100
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Qy   2101  TTATGTCATAGGAGGAAAACTACATACTTGTTCAGATAAGATTCTTAGTGCTGTCATTTTG   2160
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Qy   2161  TCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAATC-AAGTACAGTCTACG   2219
Db  33817  TCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAATCAAAGGTACAGTCTACG  33876

Qy   2220  GAGGAACTCTCTATTACCAGCACACAACGAAACCTATATCTTCCTTCCTTGCAAACTACGGC   2279
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Qy   2280  CTTGTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCCTTTTCAGGAAAACCTTAGCT   2339
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Qy   2340  ACACCCCATACGGATAACGATCTGAAAACCAAGTATACAACACATATCCTACTGTTAAAGGAA   2399
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Qy   2400  GCTCGGGGAATGATAGTTCGCTTTAGAATTGATGTGGAAGAGCTCCGATTTGCTTAGATG   2459
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Qy   2460  AAAGTGCTCTATTTGAGCAGTACATGCCCCTTCATGAAATTGCAGTTTGTCTATGCACATC   2519
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Qy   2880  AATTCTAATGCGTTAGCTTTGGTAAAGAAGTCCATACATCGAAGGGAAAAGAGCTTTTAA   2939
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Qy   2940  GATTTCTTGAAGGCTCTTTTCGATTTCGATTTCCATTTTAGTGTTTTGCTAAAACACTTT   2999
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Qy   3000  C 3000
Db  34657  C 34657
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RESULT 6

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ACCESSION   A81835
VERSION     A81835.1  GI:6731868
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2787)
  AUTHORS   Madsen,A. and Birkelund,S.
  TITLE     NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA PNEUMONIAE
  JOURNAL   Patent: WO 9858953-A 9 30-DEC-1998;
            MADSEN ANNA SOFIE (DK); BIRKELUND SVEND (DK)
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Matches 2780;  Conservative    0;  Mismatches    0;  Indels    7;  Gaps    0;
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RESULT 7

AX349497

LOCUS   AX349497   2241 bp   DNA   linear   PAT   06-FEB-2002

DEFINITION Sequence 20 from Patent WO0202606.

ACCESSION   AX349497

VERSION   AX349497.1   GI:18615355

KEYWORDS   .

SOURCE   Chlamydophila pneumoniae

  ORGANISM Chlamydophila pneumoniae

            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.

REFERENCE   1

  AUTHORS   Ratti,G. and Grandi,G.

  TITLE   Immunisation against Chlamydia pneumoniae

  JOURNAL   Patent: WO 0202606-A 20 10-JAN-2002;

            Chiron S.p.A. (IT)

FEATURES   Location/Qualifiers

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ORIGIN

Query Match   74.7%; Score 2241; DB 6; Length 2241;

Best Local Similarity 100.0%;

Matches 2241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AUTHORS   Read,T.D., Myers,G.S., Brunham,R.C., Nelson,W.C., Paulsen,I.T.,
          Heidelberg,J., Holtzapple,E., Khouri,H., Federova,N.B., Carty,H.A.,
          Umayam,L.A., Haft,D.H., Peterson,J., Beanan,M.J., White,O.,
          Salzberg,S.L., Hsia,R.C., McClarty,G., Rank,R.G., Bavoil,P.M. and
          Fraser,C.M.
TITLE     Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC):
          examining the role of niche-specific genes in the evolution of the
          Chlamydiaceae
JOURNAL   Nucleic Acids Res. 31 (8), 2134-2147 (2003)
MEDLINE   22569155
PUBMED    12682364
REFERENCE 2  (bases 1 to 300512)
AUTHORS   Read,T., Myers,G., Brunham,R., Nelson,W., Paulsen,I.,
          Heidelberg,J., Holtzapple,E., Khouri,H., Federova,N., Carty,H.,
          Umayam,L., Haft,D., McClarty,G., Rank,R., Bavoil,P. and Fraser,C.
TITLE     Direct Submission
JOURNAL   Submitted (29-OCT-2002) The Institute for Genomic Research, 9712
          Medical Center Dr, Rockville, MD 20850, USA
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Qy    611 ATCACCGCAAAAACTCTTCATTAACAGGGACTACAATGTCAGCTCTGTTTCTGAAAAT 670
Db  24107 ATTTCTTGCAAAGCTTTTTCTCAACGGCTCGAGCAGCGGAAATTAGCTTCACCACCAAC 24048

Qy    671 ACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTACCATTACTGGAAAC 730
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Db  23987 CAAGGAAAAGTCATATATTTCTGGAAATACTGCCGTGAATTCTGGAGGAGCAGTATATGCA 23928

Qy    791 GAAGCCTGGTGACTATTTCTAATAATGCTAAAGTTCCTTTATTGACAATAAGTCACA 850
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Qy    851 GGAGCCGAGCTCTCAACAACGGGGGATATGTCAGGAGGTGCTATCTGTGCTTATAAAACT 910
Db  23867 GG--------AACAACAGATGCTTGGGCCGTATCATTCGCGGGCTATCATCAGCAACAAACA 23823

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Qy    971 TCGACAACAGCGGGGAGGAGCTATCTATGTGAAACTGGCTTCCGGAGGACTT 1030
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Qy   1208 AGTGCAAAGATGACACAGCTTTGCGTTCTGCTGGTAGCCAATCTACTTCTATGATCCC 1267
Db  23525 GGCTCTTCTAATTTTGATTGATGCAGTAGACAAAGCTCTCGGAAAAACTCCAGAGAGAC 23466

Qy   1268 ATAACTACGGATCATCCACAACAGTTACAGTCTTACAGATGTCTTAAAAGTTAATGAGACTCCGGCA 1327
Db  23465 AATGGGAAATTCGTAAATTTACGCGCGGCTTCTGGAAACACTCTTACCTTTTACGATCCT 23418

Qy   1328 GATTCTGCACTACAATATACAGGGGAACTCATCTTCACCAGGAGAAAAGTATCAGAGACA 1387
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Qy   1388 GAGGCCGCGCAGATTCTCAGTTCATCAGTTCTTACTTCGAACTCCTGTAACTCTTTCAGGA 1447
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Qy   1448 GGTACTCTATCTTTAAAACATGGACTCTGCAGACTTCAGGCATTCAACAGCAGCA 1507
Db  23297 GGAGAGCTTATCTTAAGAACGGTGTGGAAGTACTCT---AGAACCTGCAAAAGCTAGCACG 23238

Qy   1508 GATTCTCGTCTCGAAATGTTTGATTTTGATTGATGCGGAATACTTCTGATTTTCGTCAGC 1564
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Qy   1565 ATAAACAATTTGGTCATTAACATCAGTTCTATAGAGCGGTGCAAAGAAGGCAAAAATAGAA 1624
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Db  21977  CTTGCTAGACAAGCTTTCATATAATTCGTGCTGGCCACCATTATTGCCGTAACATCTGGATTT  21918
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Qy   2804  GAAGCCTTTAGCCAATTTCTTTGAATTGCGTGGGTCATCTCGCGAATTACAATGTAGAC     2863

Db  21917  GAGATGTTCAGTCAGTTGGTTCGAATTACGAAGCTCTTCAAGAGAATTACAACGTAGAT  21858
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Qy   2864  TTAGGAGCAAAATACCAATTCTAA  2887
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Db  21857  CTTGGAGCTAAGGTCTCTTTCTAA  21834

RESULT 9
AX662119
LOCUS       AX662119          2781 bp    DNA       linear   PAT 22-MAR-2003
DEFINITION  Sequence 56 from Patent WO02053588.
ACCESSION   AX662119
VERSION     AX662119.1  GI:29163057
KEYWORDS
SOURCE      Chlamydophila psittaci
  ORGANISM  Chlamydophila psittaci
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
REFERENCE   1
  AUTHORS   Johnston,S.A., Stemke-Hale,K., Sykes,K.F. and Kaltenboeck,B.
  TITLE     Methods and compositions for vaccination comprising nucleic acid
            and/or polypeptide sequences of chlamydia psittaci
  JOURNAL   Patent: WO 02053588-A 56 11-JUL-2002;
            BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
FEATURES             Location/Qualifiers
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                     /organism="Chlamydophila psittaci"
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BASE COUNT      818 a    555 c    610 g    798 t
ORIGIN

Query Match        18.2%;  Score 546.6;  DB 6;  Length 2781;
Best Local Similarity   53.7%;  Pred. No. 3.8e-117;
Matches 1390;  Conservative  0;  Mismatches 1134;  Indels  63;  Gaps  10;
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Qy   328  TTTTAACAACTAAGGGCGATTTCACTTTCACAGTAAGGGAACTCTCTATTGTTCCA   387
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Db   231  TTTTGTTCAGATCGCAGACACACCTAACTTTCAAAGGGAACAACACCATAGCTTATCCATAAC   290

Qy   388  AACGGTGGATGCAGGGAGCTGCGTCTGAGCAGGGGCTGCGTGTTAACGCAGCGTGTGGTAGATAAATC   447
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Db   291  GAACCGCGAATGCCGGAGCTAATCC---TGCCGGAATTAACGTTAACACTGCCGATAAGAT   347

Qy   448  TACCACGTTTATAGGGTTTTCTTCGCTATCTTTATTGCGTCTCCTGGAAGTTCGATAAC   507
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Db   348  TCTTACGCTGACAGATTTTTCTGACTTTTCCTAAGTTGAGCTTTAAGGAATGGCTTTAAGGAATG   407

Qy   508  TACCGGCAAAGGAGCCGTTAGCTGCTCTACGGGTAGCTTGAGTTTTGACAAAAAATGTCAG   567
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Db   408  TACTGGAAAAGGGGGC---TATGAAATCCGGAGGAGCATTAGGCGGAATAATGCCAC   464

Qy   568  TTTGCTTCCTCAGCAAAAACTTTCAACGGATAATGGCGGTGCTATCACCGCAAAAACTCT   627
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Db   465  TATTCTGTTTGATCAGAACTATTCCGCTCGAGCAAATGGTGAGCCATCTCTTGCAAAGCTTT   524

Qy   628  CGGAGCCATTCAGATGTCCGATGCCCTTACCATTACTGCGAAACCTCCTCAAAGAAAGG   687
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Db   525  TGGAGCGATTCGTGCTCACGGGAATACGTCATCTTTCGGACAACCAATCAGCACAATCGAGAT   584

Qy   688  CGGAGCCATTCAGATGTCCGATGCCCTTACCATTACTGCGAAACCAAGGGGAAGTCTTTT   747
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Db   585  TGGAGCGATTCGTGCTCACGGGAATAGCTCATCTTTCGGACAACAAGGCACAATCGAT   644

Qy   748  TTCTGACAATACTTCTTCGGATTCTGGAAGTTCGCAATTTTTACAGAAGCCTCGGTGACTAT   807
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LOCUS   AX666191   2781 bp   DNA   linear   PAT 26-MAR-2003
DEFINITION   Sequence 56 from Patent WO0247718.
ACCESSION   AX666191
VERSION   AX666191.1 GI:29290994
KEYWORDS   .
SOURCE   Chlamydophila psittaci
  ORGANISM   Chlamydophila psittaci
              Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
REFERENCE   1
  AUTHORS   Johnston,S.A.
  TITLE   Methods and compositions for vaccination comprising nucleic acid
              ad/or polypeptide sequences of i(chlamydia)
  JOURNAL   Patent: WO 0247718-A 56 20-JUN-2002;
              BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
FEATURES   Location/Qualifiers
     source   1..2781
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                     /mol_type="genomic DNA"
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BASE COUNT   818 a   555 c   610 g   798 t
ORIGIN

Query Match   18.2%;   Score 546.6;   DB 6;   Length 2781;
Best Local Similarity 53.7%;   Pred. No. 3.8e-117;
Matches 1390; Conservative   0; Mismatches 1134; Indels 63; Gaps 10;

Qy   328 TTTTAACACATAAGGGCGATTGACTTTCACAGGTAACGGAACTCTCTATTGTTCCA 387
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Db   231 TTTTGTTCAGACTGCAGACAACCTAACTTCAAAGGGACAACAACCATAGTTATCATAAC 290

Qy   388 AACGGTGATGCAGGAGGGACTGGTAGCAGGGGCGTCGTAACAGCAGCCGTTGGGTAGATAAATC 447
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Db   291 GAACGCGAATGCCCGAGCTAATCC---TGCGGGAATTAACGTTAACACTGCCGATAAGAT 347

Qy   448 TACCACGTTTATAGGGTTTCTTCGCTATCTTTATTGCGTCTCCTGGAAGTTCGATAAC 507
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Qy   508 TACCGGCAAAGGAGCCGTTAGCTGCTCTACGGGTAGCTTGAGTTTGACAAAAAATGTCAG 567
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Db   408 TACTGGAAAAGGGGC---TATGAAATCCCGAGCAAAGGCATTAAACTTAGCGAATAATGCCAG 464

Qy   568 TTTGCTCTTCAGCGAAAACTTTTCAACGGTATTCCGCTGCTATCACGCGAAAAACTCT 627
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Qy   628 TTCATTAACAGGGACTACAATGTCAGCTCGTTTCTGAAAATACCTCCTCAAAGAAAGG 687
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Db   525 TTCTCTAACCGGCTGCGAGCAAAGAAATCAGCTTCACCCACTAACTGGAAAAAAAGG 584

Qy   688 CGGAGCCATTCAGACTTCCGATGCCCTTACCATTACTGAAAACCAAGGGGAAGTTCTCTTT 747
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Db   585 TGGAGCGGATTTGCTCTGCTCTACGGGAATAGCTCATCTTTCGGACAACCAAGGCACAATCAGATT 644

Qy   748 TTCTGACAATATCTTCTTGGAGATTCTCGAGCTGCAATTTTACGAGAAGCTCGCTGGGTGACATAT 807
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Db   645 TTCTGGGACAACTGCTGTGAAT-TCTGGGGAGCAGTTATTATCAGAAAGCTTCATGCTGACGAT 704

Qy   808 TTCTAATAATGCTAAAGTTCCTTTATTGACAATAAGTCACAGGAGCCAGCTCCTCAAC 867
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Db   705 TGCAGGTAACAACCACCGTGCTTAGCTAACCTCTGGTGTTTTAGCAACAACAGGTTCCGGTTCATCT------ 756

Qy   868 AACGGGGGATATGTCAGGAGGTGCTATCTGTGTTATAAAACTAGTACAGATACTAAGGT 927
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Db   757 ------GATGGTTGCGGTGGA-CATCATATATTGATTTTTGAGGAAAATACTTCTTCAGCAAAAGCAGGTCGC 809

Qy   928 CACCCTCACTGGAAATCAGATTGACTGCTTCCGGAGGACTTCCGTGGCTTCCTACCCTAT 987
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Db   810 TACTATAAGGAGTAACAAAGTCTTGATTTTGATTTTTGAGGAAAATACTTCTTCAGCAAAAGGTCG 869

Qy   988 AGCTATCTATGTGAAAAAGCTGAACTGGCTTCCGGAGGACTTACCCTATTCAGTAGAAA 1047
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Db   870 AGCGATTTACCACCGATAAACTCATATTGACTTCTGGTGGCGTCTGGGGCCTACGCGGCATTTATCAATAA 929

Db   1755 AATCTTTACCTGGAATAAACAAGGATATGTTCCAAATCCTGAACGTCGTGCTCCGCTAGT 1814
Qy   1930 CCCTAATAGCTTATGGAATGCATTTATAGATATTAGCTCTCCCATTATCTTATGGAGAC 1989
Db   1815 ACTCAAATAGCCCTTGGGGATCCTTTATAGATTTACGTCTCATTCAAGATGTCTTGGAACG 1874
Qy   1990 TGCAAACCAAGGGTGC--AGGGAGACCGGTTGC--AGGGAGACACGTCGTGGTTGTGTGGGTCTCTGGGAATTGGGAACTT 2046
Db   1875 TAGTGTTGATAGTATTCTTGAGACACGTTGTGGGTTCTCTGGGAATTGGGGAACTT 1934
Qy   2047 CTTCCATAAGGAGTAGTACAAAAACACGACGCCGGTTTCGCCATTTGAGTGGCGGTTATGT 2106
Db   1935 CTTCCATAAAGATCGGAATGCTGAAAATCGCAAATTCCGTCATATATCGGGGGATATGT 1994
Qy   2107 CATAGGAGGGAAACCTACATACTTGTTCAGATAAGATCTTCAGTGTGCTGCAGCT 2166
Db   1995 GTTAGGGAGCGATAGAGACTACTTGTAGCTAAGGATACTCCTTAGTGTGGCTTTCTCAGTT 2054
Qy   2167 CTTTGGAGAGATAGAGACTACTTGTAGCTAAGGATACAGTCTACGGAGGAAC 2226
Db   2055 ATTTGCAAAGATAAAGACTACCTTGTAAGCAAGAACGACGCCGCAAACGTCTATGCGGGTTC 2114
Qy   2227 TCTCTATTACCAGCA------CAACGAAACCTATATCTCTCTTCCTTGCAAACTACCGGCC 2280
Gap ||| ||| |||
Db   2115 TGTATATTATCAGCATGTGAGCCAGTTTGATGATCTCCACGCGGTTATTAATGGGCCTAA 2174
Qy   2281 TTGTTCGTTGCTTTATGTCCTACACAGAGATTCCTGTTCTCTTTTCAGGAAAACCTTAGCTA 2340
Db   2175 CACGTGTTGTTCAGGGTTTCTAAAGAGATTCCTATTTTTCTTGGATGCACAAATTACCTA 2234
Qy   2341 CACCCCATACGGATAACGATCTGAAAACCAAGTAGTACAACATATCCTACTGTTAAAGGAAG 2400
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Qy   2401 CTGGGGGAATGAGTAGTTTCGCTTTAGAATTCGGTGGAAGAGCTCCGATTTGCTTAGATGA 2460
Db   2295 TTGGGGTAATGATTGATACCCTGGGCTTAACTTGTCTGACTATCTACTACTACTGCTTTTAG 2354
Qy   2461 AAGTGCTCTATTTGAGCAGTAGCATGCCCCTTCATGAAATTGCCAGTTTGTCTATGCACATCA 2520
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Qy   2521 GGAAGGTTTAAAAGAACAGGAACAGAGAGTTCGCTGGAAGTTGGAAGTAGCCGTCTTGTGAA 2580
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Qy   2581 TCTTGCCTTACCTATCGGGATCCGATTTGTGATAAGGAATCAGACTGCCAAGATGCAACGTA 2640
Db   2475 CGTTTCTGTACCTATAGGTATAAAAATTTGAGAAATTTGAGAAGCTATCTTCTCAA 2534
Qy   2641 CAATCTAACTCTTGGTATATACTGTGATCTTGTTCGTAGTGAACCCCGACTGTACGACAAAC 2700
Db   2535 TGATCTTCACTGACTGCTCGTCTACCGGTCATAATCCAAGCTGTGATGACAGG 2594
Qy   2701 ACTGCGAATTAGCGGTGATTCTTCGGAATTTGGGAAAACCTTCGCAAGGACAAGCTTT 2760
Db   2595 ATTGGCGATCAATGACGTTTCCTGGTTAACCACAGCTACGAATCTTGCTAGACAAGCTTT 2654
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Db   2655 CATAGTTGCGCCGCGGTAACCATATTTCCTTAACCTCTGGTGTCTTGAGATGTTCAGTTCAGT 2714
Qy   2821 TTCTTTTGAATTGCTGGGTCATCTCGCAATCTCGCAATCAAATGTAGACTTAGGAGCAAAATACCA 2880
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Qy   2881 ATTCTAA 2887
Db   2775 GTTCTAA 2781

RESULT 10
AX666191

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Qy  1048  TAGTGTCAATGGAGGTACAGCTCCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGA  1107
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Qy  1108  ATTGAGTTATCCGCCGATAGTGGTGACAATTGTCTTTTTAGGGA---TACAGTCACTTC  1164
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Db  1047  AGACAAATGCTACAATAAAAGAAATGCCATTAACATTGAAGGCAATGGTAAATTCGTCAA  1106

Qy  1225  TTTGCGTTCTGCTGGTAGAGCCATCTACTTCTATGATCCCATAACTACAGATCATC------  1284
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Qy  1285  CACAACAGTTACAGATGTCTTAAAGTGTAATGAGACTCCCGCAGATTCTGCACTACAATA  1344
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Db  1160  ----AAGGTAAATGCTGCTGATCTTCTCTCACTTTGAATAAAGCTGAGGGTGATAAAACGTA  1214

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Db  1215  TAATGGAAGAATTATTTTTTCAGGAGAAAAAGCTCACTCGAGAACAAGCTGCTGTGTGCGGA  1274

Qy  1405  AAATCTTACTTGAAGCTACTACAGCCCTGTAACTCTTTCAGGAGTACTCTATCTTTAAA  1464
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Db  1335  CAGCCGGTGTGGAAGTAGAAGCAGTCGTGCAAAAAACCAGTCGTGCAAACAGCAGCAGGATCTTCAA  1394

Qy  1525  GGACGTAGGAACTACTCTA---GAACCTGCTGATACTAGCAGCCATAAACAAATTTGGTCAT  1581
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Qy  1582  TAACATCAGTTCTATAGACGGTGCAAAAAATAGAAAGCAAAATAGAAACCAAAGCTACGTCAA  1641
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Db  1635  GACAACAACGCGCCTAGTCATGTTGTGTTGCTTGAAAACCCACTATGGTTATCA  1694

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Db  1695  AGGAAACTGGTCGTGTCAGTTGGGTCAAAGAATAACTGATCCTAAAACACAAACAGC  1754

Qy  1870  AACCTTCAACTGGACTAAAACTGGCTATATTCCTAATCCCGAGCGTATCGGCTCTTTAGT  1929
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Db  1755  AATCTTTACCTGGAATAAAAAAACAGGATATGTTCCAAATCCTGAACGTCGTCCGCTAGT  1814

Qy  1930  CCCTAATAGCTTATGGAATGCATTTATAGATATTATAGAATCCCTCCATTATCTTATGGAGAC  1989
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Db  1815  ACTCAATAGCCTTTGGGGATCCTTTATACGTTCTTATTCAAGATGTCTTGGAACG  1874

Qy  1990  TGCAAACGAAGGGTTGC---AGGGAGACCGTGCTTTTGGTGCTGGATTATCTAACTT  2046
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Db  1875  TAGTGTTGATAGTATTCTTGAGACACGTCGTGGTTCTCTGGTTGTGTCTCTGGAATGT  1934

Qy  2047  CTTCCATAAGGATAGTATGATAGATACAAAAACACGACGCGGGTTTCGCCATTTGAGTGCGGTTATGT  2106
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Db  1935  CTTCCATAAAGATCGGAATGCTGAAAATCCGTGAAAATCCCTGATATCAGTTCGGGGATATGT  1994

Qy  2107  CATAGAGGAGGAAACCTACATACTTGTTCAGATAAGATTCTTAGTGCTGCATTTGTCAGCT  2166
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Qy  2227  TCTCTATTACCAGCA------CAACGAAACCTATATCTCTTCCTTGCAAACTACGGCC  2280
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Db  2115  TGTATATTATCAGCATGTGAGCAAGTTTGATGATCCTCACGCGTAGTTAATTTAATGGGCTAA  2174

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Db  2235  TTGCCCACCGGCCAACAACACGTCCTATACCTACTGTCTTAACTTTGCTACTAGCGGTACCTATCCCGGTATTTAG  2294

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REFERENCE   2  (bases 1 to 4926)
AUTHORS     Longbottom,D.
TITLE       Direct Submission
JOURNAL     Submitted (25-SEP-1996) Moredun Research Institute, 408 Gilmerton
            Road, Edinburgh EH17 7JH, Scotland, UK
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Matches 1390;   Conservative 0;   Mismatches 1134;   Indels 63;   Gaps 10;

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VERSION     AE002192.2  GI:8163405
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  ORGANISM  Chlamydophila pneumoniae AR39
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
REFERENCE   1  (bases 1 to 12676)
  AUTHORS   Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F.,
            White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T.,
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            Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J.,
            McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
  TITLE     Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
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  JOURNAL   Nucleic Acids Res. 28 (6), 1397-1406 (2000)
  MEDLINE   20150255
   PUBMED   10684935
REFERENCE   2  (bases 1 to 12676)
  AUTHORS   Read,T.D., Brunham,R.C., Shen,C., Gill,S.R., Heidelberg,J.F.,
            White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T.,
            Berry,K., Bass,S., Linher,K., Weidman,J., Khouri,H., Craven,B.,
            Bowman,C., Dodson,R., Gwinn,M., Nelson,W., DeBoy,R., Kolonay,J.,
            McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAR-2000) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA
COMMENT     On Jun 1, 2000 this sequence version replaced gi:7189226.
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ORIGIN

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REFERENCE 1
  AUTHORS Shirai,M., Hirakawa,H., Ouchi,K., Tabuchi,M., Kishi,F., Kimoto,M.,
           Takeuchi,A., Nishida,J., Shibata,K., Fujinaga,R., Yoneda,H.,
           Matsushima,H., Tanaka,C., Furukawa,S., Miura,K., Nakazawa,A.,
           Ishii,K., Shiba,T., Hattori,M., Kuhara,S. and Nakazawa,T.
  TITLE   Comparison of outer membrane protein genes omp and pmp in the whole
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           the United States
  JOURNAL J. Infect. Dis. 181 Suppl 3, S524-S527 (2000)
   MEDLINE 20298986
   PUBMED 10833753
REFERENCE 2
  AUTHORS Shirai,M., Hirakawa,H., Kimoto,M., Tabuchi,M., Kishi,F., Ouchi,K.,
           Shiba,T., Ishii,K., Hattori,M., Kuhara,S. and Nakazawa,T.
  TITLE   Comparison of whole genome sequences of Chlamydia pneumoniae J138
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  JOURNAL Nucleic Acids Res. 28 (12), 2311-2314 (2000)
   MEDLINE 20330349
   PUBMED 10871362
REFERENCE 3 (bases 1 to 300650)
  AUTHORS Shirai,M.
  TITLE   Direct Submission
  JOURNAL Submitted (04-JUL-2000) Mutsunori Shirai, Yamaguchi University
           School of Medicine, Department of Microbiology; 1-1-1
           Minamikogushi, Ube, Yamaguchi 755-8505, Japan

COMMENT   (E-mail:mshirai@po.cc.yamaguchi-u.ac.jp, Tel:81-836-22-2227,
           Fax:81-836-22-2415)
           On or before Sep 15, 2000 this sequence version replaced
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gene
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Best Local Similarity 53.0%;   Pred. No. 9.1e-114;
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Db    207675  TACTGAATAGACTATACTCCTGACACAGAGATATAACCTCTGCAAAACCTTGGGGATTCGG-  207617

Qy       307  CACAGCAAATCACAAAAAGCTGTTTAACACACTAAGGGCGATTTGACTTTCACAGGTAA  366
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Db    207616  --CAGCTTTAACGAAGGGTTGTTTTCTGACACTACGGGAATCTTTAAGCTTTGCCGGTAA  207559

Qy       367  CGGGAACTCTCTATTGTTCCAAACGTGGATGCAGGGACTGTAGCAGGGGCGTGCTGTTAA  426
              ||||| ||||| |||||| || | || ||| | | |||| |||| |||  || | |||||
Db    207558  GGGGTACTCACTTTCTTTTTTAAATATTAAGCTCTAGTGCTGAAGGCGCAGCACTTTCTGT  207499

Qy       427  CAGCAGCGCTGGTGTAGATAAAATCTACCACGTTTATAGGGTTTCGAGTCTAACTTTTTTATTGC  486
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Qy       487  GTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGCGGTTAGCTGCTTAGCTGCGGTAGCTT  546
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Qy       547  GAGTTTGACAAAAAATGTCAGTTTGCTTCAGCAAAAAACTTTCAACGGATAATGGCGG  606
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Qy       667  AAATA-------------CCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTAC  717
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Qy       718  CATTACTGGAAACCAAGGAGAGTCTCTTTTTCTGACAACTACTTCTTCGGATTCTGGAGC  777
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Qy       778  TGCAATTTTTACAGAAGCCTCGGTGACTATTTCTAATAAATGCTAAAGTTTCCTTTATTGA  837
              |||| |||| ||| |||| || | | |||| ||| || |||| |||| |||||  |||| |
Db    207141  AGCTATAAATAGACACAGGAAAACTGTACAATTACAGGGAATACGTCCTTCTTGTATTTTCTGA  207082

Qy       838  CAATAAGGTCACAGGAGCGAGCCTCCTCAACAACGGGGATAAGTCAGGAGGTGCTATCTG  897
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Qy       958  CAGCAACAATACATCGACAACAGCGGAGCAGAGCTATCTATGTGAAAAGCTCGAACTGGC  1017
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Qy    1018  TTCCGGAGGACT------TACCCTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCC  1071
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Db  206934  TTCCGGGGGGGGGGGTATCCCTTTTCTAACAATATAGTCCAAGAGTCCAAGCAGG      206875

Qy    1072  TAAAGGTGGAGCCATAGTCATGAAGATAGTGGGGAATTGAGTTTATCCGCGATAGTGG    1131
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Db  206874  TAATGGTGGAGCCATTCTATACTGGCTGGAGAGTGTAGTCTTTCAGCAGAAGCAGG      206815

Qy    1132  TGACATTGTCTTTTAGGGAATACAGTCACTCTACTCC---TGGGACGAATAGAAG       1188
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Db  206814  GGACATTACCTTCAATGGGATGGCCATTGTCAACTACAACCACCAAACTACGAAAGAAA   206755

Qy    1189  TAGTATCGACTTAGGAACGAGTGCAAAGATGACAGCTTGCGTTCGTCGCTGGTGTGTAGAGC 1248
            |||| || ||  |||| | || |||||||  ||  |||||| |  |              
Db  206754  TTCTATTGACATAGGATCCTACTGCAAAGATCACGAATTTACGTGCAATATCTGGGCATAG  206695

Qy    1249  CATCTACTTCATCTGATGATCCATAACTACAGGATCATCCACAACAGTTACAGATGTCTTAAA 1308
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Db  206694  CATCTTTTTTCTACGATCCGATTACTGCTAATACGGCTGCGAGAGTCTTTCTACAGATACTTTAAA 206635

Qy    1309  AGTTAATGAGACTCCGGCAGATTCTGCACTACATATATCAGGGAACATCATCTTCACAGG   1368
                                                                        
Db  206634  TCTCAATAAGGCTGATGCAGGTAATAGTACAGATTATATAGTGGTGATCGATTGTTTTTCTGG 206575

Qy    1369  AGAAAAGTTATCAGAGACAGAGGCCGCCAGATTCTAAAAATCTTAACTTCGAAGCTACTACA  1428
            ||||||  | ||| |||| |||| |                                   
Db  206574  TGAAAAGCTCTCTGAAGATGAAGCTCTGAGCAACACCTCACTTCTACGCTGAGAGCA      206515

Qy    1429  GCCTGTAACTCTTTCAGGAGTACTCTATCTTTAAAACATGAGTGACTCTGCAGACTCA     1488
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Db  206514  GCCTGTAACTCTCAAGGTAAATTTAGTACTTAAACGTGTGTCACTCTCGATACGAA      206455

Qy    1489  GGCATTCACTCAACAGGCAGATTCTCGTCTCGAAATGACGTAGGAACTACTCTAGAACC    1548
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Qy    1549  ---TGCTGATACTAGCACCATAAAACAATTGGTCATTAACAATCAGTTCTATAGACGGTGC  1605
                                                                        
Db  206394  AGTGACAGAGGAGGTCACTTTAACAGGTCTTTCCGTAGACTCTTTAGGCGGAGGG        206335

Qy    1606  AAAGAAGGCAAAAATAGAAAACCAAAGTCACGTCAAAAAATCTGACTTTATCTGGAACCAT  1665
                                                                        
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Qy    1666  CACTTTATTGGGACCCGACGGGCAAGTTTTATGAAGAAATCATAGTTTAAGAAATCCTCAGTC 1725
                                                                        
Db  206274  TCTTCTTTGGATAACCAAAGGGAATGCTTATGGAAAATTACACGACTTAGGAAAAAACTTCAAGA 206215

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Db  206214  CTTTTCATTGTGCAGCTCTCGTGCTCTGGGTATGCCACAACTACAGATGTTCCAGCGGT    206155

Qy    1786  TCCTATAATGGGTGAGAAATTCCATTACGGCTATCCAGGGGAACTTGGGGCCCAATTGTTTG 1845
            |||||  | |                                                   
Db  206154  TCCTACAGTAGCAACTCCTACGCACTATGGGTATCAAGGGTACTTGGGGAATGACTTGGGT   206095

Qy    1846  GG--------GGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAAAACTGG       1893
            ||                                                          
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Qy    1894  CTATATTCCTAATCCCGAGCGTATCGGCTCTTGGTCTTCCTAATAGCTTATGGAATGCATT  1953
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Qy    1954  TATAGATATTAGCTCCTCTCCATTATCTTCATTGGAGACTGCAAACGAAGGGGTTGCAGGGAGA 2013
                                                                        
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Qy    2014  CCGTGCTTTTTGGTGTGCTGATTATCCATCCTTCCTCCATAAGGATGAGTAAAGAGATAAGAAGGGGAAAA 2073
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Db  205914  TCGAGCGCTTCTGGGCTGCGGGAGTGCCGGGAGTCGCCCAATTTCTTAGAGATAAAGATAAAGAAGGGGAAAA 205855
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Qy    2134  AGATAAGATTCTTAGTGCTGCATTTGTCAGCTCTTGGAAGAGATAGAGACTACTTTGT     2193
            |||| | |||| |||  ||  |||  |||| ||  |||  || || |||  |||  ||   
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Qy    2194  AGTTAAGAATCAAGGTACAGTCTACGGAGGAACTCTCTATTACCCAGCACAACGAAAACCTA  2253
                                                                        
Db  205734  CGCTAAAAATCATACTGATAGCCTATGCCAGGAGCCTTCTATATCTCTATATCAACACATTACAGAATG 205675

Qy    2254  TATCTCCTTCCTCCTTGCAAACTACGGCCCTTGTTCGTTCGTTCGTTGTCTATGTTCCTACAGAGATTCC 2313
                                                                        
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Qy    2314  TGTTCTCTTTCAGGAAACCTTAGCTACCACCATAACGATAACGATCTGAAAACCAAGTA     2373
                                                                        
Db  205617  CCTCGTTTTAGAGGGCAGCTCGCTTATAGCCAGTCACGTCAGTAGTAATGATCTGAAGACAAAGTA 205558

Qy    2374  TACAACATATCTACTGTTAAAGGAAGCTGGGGAGTGAATGATAGTTTCGCTTTAGAATTCGG  2433
                                                                        
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Qy    2434  TGGAAGAGCTCCGATTTGCTTAGATGAAAGTGCTCATTGCTCTAGTAAAAATCCTGAAATCCTGAATACCTTCAT 2493
                                                                        
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Qy    2494  GAAATTGCAGTTTGTCTATGCACATCAGGGAGAGGTTTTAAAGAACAGGGAACAGAAGCTCG  2553
                                                                        
Db  205437  CAAACTGAATCTGACTATATACGTCGAGGAAGCGAGGAAAAGTACAGAAGGAAG          205378

Qy    2554  TGAATTTGGAAGTAGCCGTCTTGTGATCTTGCCTTACCTATCGGATCCGATTTGATAA     2613
                                                                        
Db  205377  ATCTTTTTGATGACAGCAACCTCTTCAATTTATCTTTGCTATAGGGGTGAAGTTTGAGAA   205318

Qy    2614  GGAATCAGACTGCCAAGATGCAACGTACAAATCAATCTAACTCTTGGTTATACTGTGGAATCTTGT 2673
                                                                        
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Qy    2734  CGGTACGAATTTGGCAAGACAAGCTTTAGTCCTTCGTGCAGGAACCATTTTTGCTTAA     2793
                                                                        
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Qy    2794  CTCAAATTTGAAGCTTAGACGCTTGTGCTTTGAATGGCTGGGTCATCTCGCAATTA       2853
                                                                        
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DEFINITION  Chlamydia pneumoniae section 44 of 103 of the complete genome.
ACCESSION   AE001628 AE001363
VERSION     AE001628.1  GI:4376730
KEYWORDS    .
SOURCE      Chlamydophila pneumoniae CWL029
  ORGANISM  Chlamydophila pneumoniae CWL029
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REFERENCE   1 (bases 1 to 10757)
  AUTHORS   Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Hyman,R.W.,
            Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S.
  TITLE     Comparative genomes of Chlamydia pneumoniae and C. trachomatis
  JOURNAL   Nat. Genet. 21 (4), 385-389 (1999)
  MEDLINE   99206606
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PUBMED   10192388
REFERENCE   2 (bases 1 to 10757)
AUTHORS   Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Olinger,L.,
            Grimwood,J., Davis,R.W. and Stephens,R.S.
TITLE   Direct Submission
JOURNAL   Submitted (01-DEC-1998) Program in Infectious Diseases, University
            of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA
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BASE COUNT   3228 a   2459 c   2065 g   3005 t
ORIGIN

Query Match   17.7%; Score 531.2; DB 1; Length 10757;
Best Local Similarity   53.0%; Pred. No. 1.5e-113;
Matches 1415; Conservative   0; Mismatches 1183; Indels 74; Gaps   10;

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Qy  1133  GACATTGTCTTTTTAGGGAATACCAGTCACTTCTACTACTCC---TGGGACGGAATAGAAGT  1189
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Qy  1190  AGTATCGACTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTCGTGATAGGCC  1249
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Db  6574  TCTATTGACATAGGATCTCACTTGAGAGATCACGAAGTTCAACGGATTCAATATCTGGCATAGC  6515

Qy  1250  ATCTACTTCTATGATCCCATAACTACAGGAGTCCAATATCTCCACAAACAGTTACGACAGTGTCTTAAAAA  1309
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Qy  1310  GTTAATGAGACTTCCGGCACAGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAGGA  1369
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Db  6454  CTCAATAAGGCTGATGCAGTGACAGAGCTCTGAAGTGAAGGTGTTGCAGAAAATCTTAGCCTTGGA  6395

Qy  1370  GAAAAGTTATCAGAACAGAGAGCCGCAGAGTTCTAAAAATCTTAACTTCGAAGCTACTACAG  1429
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Qy  1430  CCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAACATGAGAGTGACTCTGCAGACTCAG  1489
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Qy  1490  GCATTCACTCACCAACAGGAGCAGATTCGTCGTCAAAAATGGACTAGGAACTACTCTAGACC-  1548
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Qy  1549  --TGCTGATATAGTAGCACCATAAACAATTTGGTCATTAACACATCAGTTCTATTACACGCGGTGCA  1606
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Qy  1667  ACTTTATTGGACCCGACGGGCACGTTTATGAAAATCATAGTTTAAGAAAATCCAGTCC  1726
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Qy  1847  G------GGACAGGGGCTTCACGACTGCAACCTCACTGGACTAAAACTGGC  1894
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Qy  2435  GGAAGAGCTCCGATTTGCTTAGATGAAAGTGCTCTATTTGAAGTACATGCCCTTCATG  2494
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KEYWORDS    .
SOURCE      unidentified
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            unclassified.
REFERENCE   1  (bases 1 to 2815)
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AUTHORS    Madsen,A. and Birkelund,S.
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JOURNAL    Patent: WO 9858953-A 3 30-DEC-1998;
           MADSEN ANNA SOFIE (DK); BIRKELUND SVEND (DK)
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                /db_xref="taxon:3264"
BASE COUNT       790 a       575 c       626 g       824 t
ORIGIN

Query Match       17.7%;  Score 530.2;  DB 6;  Length 2815;
Best Local Similarity       52.9%;  Pred. No. 2.7e-113;
Matches 1415;  Conservative       0;  Mismatches 1183;  Indels       75;  Gaps       10;

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          |||||  ||| |||| || | | | |||  ||||  | || ||||   |||||| ||||
Db    156 TACTGGAATAGACTATACTCTGACAGAGATATAACCTGCAAAACCTTGGGATTCGG- 214

Qy    307 CACAGCAATCACAAAAAGCTGTTTTAACAACACTAGGGCGATTTGACTTTCACAGGTAA 366
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Db    215 --CAGCTTTAACGAAGGGTGTGTTTTTCTGACACTACGGAAATCTTTAAGCTTGCCGGTAA 272

Qy    367 CGGGAACTCTCTATTGTTCCAAACGGTGGATGCAGGGACTGTAGCAGGGTGCTCGTTAA 426
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Db    273 GGGGTACTCCACTTTCTTTTCTTTTAAAATATTAAGTCTAGTAGTGCTGAAGGCGCAGCACTTTCTGT 332

Qy    427 CAGCAGCGTGTAGATAAAATCTACCACGTTTATAGGGTTTTCTTCGCTATCTTTTATTGC 486
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Qy    487 GTCTCCTGGAAGTTCGATAACTACCCGGCAAAGGAGGAGCCCGTTAGCTGCTGCTACGGGTAGCTT 546
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Qy    898 TGCTTATAAAACTAGTACAGATACTAAGGTCACCCCACTGGAAATCAGATGTTACTCTT 957
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Qy   1489 GGCATTCACTCACAGGCAGATTCTCGTCTGCAAATGGGTTTTCTTTGCTATCTTTTATTGC 1548
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Qy   1549 ---TGCTGATACTAGACACCATAAACAATTTGGTCATTAACATCAGTTCTATACGCGTGC 1605
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          Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          December 16, 2003, 12:10:57 ; Search time 752 Seconds
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          25: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	3000	100.0	3000	AAA27021	Chlamydia pneumoni
2	2975.4	99.2	1230025	AAX91990	Nucleotide sequenc
3	2775.8	92.5	2787	AAX06820	Chlamydia pneumoni
4	2241	74.7	2241	ABL91193	Chlamydia pneumoni
5	546.6	18.2	2781	ABQ84775	Chlamydia psittaci
6	546.6	18.2	2781	ABQ78033	Chlamydia polynucl
7	546.6	18.2	2781	ABX99200	C. psittaci genomi
8	531.2	17.7	273254	AAC81914	Chlamydia pneumoni

No.	Score	%	Length	Pred	DB ID	Description
9	530.2	17.7	2815	20	AAX06817	Chlamydia pneumoni
10	527	17.6	2787	24	ABL91231	Chlamydia pneumoni
11	524.6	17.5	2957	21	AAZ61509	DNA encoding the C
12	523	17.4	534	21	ABL91192	Chlamydia pneumoni
13	522.2	17.4	2757	20	AAX06821	Chlamydia pneumoni
14	518.2	17.3	2950	21	AAA30851	Chlamydia antigen
15	516.6	17.2	2787	24	ABL91200	Chlamydia pneumoni
16	516.6	17.2	273254	21	AAC81914	Chlamydia pneumoni (c)
17	515.2	17.2	2784	21	AAA30852	Chlamydia antigen
18	515	17.1	2787	20	AAX06822	Chlamydia pneumoni
19	514	17.1	2793	20	AAX06823	Chlamydia pneumoni
20	514	17.1	3000	24	ABL91206	Chlamydia pneumoni
21	513.6	17.1	3000	21	AAA30853	Chlamydia antigen
22	512.6	17.1	2950	21	AAA30849	Chlamydia antigen (c)
23	509.8	17.0	1230025	20	AAX91990	Nucleotide sequenc
24	506.6	16.9	3050	21	AAA48838	Chlamydia pneumoni
25	506	16.9	3000	20	AAX06828	Chlamydia pneumoni
26	503.6	16.8	2811	24	ABL91260	Chlamydia pneumoni
27	491.8	16.4	2790	21	AAA30854	Chlamydia antigen
28	477	15.9	2808	21	AAA48839	Chlamydia antigen
29	469.4	15.6	2784	24	AAA30850	Chlamydia antigen
30	465.8	15.5	2787	24	ABL91241	Chlamydia pneumoni
31	465.8	15.5	2950	21	AAA30847	Chlamydia antigen
32	465.8	15.5	3200	20	AAX06816	Chlamydia pneumoni
33	435.8	14.5	2784	21	AAA30848	Chlamydia antigen
34	389	13.0	3050	21	AAZ61508	DNA encoding the C
35	378.4	12.6	2838	20	AAX06827	Chlamydia pneumoni
36	348.8	11.6	2750	21	AAA28690	C. pneumoniae CPN1
37	348.4	11.6	2520	24	ABQ84758	Chlamydia psittaci
38	348.4	11.6	2520	25	ABQ78016	Chlamydia polynucl
39	348.4	11.6	2520	25	ABX99183	C. psittaci genomi
40	345	11.5	2526	21	AAA28691	C. pneumoniae CPNI
41	345	11.5	2526	24	ABL91253	Chlamydia pneumoni
42	340.2	11.3	2526	20	AAX06819	Chlamydia pneumoni
43	289	9.6	1065	24	ABL91191	Chlamydia pneumoni
44	284	9.5	1188	24	ABL91194	Chlamydia pneumoni
45	273.2	9.1	3052	20	AAX06818	Chlamydia pneumoni

ALIGNMENTS

```
RESULT 1
AAA27021
ID   AAA27021 standard; DNA; 3000 BP.
XX
AC   AAA27021;
XX
DT   11-AUG-2000  (first entry)
XX
DE   Chlamydia pneumoniae 98kD putative outer membrane protein gene.
XX
KW   Chlamydia; antigen; vaccine; infection; outer membrane protein; ds.
XX
OS   Chlamydia pneumoniae.
XX
FH   Key          Location/Qualifiers
FT   CDS          101..2887
FT                /*tag= a
FT                /product= "98kDa putative outer membrane protein"
XX
PN   WO20026237-A2.
XX
PD   11-MAY-2000.
XX
PF   29-OCT-1999;  99WO-GB03579.
XX
PR   29-OCT-1998;  98US-0106070.
PR   01-MAR-1999;  99US-0122066.
PR   27-OCT-1999;  99US-0428122.
XX
PA   (CONN-) CONNAUGHT LAB LTD.
XX
```

PI Murdin AD, Oomen RP, Dunn PL;
XX
DR WPI; 2000-365569/31.
DR P-PSDB; AAY94327.
XX
PT Novel Chlamydia 98 kDa putative outer membrane protein antigen, used
PT for vaccination and protection against Chlamydia infection -
XX
PS Claim 1; Fig 1; 93pp; English.
XX
CC The present sequence is the 98kDa putative outer membrane protein gene
CC from Chlamydia pneumoniae. The genomic sequence was amplified using two
CC PCR primers. The 5' primer contains a NotI restriction site, a ribosome
CC binding site, an initiation codon and a sequence close to the 5' end of
CC the 98kDa putative outer membrane protein coding sequence. The 3' primer
CC contains the sequence encoding the C-terminal sequence of the putative
CC outer membrane protein and a BsrGl restriction site. The stop codon was
CC excluded and an additional nucleotide was inserted to obtain an in-frame
CC C-terminal fusion with the Histidine tag. The PCR product was cloned
CC into a eukaryotic expression vector (pCA-Myc-His) by restricting both
CC the vector and the PCR product with NotI and BamHi and performing a
CC ligation reaction. This expression vector was injected intramuscularly
CC and intranasally into mice, which were subsequently inoculated with
CC Chlamydia pneumoniae. The chlamydial lung titers of the immunised mice
CC were lower than those of the controls. Thus the 98kDa putative outer
CC membrane protein can be used as a vaccine to provide protection against
CC Chlamydia infections, especially Chlamydia pneumoniae infections.
CC The polypeptide may also be administered orally to treat Chlamydia
CC infection. The present sequence may also be used in the
CC construction of attenuated Chlamydia strains that can over-express the
CC gene or express it in a non-toxic form.
XX
SQ Sequence 3000 BP; 871 A; 617 C; 634 G; 878 T; 0 other;

Query Match   100.0%;   Score 3000;   DB 21;   Length 3000;
Best Local Similarity   100.0%;   Pred. NO.0;
Matches 3000;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

```
Qy         1 CGGTCCTTACCTAGTAGAGGTTGAGTGAATTCTTGACTTGTTCTCCCTATTGGTGTATCT 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 CGGTCCTTACCTAGTAGAGGTTGAGTGAATTCTTGACTTGTTCTCCCTATTGGTGTATCT 60

Qy        61 CTTAAAATATTAAATTCAAAATCAAAGTATATATTTACAAATGAAGTCTTCTTTCCCCAA 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CTTAAAATATTAAATTCAAAATCAAAGTATATATTTACAAATGAAGTCTTCTTTCCCCAA 120

Qy       121 GTTTGTATTTTCTACATTTGCTATTTTCCCTTTGCTATGATTGCTACCGAGACAGTTTT 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GTTTGTATTTTCTACATTTGCTATTTTCCCTTTGCTATGATTGCTACCGAGACAGTTTT 180

Qy       181 GGATTCAAGTGCGGAGTTCGATGGGAATAAAAATGGTAATTTTTCAGTTCGTGAGAGTCA 240
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Db       181 GGATTCAAGTGCGGAGTTCGATGGGAATAAAAATGGTAATTTTTCAGTTCGTGAGAGTCA 240

Qy       241 GGAAGATGCTGGAACTACCTATTTAAGGGAAATGTCACTCTAGAAATATTCCTGG 300
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Db       241 GGAAGATGCTGGAACTACCTATTTAAGGGAAATGTCACTCTAGAAATATTCCTGG 300

Qy       301 AACAGGCACAGCAATACACAAAAAGCTGTTTTAACAACACTAAGGCGATTTGACTTTCAC 360
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Db       301 AACAGGCACAGCAATACACAAAAAGCTGTTTTAACAACACTAAGGCGATTTGACTTTCAC 360

Qy       361 AGTAACGGGAGAACTCATTGTTCCAAACGGTCGAGCTGCGCAGGGGCTGC 420
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Db       361 AGTAACGGGAGAACTCATTGTTCCAAACGGTCGAGCTGCGCAGGGGCTGC 420

Qy       421 TGTTAACAGCAGCGGTGGTAGATAAATCTACCACGTTTATAGGGTTTCTCGCTATCTTT 480
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Db       421 TGTTAACAGCAGCGGTGGTAGATAAATCTACCACGTTTATAGGGTTTCTCGCTATCTTT 480

Qy       481 TATTGCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGGAGCCGTTAGCTGCTCACGGG 540
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Db       481 TATTGCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGGAGCCGTTAGCTGCTCACGGG 540
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Qy       541 TAGCTTGAGTTGACAAAAAATGTCAGTTTGCTCTTCAGCAAAAAATTTTTCAACCGATAA 600
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Db       541 TAGCTTGAGTTGACAAAAAATGTCAGTTTGCTCTTCAGCAAAAAATTTTTCAACCGATAA 600

Qy       601 TGGCGGTGCTATCACCGCAAAAACTCTTTCATTAACAGGACTACAAATGTCAGTCTGTT 660
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Db       601 TGGCGGTGCTATCACCGCAAAAACTCTTTCATTAACAGGACTACAAATGTCAGTCTGTT 660

Qy       661 TTCTGAAAATACCTCCTCAAAGAAAGGAGGCGGAGCCATTCCGATGCCCTTACCAT 720
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Qy       721 TACTGGAAACCAAGGGAAGTCTCTTTTCTGACAATACTTCTCGGAGTTCTGGAGCTGC 780
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Db       721 TACTGGAAACCAAGGGAAGTCTCTTTTCTGACAATACTTCTCGGAGTTCTGGAGCTGC 780

Qy       781 AATTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTCCTTTATTGACAA 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 AATTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTCCTTTATTGACAA 840

Qy       841 TAAGGTCACAGGAGGAGCTCCTCAACACGGGGATATGTCAGGAGGTGCTATCTGTGC 900
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Db       841 TAAGGTCACAGGAGGAGCTCCTCAACACGGGGATATGTCAGGAGGTGCTATCTGTGC 900

Qy       901 TTATAAAACTAGTACAGATACTAAGGTCACCCTACTGAAATCAGATGTTACTCTTCAG 960
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Db       901 TTATAAAACTAGTACAGATACTAAGGTCACCCTACTGAAATCAGATGTTACTCTTCAG 960

Qy       961 CAACAATACATCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTC 1020
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Db       961 CAACAATACATCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTC 1020

Qy      1021 CGGAGGACTTACCCTATTCAGTAGAAATAGTGTCAATGAGGTACAGCCTCCTAAAGGTGG 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 CGGAGGACTTACCCTATTCAGTAGAAATAGTGTCAATGAGGTACAGCCTCCTAAAGGTGG 1080

Qy      1081 AGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 AGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGT 1140

Qy      1141 CTTTTTAGGGAATACAGTCACTTCTACTACTCCTGGGACGAATAGAAGTAGTATCGACTT 1200
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Db      1141 CTTTTTAGGGAATACAGTCACTTCTACTACTCCTGGGACGAATAGAAGTAGTATCGACTT 1200

Qy      1201 AGGAACGAGTGCAAAGATGACAGCTTGGCTTCTGCGTCTGCGTGGTAGAGCCATCACTTCTA 1260
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Db      1201 AGGAACGAGTGCAAAGATGACAGCTTGGCTTCTGCGTCTGCGTGGTAGAGCCATCACTTCTA 1260

Qy      1261 TGATCCCATAACTACAGATCATCCACAACAGTTACAGATGTCTTAAAGTTAATGAGAC 1320
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Qy      1321 TCCGGCAGATTCTGCACTACAACATATACAGGGAACAATCATCTTCACAGGAAAAGTTATC 1380
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Db      1321 TCCGGCAGATTCTGCACTACAACATATACAGGGAACAATCATCTTCACAGGAAAAGTTATC 1380

Qy      1381 AGAGACAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACACGCCTGTAACTCT 1440
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Db      1381 AGAGACAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACACGCCTGTAACTCT 1440

Qy      1441 TTCAGGAGTACTCTATCTTAAAACATGGAGTGACTTCTCGCAGGACTCACTCA 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 TTCAGGAGTACTCTATCTTAAAACATGGAGTGACTTCTCGCAGGACTCACTCA 1500

Qy      1501 ACAGGCAGATTCCGTCTCGAAATGACGTAGGAACTGCTACTACTAG 1560
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Db      1561 CACCATAAACAATTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGAGGCAAAAAT 1620
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Qy  1621  AGAAACCAAAGCTACGTCAAAAAATCTGACTTTATCTGGAACCATCACTTATTGGACCC  1680
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Db  1621  AGAAACCAAAGCTACGTCAAAAAATCTGACTTTATCTGGAACCATCACTTATTGGACCC  1680

Qy  1681  GACGGGCACGTTTTATGAAAATCATAGTTAAGAAATCCTCAGTCCTACGACATCTTAGA  1740
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Db  1681  GACGGGCACGTTTTATGAAAATCATAGTTAAGAAATCCTCAGTCCTACGACATCTTAGA  1740

Qy  1741  GCTCAAAGCTTCTGGAACTGTACAAGCACCGCAGTGACTCCAGATCCTATAATGGGTGA  1800
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Db  1741  GCTCAAAGCTTCTGGAACTGTACAAGCACCGCAGTGACTCCAGATCCTATAATGGGTGA  1800

Qy  1801  GAAATTCATTAGGCTATCAGGGAACTTGGGCCCAATTGTTTGGGGGACAGGGGCTTC  1860
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Db  1801  GAAATTCATTACGGCTATCAGGGAACTTGGGCCCAATTGTTTGGGGGACAGGGGCTTC  1860

Qy  1861  TACGACTGCAACCTCAACCTCAACTGGACTAAAACTGCTATATTCCTAATCCGAGCGTATCGG  1920
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Db  1861  TACGACTGCAACCTCAACCTCAACTGGACTAAAACTGCTATATTCCTAATCCGAGCGTATCGG  1920

Qy  1921  CTCTTTAGTGTCCCTAATAGCTTATGGAATGCATTTATAGAGTATTTAGAGTGCTCTCCTCCATTATCT  1980
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Db  1921  CTCTTTAGTGTCCCTAATAGCTTATGGAATGCATTTATAGAGTATTTAGAGTGCTCTCCTCCATTATCT  1980

Qy  1981  TATGGAGACTGCAAACGAAGGGTTGCAGGGAGACCGTGCTTTTGGTGTGCTGGATTATC  2040
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Db  1981  TATGGAGACTGCAAACGAAGGGTTGCAGGGAGACCGTGCTTTTGGTGTGCTGGATTATC  2040

Qy  2041  TAACTTCTTCCATAAGGATAGTACAAAAACACGACGCGGGGTTTCGCCATTTGAGTGGCGCG  2100
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Db  2041  TAACTTCTTCCATAAGGATAGTACAAAAACACGACGCGGGGTTTCGCCATTTGAGTGGCGCG  2100

Qy  2101  TTATGTCATAGGAGGAGGAACCTACACTGTTCAGATAAGATTCTTAGTGCTGCATTTG  2160
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Db  2101  TTATGTCATAGGAGGAGGAACCTACACTGTTCAGATAAGATTCTTAGTGCTGCATTTG  2160

Qy  2161  TCAGCTCTTTGGAAGAGAGTAGAGACTACTTTGTAGCTAAGAATCAAGTACAGTCTCACGG  2220
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Db  2161  TCAGCTCTTTGGAAGAGAGTAGAGACTACTTTGTAGCTAAGAATCAAGTACAGTCTCACGG  2220

Qy  2221  AGGAACTCTCTATTACCAGCACAACGAAACCTATATCTCCTTGCAAACTACGGGCC  2280
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Db  2221  AGGAACTCTCTATTACCAGCACAACGAAACCTATATCTCCTTGCAAACTACGGGCC  2280

Qy  2281  TTGTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCTCTTTTCAGGAAAACCTTAGCTA  2340
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Db  2281  TTGTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCTCTTTTCAGGAAAACCTTAGCTA  2340

Qy  2341  CACCCATACGGATAACGATCTGAAAACCAAGTATACAACATATCCTACTGTTAAAGGAAG  2400
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Db  2341  CACCCATACGGATAACGATCTGAAAACCAAGTATACAACATATCCTACTGTTAAAGGAAG  2400

Qy  2401  CTGGGGGAATGATAGTTTCGCTTTAGAATTCGGTGGAAGAGCTCCGATTTGCTTAGATGA  2460
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Db  2401  CTGGGGGAATGATAGTTTCGCTTTAGAATTCGGTGGAAGAGCTCCGATTTGCTTAGATGA  2460

Qy  2461  AAGTGCTCTATTTGAGCAGTACACAGGGAACAGGGAACTCGTGAATTGGAAGTAGCACATCA  2520
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Db  2461  AAGTGCTCTATTTGAGCAGTACACAGGGAACAGGGAACTCGTGAATTGGAAGTAGCACATCA  2520

Qy  2521  GGAAGGTTTAAAGAACAGGGAACAGGGAACTCGTGAATTTGGAAGTAGCCGTCTTGTGAA  2580
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Db  2521  GGAAGGTTTAAAGAACAGGGAACAGGGAACTCGTGAATTTGGAAGTAGCCGTCTTGTGAA  2580

Qy  2581  TCTTGCCTTACCTATCTGGGATCCGATTTGATAAGGAATCAGACTGCCAAGATGCAACGTA  2640
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Db  2581  TCTTGCCTTACCTATCTGGGATCCGATTTGATAAGGAATCAGACTGCCAAGATGCAACGTA  2640

Qy  2641  CAATCTAACTTCTTGGTTATACTTCGTTGTTCGTTACCCCGACTGTACGACGACAAC  2700
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Db  2641  CAATCTAACTTCTTGGTTATACTTCGTTGTTCGTTACCCCGACTGTACGACGACAAC  2700

Qy  2701  ACTGCGAATTAGCGGTGATTCTTGGAAAACCTTCGGTTACGAATTTGCCAAGACAAGCTTT  2760
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Db  2701  ACTGCGAATTAGCGGTGATTCTTGGAAAACCTTCGGTTACGAATTTGCCAAGACAAGCTTT  2760

Qy  2761  AGTCCTTCGTGCAGGGAACCATTTTGCTTAACTCAAATTTGAAGCCTTTAACTCAAATTTGAAGCCAATT  2820
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Db  2761  AGTCCTTCGTGCAGGGAACCATTTTGCTTAACTCAAATTTGAAGCCTTTAACTCAAATTTGAAGCCAATT  2820

Qy  2821  TTCTTTGAATTGCTGCGGTCATCTCGCAATTACAATGTAGACTTAGGAGCAAAATACCA  2880
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Db  2821  TTCTTTGAATTGCTGCGGTCATCTCGCAATTACAATGTAGACTTAGGAGCAAAATACCA  2880

Qy  2881  ATTCTAATGCGTTAGCTTTGGTAAAGAGCTCCATACATCGAAGGGAAAAGAGCTTTTAG  2940
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Db  2881  ATTCTAATGCGTTAGCTTTGGTAAAGAGCTCCATACATCGAAGGGAAAAGAGCTTTTAG  2940

Qy  2941  ATTTCTTGAAGGCTCTTTTCGATTTCGATTTCGATTTCCATTTTAGTGTTTTGCTAAAACACTTTC  3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  ATTTCTTGAAGGCTCTTTTCGATTTCGATTTCGATTTCCATTTTAGTGTTTTGCTAAAACACTTTC  3000
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RESULT 2

```
AAX91990
ID   AAX91990 standard; DNA; 1230025 BP.
XX
AC   AAX91990;
XX
DT   13-SEP-1999   (first entry)
XX
DE   Nucleotide sequence of the complete genome of Chlamydia pneumoniae.
XX
KW   Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW   sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW   vaccine; neutralising epitope; ss.
XX
OS   Chlamydia pneumoniae.
XX
PN   WO9927105-A2.
XX
PD   03-JUN-1999.
XX
PF   20-NOV-1998;   98WO-IB01890.
XX
PR   04-NOV-1998;   98US-0107078.
PR   21-NOV-1997;   97FR-0014673.
XX
PA   (GEST ) GENSET.
XX
PI   Griffais R;
XX
DR   WPI; 1999-357842/30.
XX
PT   Genome sequence of Chlamydia pneumoniae
XX
PS   Claim 1; Page 291-611; 1912pp; English.
XX
CC   The present sequence represents the complete genome of Chlamydia
CC   pneumoniae, and encodes proteins AAY34584-Y35879. C. pneumoniae causes
CC   respiratory disease such as pneumonia and bronchitis and is thought
CC   to be a contributing factor in heart disease, sarcoidosis, sinusitis,
CC   purulent otitis media, erythema nodosum or pharyngitis. The polypeptides
CC   encoded by the open reading frames of the C. pneumoniae genome (see
CC   AAY34584-Y35879) can be used in immunogenic compositions as vaccines.
CC   Vectors containing C. pneumoniae nucleotides sequences can also be
CC   used as immunogenic compositions, especially where the vector directs
CC   the expression of a neutralising epitope of C. pneumoniae.
XX
SQ   Sequence 1230025 BP; 367213 A; 249833 C; 249013 G; 363589 T; 377 other;
```

```
Query Match             99.2%;  Score 2975.4;  DB 20;  Length 1230025;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches  2998;  Conservative   0;  Mismatches   0;  Indels   1;  Gaps   2;

Qy      1  CGCTCTTCTTACCCTAGTAGAGGTTGAGTGAATTCTTCGACTTGTTCTCCTATTGGTGTATCT  60
```

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Db  31658 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 31717
          CGCTCTTACCTAGTAGAGGTTGAGTGAATTTCTTGACTTGTTCTCCCATTGGTGTATCT

Qy     61 CTTAAAATATTAAAATCAAAATCAAAATCAAAGTATATATATTTACAATGAAGTCTTCTTCCCCAA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  31718 CTTAAAATATTAAAATCAAAATCAAAGTATATATATTTACAATGAAGTCTTCTTCCCCAA 31777

Qy    121 GTTTGTATTTTCTACATTTGCTATTTTCCCTTTGTCTATGATTGCTACCGAGACAGTTTT 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  31778 GTTTGTATTTTCTACATTTGCTATTTTCCCTTTGTCTATGATTGCTACCGAGACAGTTTT 31837

Qy    181 GGATTCAAGTGCGAGTTCGATGGAATAAAAATGTAATTTTCAGTTCGTGAGAGTCA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  31838 GGAAGGATGCGAGTGCGAGTTCGATGGAATAAAAATGTAATTTTCAGTTCGTGAGAGTCA 31897

Qy    241 GGAAGATGCTGGAACTACCTACCTATTTAAGGGAAATGTCACTCTAGAAAATATTCCTGG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  31898 GGAAGATGCTGGAACTACCTACCTATTTAAGGGAAATGTCACTCTAGAAAATATTCCTGG 31957

Qy    301 AACAGGCACAGCAATCACAAAAAGCTGTTTTAACAACACTAAGGGCGATTTGACTTTCAC 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  31958 AACAGGCACAGCAATCACAAAAAGCTGTTTTAACAACACTAAGGGCGATTTGACTTTCAC 32017

Qy    361 AGGTAACGGGAACTCTCTATTGTTCCAAACGGTGATGCAGGGACTGTAGCAGGGCTGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  32018 AGGTAACGGGAACTCTCTATTGTTCCAAACGGTGATGCAGGGACTGTAGCAGGGCTGC 32077

Qy    421 TGTTAACAGCAGCGTGGTAGTATAAATCTACCACGTTTATAGGGTTTTCTTCGCTATCTTT 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  32078 TGTTAACAGCAGCGTGGTAGTATAAATCTACCACGTTTATAGGGTTTTCTTCGCTATCTTT 32137

Qy    481 TATTGCGTCTCCTGGAAGTTCGATAACTACCGGCAAAAGAGCCGTTAGCTGCTCTACGGG 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  32138 TATTGCGTCTCCTGGAAGTTCGATAACTACCGGCAAAAGAGCCGTTAGCTGCTCTACGGG 32197

Qy    541 TAGCTTGAGTTTGACAAAAAAATGTCAGTTTGCTCTTCAGCAAAAACTTTTCAACGGATAA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  32198 TAGCTTGAGTTTGAC-AAAAATGTCAGTTTGCTCTTCAGCAAAAACTTTTCAACGGATAA 32256

Qy    601 TGGGCGGTGCTATCACCGCAAAACTCTTCATTACAGGACTACAATGTCAGCTCTGTT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  32257 TGGGCGGTGCTATCACCGCAAAACTCTTCATTACAGGACTACAATGTCAGCTCTGTT 32316

Qy    661 TTCTGAAAATACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCTTTATTGACAA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  32317 TTCTGAAAATACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCTTTATTGACAA 32376

Qy    721 TACTGGAAAACCAAGGGGGAAGTCTCTTTTCTGACAATACTTCTTCGGAGCTGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  32377 TACTGGAAAACCAAGGGGGAAGTCTCTTTTCTGACAATACTTCTTCGGAGCTGC 32436

Qy    781 AATTTTTACAGAAGCCTCGGTGACTATTTCTAAATAATGCTAAAGTTCCTTTATTGACAA 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  32437 AATTTTTACAGAAGCCTCGGTGACTATTTCTAAATAATGCTAAAGTTCCTTTATTGACAA 32496

Qy    841 TAAGGTCACAGCAGCGAGCTCCTCAACACGGGGATAGTGTCAGGAGGTGCTATCGTGTGC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  32497 TAAGGTCACAGCAGCGAGCTCCTCAACACGGGGATAGTGTCAGGAGGTGCTATCGTGTGC 32556

Qy    901 TTATAAAAACTAGTACAGATACCAACGCGGGAGGAGCTAAGGTGTCACCCCTACTCCTTC 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  32557 TTATAAAAACTAGTACAGATACCAACGCGGGAGGAGCTAAGGTGTCACCCCTACTCCTTC 32616

Qy    961 CAACAATACATCGACAACACGCGGGAGGAGCTATCGTATTCTATGTGAAAAAGCTCAACTGGCTTC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  32617 CAACAATACATCGACAACACGCGGGAGGAGCTATCGTATTCTATGTGAAAAAGCTCAACTGGCTTC 32676

Qy   1021 CGGAGGACTTACCCTATTCAGTCAGTAGAAATAGTGTCAATGGAAGTACAGCCTCCTAAAGGTGG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  32677 CGGAGGACTTACCCTATTCAGTCAGTAGAAATAGTGTCAATGGAAGTACAGCCTCCTAAAGGTGG 32736

Qy   1081 AGCCATAGCTATCGAAGATAGTGGGAATTGAGTTTATCCGCGATAGTGGTGACATTGT 1140
          |||||||||||
Db  32737 AGCCATAGCTATCGAAGATAGTGGGAATTGAGTTTATCCGCGATAGTGGTGACATTGT 32796

Qy   1141 CTTTTTAGGGAATACAGTCACTTCTACTACTCCTGGACGAATAGAAGTAGTATCGACTT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  32797 CTTTTTAGGGAATACAGTCACTTCTACTACTCCTGGACGAATAGAAGTAGTATCGACTT 32856

Qy   1201 AGGAACGAGTGCAAAGATGACAGCTTGCGTTCTGCGTTCTGCGTTCGTCGTAGAGCCATCGACTTCTA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  32857 AGGAACGAGTGCAAAGATGACAGCTTGCGTTCTGCGTTCTGCGTTCGTCGTAGAGCCATCGACTTCTA 32916

Qy   1261 TGATCCCATAACTACAGGATCATCCACAACAGTTACAGATGTCTTAAAGTTAATGAGAC 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  32917 TGATCCCATAACTACAGGATCATCCACAACAGTTACAGATGTCTTAAAGTTAATGAGAC 32976

Qy   1321 TCCGGCAGATTCTGCACTACAATATACAGGGAACAATCATCTTCACAGGAGAAAAGTTATC 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  32977 TCCGGCAGATTCTGCACTACAATATACAGGGAACAATCATCTTCACAGGAGAAAAGTTATC 33036

Qy   1381 AGAGACAGAGCCGCAGATTCTAAAAATCTTAAAAATCTTACTTCGAAGCTACTACAGGCTCAGGCGATTCACTCTC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  33037 AGAGACAGAGCCGCAGATTCTAAAAATCTTAAAAATCTTACTTCGAAGCTACTACAGGCTCAGGCGATTCACTCTC 33096

Qy   1441 TTCAGGAGTACTCTCATCTTTAAAACATGGAGCTGACTCTGCGAGACTCAGGCATTCACTCA 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  33097 TTCAGGAGTACTCTCATCTTTAAAACATGGAGCTGACTCTGCGAGACTCAGGCATTCACTCA 33156

Qy   1501 ACAGGCAGATTCTCGTTCTCGTTCTCGGAATGGACGTAGGGAACTACTCTAGAACCTGCTGCTGATACTAG 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  33157 ACAGGCAGATTCTCGTTCTCGTTCTCGGAATGGACGTAGGGAACTACTCTAGAACCTGCTGCTGATACTAG 33216

Qy   1561 CACCATAAACAATTGGTCATTAACATCAGTTCATAGACGGTGCAAAGGAGGCAAAAAT 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  33217 CACCATAAACAATTGGTCATTAACATCAGTTCATAGACGGTGCAAAGGAGGCAAAAAT 33276

Qy   1621 AGAAACCAAAGCTACGTCAAAAATCTGACTTATCTGACTTATTGACCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  33277 AGAAACCAAAGCTACGTCAAAAATCTGACTTATCTGACTTATTGACCC 33336

Qy   1681 GACGGGCACGTTTATTGAGAAATCATAGTTTAAGAAATCCTCAGTCCTACGACATCTTAGA 1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  33337 GACGGGCACGTTTATTGAGAAATCATAGTTTAAGAAATCCTCAGTCCTACGACATCTTAGA 33396

Qy   1741 GCTCAAAGCTTCTGAACTGTAACAGCAGTCCAGATCCTAATAATGGGTGA 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  33397 GCTCAAAGCTTCTGAACTGTAACAGCAGTCCAGATCCTAATAATGGGTGA 33456

Qy   1801 GAAATTCATTACGGCTATCAGGGAACTTGGGGCCCAATTGTTTGGGGACAGGGGCTTC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  33457 GAAATTCATTACGGCTATCAGGGAACTTGGGGCCCAATTGTTTGGGGACAGGGGCTTC 33516

Qy   1861 TACGACTGCAACCTTCAACTGACTAAAACTGGCTATAATCCCGAGCCGTATCGG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  33517 TACGACTGCAACCTTCAACTGACTAAAACTGGCTATAATCCCGAGCCGTATCGG 33576

Qy   1921 CTCTTTAGTCCTAAGTTTGATATAGCTCATTTATGATATTAGTCTTCTCCATTATCT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  33577 CTCTTTAGTCCTAAGTTTGATATAGCTCATTTATGATATTAGTCTTCTCCATTATCT 33636

Qy   1981 TATGGAGACTGCAAACGAAGGGTTCAGGGAGACCGTGCTTTTGGTGTGCTGGATTATC 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  33637 TATGGAGACTGCAAACGAAGGGTTCAGGGAGACCGTGCTTTTGGTGTGCTGGATTATC 33696

Qy   2041 TAACTTCTTCCATAGGAGGAAGTAGTACAAAAACACGACGCGGGTTTCGCCATTGAGTGGCCGG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  33697 TAACTTCTTCCATAGGAGGAAGTAGTACAAAAACACGACGCGGGTTTCGCCATTGAGTGGCCGG 33756

Qy   2101 TTATGTCATAGGAGGAAACCTACACTACTTGTTCAGATAAGAATTCTTAGTGCTCATTTTG 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  33757 TTATGTCATAGGAGGAAACCTACACTACTTGTTCAGATAAGAATTCTTAGTGCTCATTTTG 33816

Qy   2161 TCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAAC-AAGGTACAGTCTACG 2219
          ||||||||||
Db  33817 TCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAATCAAAGGTACAGTCTACG 33876
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PN   WO9858953-A2.
XX
PD   30-DEC-1998.
XX
PF   19-JUN-1998;   98WO-DK00266.
XX
PR   23-JUN-1997;   97DK-0000744.
XX
PA   (BIRK/) BIRKELUND S.
PA   (CHRI/) CHRISTIANSEN G.
XX
PI   Birkelund S, Christiansen G, Knudsen K, Madsen A;
PI   Mygind P;
XX
DR   WPI; 1999-105610/09.
DR   P-PSDB; AAW88421.
XX
PT   Species-specific test for identifying mammals infected with
PT   Chlamydia pneumoniae - comprises detecting antibodies specific for
PT   outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT   these proteins
XX
PS   Claim 6; Page 52-53; 115pp; English.
XX
CC   This DNA sequence codes for the novel 90.0 kDa surface exposed
CC   protein Omp8 (see AAW88421) of the human respiratory pathogen
CC   Chlamydia pneumoniae. By generating antibodies specific against C.
CC   pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
CC   was obtained which reacted with outer membrane proteins. The
CC   antibody was used to identify the genes (see AAX06816-27) encoding
CC   Omp4-Omp15 proteins (see AAW8417-28) in an expression library of
CC   C. pneumoniae DNA. The genes are situated in 2 gene clusters:
CC   Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
CC   the other, and encode polypeptides of about 89.6-100.3 kDa and
CC   about 56.1 kDa. The invention provides a new species specific test
CC   for identifying mammals (including humans) infected with Chlamydia
CC   pneumoniae. The test comprises detecting antibodies specific for
CC   Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC   membrane proteins, especially by PCR. The proteins are also used
CC   in the diagnosis of C. pneumoniae infection in mammals. The
CC   nucleic acids and proteins can also be used in the immunization of
CC   mammals, the nucleic acids being particularly useful as DNA
CC   vaccines for effecting in vivo expression of antigens. The
CC   vaccines may also prevent atherosclerosis and bronchial asthma,
CC   which are possibly associated with C. pneumoniae.
XX
SQ   Sequence 2787 BP; 811 A; 583 C; 598 G; 795 T; 0 other;

Query Match   92.5%; Score 2775.8; DB 20; Length 2787;
Best Local Similarity   99.7%; Pred. No. 0;
Matches 2780; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy   101 ATGAAGTCTCTTCCCCAAGTTGTATTTTCTACATTTGCTATTTTCCCTTTGTCTATG 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGAAGTCTCTTCCCCAAGTTGTATTTTCTACATTTGCTATTTTCCCTTTGTCTATG 60

Qy   161 ATTGCTACCGAGACAGTTTTGGATTCAAGTGCGAGTTTCGATGTGGAATAAAAATGGTAAT 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATTGCTACCGAGACAGTTTTGGATTCAAGTGCGAGTTTCGATGTGGAATAAAAATGGTAAT 120

Qy   221 TTTTCAGTTCGTGAGAGTCAGGAAGATGTGGAACTACCTATTTAAGGGAAATGTC 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TTTTCAGTTCGTGAGAGTCAGGAAGATGTGGAACTACCTATTTAAGGGAAATGTC 180

Qy   281 ACTCTAGAAAAATATTCCTGAACAGCCACAGCAATCACAAAAAGTGTTTAACAACACT 340
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ACTCTAGAAAAATATTCCTGAACAGCCACAGCAATCACAAAAAGTGTTTAACAACACT 240

Qy   341 AAGGGCGATTTGACTTTCACAGGTAACGGACGAACTCTATTGTTCCAAACGGTGGATGCA 400
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AAGGGCGATTTGACTTTCACAGGTAACGGACGAACTCTATTGTTCCAAACGGTGGATGCA 300

Qy   401 GGGACTGTAGCAGGGGCGTCGTGTTAACAGCAGCGGTGGTGAGATAAATCTACCACGTTTATA 460

Qy   2220 GAGGAACTTCTATTACCAGCACAACGAAACCTATATCTCTCTTCCTTGCAAACTACGGC 2279
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 33877 GAGGAACTTCTATTACCAGCACAACGAAACCTATATCTCTCTTCCTTGCAAACTACGGC 33936

Qy   2280 CTTGTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCTCTTTTCAGGAAACCTTAGCT 2339
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 33937 CTTGTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCTCTTTTCAGGAAACCTTAGCT 33996

Qy   2340 ACACCCATACGGATAACGATCTGAAAACCAAGTATACAACATATCCTACTGTTAAAGGAA 2399
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 33997 ACACCCATACGGATAACGATCTGAAAACCAAGTATACAACATATCCTACTGTTAAAGGAA 34056

Qy   2400 GCTGGGGAATGATGAGTTTCGCTTAGAATTCGGTGGAAGAGCTCCGATTGCTTAGATG 2459
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 34057 GCTGGGGAATGATGAGTTTCGCTTAGAATTCGGTGGAAGAGCTCCGATTGCTTAGATG 34116

Qy   2460 AAAGTGCTCTATTTGAGCAGTACATGCCCTTCATGAAATTGCAGTTTGTTGTCATGCACATC 2519
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 34117 AAAGTGCTCTATTTGAGCAGTACATGCCCTTCATGAAATTGCAGTTTGTCTATGCACATC 34176

Qy   2520 AGGAAGGTTTAAAGAACAGAGGAACAGAGGAACAGAAGCTTCGTGAATTTGGAAGTAGAGCCGTCTTGTGA 2579
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 34177 AGGAAGGTTTAAAGAACAGAGGAACAGAGGAACAGAAGCTTCGTGAATTTGGAAGTAGAGCCGTCTTGTGA 34236

Qy   2580 ATCTTGCCTTACCTATCCGGATCCGATTGATAAGGAATCAGACTGCCAAGATGCAACGT 2639
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 34237 ATCTTGCCTTACCTATCCGGATCCGATTGATAAGGAATCAGACTGCCAAGATGCAACGT 34296

Qy   2640 ACAATCTAACTCTTGGTTATACTGTGGATCTTGTTCGTAGTAACCCCGACTGTACGACAA 2699
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 34297 ACAATCTAACTCTTGGTTATACTGTGGATCTTGTTCGTAGTAACCCCGACTGTACGACAA 34356

Qy   2700 CACTGCGAATTAGCGGTGATTCTTGGAAAACCTTCGGTACGAATTTGGCAAGACAAGCTT 2759
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 34357 CACTGCGAATTAGCGGTGATTCTTGGAAAACTTCGGTACGAATTTGGCAAGACAAGCTT 34416

Qy   2760 TAGTCCTTCGTGCGAGGAACCATTTTGCTTAACTCAAATTTGAAGCCTTTAGCCAAT 2819
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 34417 TAGTCCTTCGTGCGAGGAACCATTTTGCTTAACTCAAATTTGAAGCCTTTAGCCAAT 34476

Qy   2820 TTTCTTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTAGACTTAGGAGGCAAAATACC 2879
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 34477 TTTCTTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTAGACTTAGGAGGCAAAATACC 34536

Qy   2880 AATTCTAATGCGTTAGCTTGGTAAAGAGCTCCATACATCGAAGGGAAAGAGCTTTTAA 2939
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 34537 AATTCTAATGCGTTAGCTTGGTAAAGAGCTCCATACATCGAAGGGAAAAGAGCTTTTAA 34596

Qy   2940 GATTTCTTGAAGGCTCTTTTGATTTCGATTTCGATTCCATTTTAGTTGTTTTGCTAAAACACTTT 2999
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 34597 GATTTCTTGAAGGCTCTTTTGATTTCGATTTCGATTCCATTTTAGTGTTTTGCTAAAACACTTT 34656

Qy   3000 C 3000
           |
Db 34657 C 34657

RESULT 3
AAX06820
ID   AAX06820 standard; DNA; 2787 BP.
XX
AC   AAX06820;
XX
DT   26-APR-1999 (first entry)
XX
DE   Chlamydia pneumoniae surface exposed protein Omp8 DNA.
XX
KW   Omp8; outer membrane protein 8; surface exposed protein; antigen;
KW   infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
XX
OS   Chlamydia pneumoniae.
XX

Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1381 CAGACTTCAGGCATTCACTCAACAGCGCAGATTCTCGTCTCGAAATGGACGTAGGAGAACTACT 1440
Qy GGGACTGTAGCAGGGGCTGCTGTGTTAAACAGCAGCGTGGTAGATAAATCTACCACGTTTATA 360

Qy 1541 CTAGAACCTGCTGATACTAGCACCATAAACAATTGGTCATTAACACATCAGTTCTATAGAC 1600
Db GGGTTTCTTCGCTATCTTTATTGCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGGA 520
Db 1441 CTAGAACCTGCTGATACTAGCACCATAAACAATTGGTCATTAACACATCAGTTCTATAGAC 1500
Qy GGGTTTCTTCGCTATCTTTATTGCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGGA 420

Qy 1601 GGTGCAAGAGAGGCAAAAATAGAAACCAAGCTACGTCAAAAAATCTGACTTATCTGGA 1660
Db GCCGTTAGCTGCTCTACGGGTAGCTTGAGTTGACAAAAATGTCAGTTGCTTCTCAGC 580
Qy 1501 GGTGCAAGAGAGGCAAAAATAGAAACCAAGCTACGTCAAAAAATCTGACTTATCTGGA 1560
Db GCCGTTAGCTGCTCTACGGGTAGCTTGAGTTGACAAAAATGTCAGTTGCTTCTCAGC 480

Db 1661 ACCATCACTTATTGGACCCGACGGGCACGTTTATGAAAATCATATAGTTAAGAAATCCT 1720
Qy AAAAACTTTTCAACGGATAATGGCGGTGCTATCACCGCAAAAACTCTTTCATTAACAGGG 640
Qy 1561 ACCATCACTTATTGGACCCGACGGGCACGTTTATGAAAATCATATAGTTAAGAAATCCT 1620
Db AAAAACTTTTCAACGGATAATGGCGGTGCTATCACCGCAAAAACTCTTTCATTAACAGGG 540

Qy 1721 CAGTCCTTACGACATCTTAGAGCTCAAAGCTTCTGAACTTCTGGAACTGTAACAAGCACCGCAGTGACT 1780
Db ACTACCAAATGTCAGCTCTGTTTCTGAAAATACCTCCTCAAAGAAAGGGGAGCCATTCAG 700
Db 1621 CAGTCCTTACGACATCTTAGAGCTCAAAGCTTCTGAACTTCTGGAACTGTAACAAGCACCGCAGTGACT 1680
Qy ACTACCAAATGTCAGCTCTGTTTCTGAAAATACCTCCTCAAAGAAAGGGGAGCCATTCAG 600

Qy 1781 CCAGATCCTATAATGGTGAGAAATTCCATTACGGCTATCGGAACTGGGGCCCAATT 1840
Db ACTTCCGATGCCCTTACCATTACTGGCAAGGGGAAGTCTCTTTTCTGACAATACT 760
Db 1681 CCAGATCCTATAATGGTGAGAAATTCCATTACGGCTATCGGAACTGGGGCCCAATT 1740
Qy ACTTCCGATGCCCTTACCATTACTGGCAAGGGGAAGTCTCTTTTCTGACAATACT 660

Db 1841 GTTTGGGGACCAGGGGCTTCTACGACTGCAACCTTCAACTGACTAAAACTGGCTATATT 1900
Qy TCTTCGGATTCTGGAGCTGCAATTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCT 820
Qy 1741 GTTTGGGGACCAGGGGCTTCTACGACTGCAACCTTCAACTGACTAAAACTGGCTATATT 1800
Db TCTTCGGATTCTGGAGCTGCAATTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCT 720

Qy 1901 CCTAATCCCGAGCGTATCGGCTTCTTAGTCCCTAATAGCTTATGGAATGCATTATAGAT 1960
Db AAAGTTCCTTATTGACAATAAGTCACAGGAGCGAGCTCCTCAACACGGGGGATATG 880
Db 1801 CCTAATCCCGAGCGTATCGGCTTCTTAGTCCCTAATAGCTTATGGAATGCATTATAGAT 1860
Qy AAAGTTCCTTATTGACAATAAGTCACAGGAGCGAGCTCCTCAACACGGGGGATATG 780

Qy 1961 ATTAGCTCTCTCCATTATCTTATGGGAGACTGCAAACGAGAGGGTTGCAGGGAGACCGTGCT 2020
Db TCAGGAGGTGCTATCTGTCGTTATAAAACTAGTACAGATACAAGTCACCCTCCACTCGA 940
Db 1861 ATTAGCTCTCTCCATTATCTTATGGGAGACTGCAAACGAGAGGGTTGCAGGGAGACCGTGCT 1920
Qy TCAGGAGGTGCTATCTGTCGTTATAAAACTAGTACAGATACAAGTCACCCTCCACTCGA 840

Db 2021 TTTTGGTGTGCTGGATATCTTCTTCCATAAGGATAGTACAAAAACGACGACGCGGG 2080
Qy AATCAGATGTTACTCTTCAGCAACAATACATCGAACAACAGCGGGAGGAGCTATCTCATGTG 1000
Qy 1921 TTTTGGTGTGCTGGATATCTTCTTCCATAAGGATAGTACAAAAACGACGACGCGGG 1980
Db AATCAGATGTTACTCTTCAGCAACAATACATCGAACAACAGCGGGAGGAGCTATCTCATGTG 900

Qy 2081 TTTCGCCATTTGAGTGCGCGGTTATGTCAGCTCTTGGAAGAATAGTGTCAATGAA 2140
Db AAAAAGCTCGAACTGCTTCCGGAGGACTTACCCTATTCAGTAGAAAATAGTGTCAATGA 1060
Db 1981 TTTCGCCATTTGAGTGCGCGGTTATGTCAGCTCTTGGAAGAATAGTGTCAATGA 2040
Qy AAAAAGCTCGAACTGCTTCCGGAGGACTTACCCTATTCAGTAGAAAATAGTGTCAATGA 960

Qy 2141 ATTCTTAGTGCTGCATTTGTCAGCTTGTCTCTTTGGAGAGATAGAGACTACTTGTAGCTAAG 2200
Db GGTACAGCTCCTAAAGGTGAGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCC 1120
Db 2041 ATTCTTAGTGCTGCATTTGTCAGCTTGTCTCTTTGGAGAGATAGAGACTACTTGTAGCTAAG 2100
Qy GGTACAGCTCCTAAAGGTGAGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCC 1020

Qy 2201 AATCAAGTACAGTCTCTATTACCAGCAGAACTCTCTATTACCAGCAACGAAACCTATATCTCT 2260
Db GCCGATAGTGGTGACATTGGTGACATTGTCTTTTAGGGAATACAGTCACTCTACTACTCCTGGGACG 1180
Db 2101 AATCAAGTACAGTCTCTATTACCAGCAGAACTCTCTATTACCAGCAACGAAACCTATATCTCT 2160
Qy GCCGATAGTGGTGACATTGGTGACATTGTCTTTTAGGGAATACAGTCACTCTACTACTCCTGGGACG 1080

Db 2261 CTTCCTTGCAAACTACCGCCTTGTTGTCTTATGTTCTTACAGAGATTCCTGTTCTC 2320
Qy AATGAAGTAGTATCGACTTAGGAACGAGGTGCAAAGATGCAAGTCTTGCGTTCTGCTGCT 1240
Qy 2161 CTTCCTTGCAAACTACCGCCTTGTTGTCTTATGTTCTTACAGAGATTCCTGTTCTC 2220
Db AATGAAGTAGTATCGACTTAGGAACGAGGTGCAAAGATGCAAGTCTTGCGTTCTGCTGCT 1140

Qy 2321 TTTTCAGGAAACCTTAGCTACACCCATACGGATAACGATCTGAAAACCAAGTATACAACA 2380
Db GGTAGAGCCATCCATTCTTATGATCCATACTACTACAGAGGATCATCCACAACAGTTACAGAT 1300
Db 2221 TTTTCAGGAAACCTTAGCTACACCCATACGGATAACGATCTGAAAACCAAGTATACAACA 2280
Qy GGTAGAGCCATCCATTCTTATGATCCATACTACTACAGAGGATCATCCACAACAGTTACAGAT 1200

Qy 2381 TATCCTACTGTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTAGAATTCGGTGGAAGA 2440
Db GTCTTAAAAGTTAATGAACTCTCCTGGCCCAGATTCTAAACTATACAGGAACATCATC 1360
Db 2281 TATCCTACTGTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTAGAATTCGGTGGAAGA 2340
Qy GTCTTAAAAGTTAATGAACTCTCCTGGCCCAGATTCTAAACTATACAGGAACATCATC 1260

Qy 2441 GCTCCGATTTGCTTAGATGAAAGTGCTCTATTGAGCAGTACATGCCCTTCATGAAATTG 2500
Db TTCACAGGAGAAAAGTTATCAGAACAGAGGCCCGAGATTCTAAAAATCTTACTTCGAAG 1420
Db 2341 GCTCCGATTTGCTTAGATGAAAGTGCTCTATTGAGCAGTACATGCCCTTCATGAAATTG 2400
Qy TTCACAGGAGAAAAGTTATCAGAACAGAGGCCCGAGATTCTAAAAATCTTACTTCGAAG 1320

Db 2501 CAGTTTGTCTATGCACATCAGGAAGGTTTAAAGAACAGAGGTTTAAAGAACAGAAGAGCTCGTGAATTT 2560
Qy CTACTACAGGCCTGTAACTCTTTCAGGAGTCTTTCAGGAGAGGTTACTGGAGTGACTCTG 1480
Qy 2401 CAGTTTGTCTATGCACATCAGGAAGGTTTAAAGAACAGAGGTTTAAAGAACAGAAGAGCTCGTGAATTT 2460
Db CTACTACAGGCCTGTAACTCTTTCAGGAGTCTTTCAGGAGAGGTTACTGGAGTGACTCTG 1380

Qy 2561 GGAAGTAGCCGGTCTTGTGAATCTTGCCTTACCTATCCGGATCCGATTTGATAAGGAATCA 2620
Db CAGACTTCAGGCATTCACTCAACAGCGCAGATTCTCGTCTCGAAATGGACGTAGGAACTACT 1540
Db 2461 GGAAGTAGCCGGTCTTGTGAATCTTGCCTTACCTATCCGGATCCGATTTGATAAGGAATCA 2520

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Qy   2621 GACTGCCAAGATGCAACGTACAATCTAACTCTTGGTTATACTGTGGATCTTGTTCGTAGT 2680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 GACTGCCAAGATGCAACGTACAATCTAACTCTTGGTTATACTGTGGATCTTGTTCGTAGT 2580

Qy   2681 AACCCGACTGTACGACAACACTGCGAATTAGCGGTGATTCTTGGAAAACCTTCGGTACG 2740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 AACCCGACTGTACGACAACACTGCGAATTAGCGGTGATTCTTGGAAAACCTTCGGTACG 2640

Qy   2741 AATTTGGCAAGACAAGCTTAGTCCTTCGTGCGCAGGGAACCATTTTGCTTTAACTCAAAT 2800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 AATTTGGCAAGACAAGCTTAGTCCTTCGTGCGCAGGGAACCATTTTGCTTTAACTCAAAT 2700

Qy   2801 TTTGAAGCCTTAGCCAATTTCTTTGAATTGCGTGGTCATCTCGCAATTACAATGTA 2860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 TTTGAAGCCTTAGCCAATTTCTTTGAATTGCGTGGTCATCTCGCAATTACAATGTA 2760

Qy   2861 GACTTAGGAGCAAAATACCAATTCTAA 2887
          ||||||||||||||||||||||||||
Db   2761 GACTTAGGAGCAAAATACCAATTCTAA 2787
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RESULT 4

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ABL91193
ID   ABL91193 standard; DNA; 2241 BP.
XX
AC   ABL91193;
XX
DT   29-JUL-2002  (first entry)
XX
DE   Chlamydia pneumoniae cp0015 ORF DNA, SEQ ID NO:20.
XX
KW   Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KW   human respiratory disease; cardiovascular disease; atherosclerosis;
KW   coronary artery disease; carotid artery stenosis; myocardial infarction;
KW   cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW   strain CWL029; open reading frame; ORF; gene; ds.
XX
OS   Chlamydia pneumoniae.
XX
FH   Key            Location/Qualifiers
FT
FT   CDS            1..2241
FT                  /*tag= a
FT                  /product= "cp0015"
XX
PN   WO20202606-A2.
XX
PD   10-JAN-2002.
XX
PF   03-JUL-2001; 2001WO-IB01445.
XX
PR   03-JUL-2000; 2000GB-0016363.
PR   11-JUL-2000; 2000GB-0017047.
PR   21-JUL-2000; 2000GB-0017983.
PR   07-AUG-2000; 2000GB-0019368.
PR   18-AUG-2000; 2000GB-0020440.
PR   14-SEP-2000; 2000GB-0022583.
PR   10-NOV-2000; 2000GB-0027549.
PR   22-DEC-2000; 2000GB-0031706.
XX
PA   (CHIR-) CHIRON SPA.
XX
PI   Ratti G, Grandi G;
XX
DR   WPI; 2002-154726/20.
DR   N-PSDB; ABB90535.
XX
PT   Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT   medicament for treatment or prevention of infection due to Chlamydia,
PT   preferably Chlamydia pneumoniae, and for diagnostic purposes -
XX
PS   Claim 5; Page 50; 364pp; English.
XX
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CC   Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
CC   pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
CC   them. The proteins are predicted to be immunogenic and may therefore be
CC   useful in vaccine production and for diagnostic purposes. Chlamydia
CC   pneumoniae is a common cause of respiratory disease in humans, and is
CC   also involved in the development of cardiovascular diseases such as
CC   atherosclerosis, coronary artery disease, carotid artery stenosis,
CC   myocardial infarction, cerebrovascular disease, aortic aneurysm,
CC   claudication and stroke. The proteins and nucleic acids of the invention
CC   may be used in vaccines and pharmaceutical compositions for the
CC   prevention or treatment of chlamydial infections, particularly chlamydia
CC   pneumoniae infections. The proteins may also be used in the detection of
CC   Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
CC   DNA probe assay or blotting techniques for determining Chlamydia
CC   pneumoniae gene expression. The present sequence represents a
CC   specifically claimed DNA which encodes a Chlamydia pneumoniae protein of
CC   the invention.
XX
SQ   Sequence 2241 BP; 660 A; 475 C; 478 G; 628 T; 0 other;
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Query Match             74.7%;  Score 2241;  DB 24;  Length 2241;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 2241;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    647 ATGTCAGTCTGTTTTCTGAAAATCCTCCAAGAAAATCCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCC 706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGTCAGTCTGTTTTCTGAAAATACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCC 60

Qy    707 GATGCCCTTACCATTACTGGAAACCAAGGGGAAGTCTCTTTTTCTGACAATACTTCTTCG 766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GATGCCCTTACCATTACTGGAAACCAAGGGGAAGTCTCTTTTTCTGACAATACTTCTTCG 120

Qy    767 GATTCTGGAGCTGCAATTTTACAGAAGCCTCGGTGACTATTCTTAATAATGCTAAAGTT 826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GATTCTGGAGCTGCAATTTTACAGAAGCCTCGGTGACTATTCTTAATAATGCTAAAGTT 180

Qy    827 TCCTTTATTGACAATAAGGTCACAGGAGCGCAGGCAGCTCCTCAACACGGGGATATGTCAGGA 886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCCTTTATTGACAATAAGGTCACAGGAGCGCAGGCAGCTCCTCAACACGGGGATATGTCAGGA 240

Qy    887 GGTGCTATCGTGCTTATAAAACTAGTACAGATACTAAGGTCACCCTACTGAAAATCAG 946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GGTGCTATCGTGCTTATAAAACTAGTACAGATACTAAGGTCACCCTACTGAAAATCAG 300

Qy    947 ATGGTTACTCTTCAGCAACAATACAATCATCGACAACAGCGGAGGAGTCATCATGTGAAAAAG 1006
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ATGGTTACTCTTCAGCAACAATACAATCATCGACAACAGCGGAGGAGTCATCATGTGAAAAAG 360

Qy   1007 CTCGAACTGGCTTCCGGAGGACTTACCCTATTCAGTGAGAAATAGTGTCAATGAGGAGTACA 1066
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CTCGAACTGGCTTCCGGAGGACTTACCCTATTCAGTGAGAAATAGTGTCAATGAGGAGTACA 420

Qy   1067 GCTCCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGAT 1126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GCTCCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGAT 480

Qy   1127 AGTGGTGACATTGTCTTTTTAGGGAATACAGTCACTTCACTCCTGGGACGAATAGA 1186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AGTGGTGACATTGTCTTTTTAGGGAATACAGTCACTTCACTCCTGGGACGAATAGA 540

Qy   1187 AGTAGTATCGACTTAGGAACGAGTGCAAAGATGCAAGATGCAAGATGCAAGCTTTGCCTTCTGCGTTGGTAGA 1246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AGTAGTATCGACTTAGGAACGAGTGCAAAGATGCAAGATGCAAGCTTTGCCTTCTGCGTTGGTAGA 600

Qy   1247 GCCATCTACTTCTATGATCCCATAACTACAGGATGATCCATACAGATTACAGATGTCTTA 1306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCCATCTACTTCTATGATCCCATAACTACAGGATGATCCATACAGATTACAGATGTCTTA 660

Qy   1307 AAAGTTAATGAGACTCCGGCAGATTCGACTACAGAATATCAGGGAACATCATCTTCACA 1366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AAAGTTAATGAGACTCCGGCAGATTCGACTACAGAATATCAGGGAACATCATCTTCACA 720

Qy   1367 GGAGAAAAGTTATCAGAGACAGAGGACGGCCGCAGATTCTAAAAAATCTTACTTCGAAGCTACTA 1426
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Db  1801 ATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTACATGCCCTTCATGAAATTGCAGTTT 1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2507 GTCTATGCACATCAGGAAGGTTTAAAGAACAGAGGAACAGAAGCTCGTGAATTTGGAAGT 2566
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 GTCTATGCACATCAGGAAGGTTTAAAGAACAGAGGAACAGAAGCTCGTGAATTTGGAAGT 1920

Qy  2567 AGCCGTCTTGTGAATCTTGCCTACCTATCGGGATCCGATTTGATAAGGAATCAGACTGC 2626
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 AGCCGTCTTGTGAATCTTGCCTACCTATCGGGATCCGATTTGATAAGGAATCAGACTGC 1980

Qy  2627 CAAGATGCAACGTACAACATCTAACTCTTGGTTATACTGTGGATCTGTTGTTCGTGAGTAACCCC 2686
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 CAAGATGCAACGTACAACATCTAACTCTTGGTTATACTGTGGATCTGTTGTTCGTGAGTAACCCC 2040

Qy  2687 GACTGTACGACAACACTGCGAATTAGCGGTGATTCTTGAAAACCTTCGGTACGAATTTG 2746
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 GACTGTACGACAACACTGCGAATTAGCGGTGATTCTTGAAAACCTTCGGTACGAATTTG 2100

Qy  2747 GCAAGACAAGCTTTAGTCCTTCGTGCAGGGAACCATTTTTGCTTAACTCAAATTTTGAA 2806
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 GCAAGACAAGCTTTAGTCCTTCGTGCAGGGAACCATTTTTGCTTAACTCAAATTTTGAA 2160

Qy  2807 GCCTTTAGCCAATTTCTTTGAATTGCGTGGGTCATCTGCAATTACAATGTAGACTTA 2866
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCCTTTAGCCAATTTCTTTGAATTGCGTGGGTCATCTGCAATTACAATGTAGACTTA 2220

Qy  2867 GGAGCAAAATACCAATTCTAA 2887
         |||||||||||||||||||||
Db  2221 GGAGCAAAATACCAATTCTAA 2241


RESULT 5
ABQ84775
ID   ABQ84775 standard; DNA; 2781 BP.
XX
AC   ABQ84775;
XX
DT   25-FEB-2003   (first entry)
XX
DE   Chlamydia psittaci antigen CP4#12 encoding DNA SEQ ID NO:56.
XX
KW   Chlamydia psittaci; vaccination; vaccine; antigen; immune response;
KW   immunisation; antibacterial; infection; gene; ds.
XX
OS   Chlamydia psittaci.
XX
FH   Key            Location/Qualifiers
FT   CDS            1..2781
FT                  /*tag=  a
FT                  /product= "antigen CP4#12"
XX
PN   WO200253588-A2.
XX
PD   11-JUL-2002.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Johnston SA,   Stemke-Hale K,   Sykes KF,   Kaltenboeck B;
XX
DR   WPI; 2002-537942/57.
DR   P-PSDB; ABP56019.
XX
PT   Vaccine for immunization of animal, preferably bovine, against
PT   Chlamydia psittaci, comprises at least one polynucleotide having a C.
PT   psittaci sequence, or at least one C. psittaci antigen -
XX
PS   Claim 14; Page 157-158; 164pp; English.
XX
CC   The present invention describes a vaccine (I) for the immunisation of an
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Db   721 GGAGAAAAGTTATCAGAGACAGAGGCCGCAGATTCTAAAAATCTTAAAAATCTTACTTCGAAGCTACTA 780

Qy  1427 CAGCCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAACATGGAGTGACTCTGCAGACT 1486
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CAGCCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAACATGGAGTGACTCTGCAGACT 840

Qy  1487 CAGGCATTCACTCAACAGGCAGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAA 1546
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 CAGGCATTCACTCAACAGGCAGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAA 900

Qy  1547 CCTGCTGATACTAGCACCCATAAACAATTGGTCATTAACATCAGTTCATAGACGGGTGCA 1606
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CCTGCTGATACTAGCACCCATAAACAATTGGTCATTAACATCAGTTCATAGACGGGTGCA 960

Qy  1607 AAGAAGGCAAAAATAGAAACCAAAGCTACGTCAAAAAATCGACTTTATCTGACCATC 1666
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 AAGAAGGCAAAAATAGAAACCAAAGCTACGTCAAAAAATCGACTTTATCTGGAACCATC 1020

Qy  1667 ACTTTATTGGACCCGACGGGCACGTTTATGAGAAATCATTAGTTTAAGAAAATCCTCAGTCC 1726
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 ACTTTATTGGACCCGACGGGCACGTTTATGAGAAATCATTAGTTTAAGAAAATCCTCAGTCC 1080

Qy  1727 TACGACATCTTAGAGTCTCAAAGCTTCTGGAACTGTAACAGCACCGCAGTGACTCCAGAT 1786
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 TACGACATCTTAGAGTCTCAAAGCTTCTGGAACTGTAACAGCACCGCAGTGACTCCAGAT 1140

Qy  1787 CCTATAATGGTGAGAAATTCCATTACGGCTATCAGGGAACTTGGGCCCAATTGTTTGG 1846
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 CCTATAATGGTGAGAAATTCCATTACGGCTATCAGGGAACTTGGGCCCAATTGTTTGG 1200

Qy  1847 GGGACAGAGGGCTTCTACGACTGCGAACCTTCAACTGGACTAAAACTGGCTATATTCCTAAT 1906
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 GGGACAGAGGGCTTCTACGACTGCGAACCTTCAACTGGACTAAAACTGGCTATATTCCTAAT 1260

Qy  1907 CCCGAGCCGTATCGGCGTCTTAGTCCCTAATAGCTTATGGAATGCATTATTAGATATTAGC 1966
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 CCCGAGCCGTATCGGCGTCTTAGTCCCTAATAGCTTATGGAATGCATTATTAGATATTAGC 1320

Qy  1967 TCTCCCATTATCTTATGGAGACTGCAAACGAGAGGGTTGCAGGGAGACCGTGCTTTTTGG 2026
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 TCTCCCATTATCTTATGGAGACTGCAAACGAGAGGGTTGCAGGGAGACCGTGCTTTTTGG 1380

Qy  2027 TGTGCTGATTATCTAACTTCTTCCATAAGGATAGTAGCACAAAAACACGACGCGGGTTTCGC 2086
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 TGTGCTGATTATCTAACTTCTTCCATAAGGATAGTAGCACAAAAACACGACGCGGGTTTCGC 1440

Qy  2087 CATTTGAGTGGGCGGTTATGTCAGCTCTTTGTTCAGATAAGAGATTCTT 2146
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 CATTTGAGTGGGCGGTTATGTCAGCTCTTTGTTCAGATAAGAGATTCTT 1500

Qy  2147 AGTGCTGCATTTTGTCAGCTCTTTGTGAAGAATAGAGACTACTTTGTAGCTAAGAATCAA 2206
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 AGTGCTGCATTTTGTCAGCTCTTTGTGAAGAATAGAGACTACTTTGTAGCTAAGAATCAA 1560

Qy  2207 GGTACACAGTCTACGGAGGAACTCTCTATTACCAGCACAACGAAACCTATATCCTCTCCT 2266
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 GGTACACAGTCTACGGAGGAACTCTCTATTACCAGCACAACGAAACCTATATCCTCTTCCT 1620

Qy  2267 TGCAAACTACGGGCCTTGTCGTTCGTTGTCTTTGTGTCTTATGTTCCTACAGAGATTCCTTTTCA 2326
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 TGCAAACTACGGGCCTTGTCGTTCGTTGTCTTTGTGTCTTATGTTCCTACAGAGATTCCTTTTCA 1680

Qy  2327 GGAAACCTTAGCTACACCCATACGGATCTGAAAACCAAGTATACACATATCCT 2386
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 GGAAACCTTAGCTACACCCATACGGATCTGAAAACCAAGTATACACATATCCT 1740

Qy  2387 ACTGTTAAAGAAGCTGGGGATGTAGTTTCGCTTGAATTGCTTAGATGATAGTT 2446
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 ACTGTTAAAGAAGCTGGGGATGTAGTTTCGCTTGAATTGCTTAGATGATAGTT 1800

Qy  2447 ATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTAGTACATGCCCCTTCATGAAATTGCAGTTT 2506
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CC   animal against Chlamydia psittaci comprising at least one polynucleotide
CC   (Ia) having a C. psittaci sequence, or at least one C. psittaci antigen
CC   (Ib), and a carrier. (Ia) and (Ib) have antibacterial activity. (I) is
CC   useful for the immunisation of a bovine. The present sequence encodes a
CC   C. psittaci antigen from the present invention.
XX
SQ   Sequence 2781 BP; 818 A; 555 C; 610 G; 798 T; 0 other;

Query Match           18.2%;  Score 546.6;  DB 24;  Length 2781;
Best Local Similarity 53.7%;  Pred. No. 4.2e-141;
Matches 1390;  Conservative  0;  Mismatches 1134;  Indels 63;  Gaps 10;
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Qy   328  TTTTAACAACTAAGGGCGATTGACTTTCACAGTAACGGGACTCTCTATTGTTCCA           387
Db   231  TTTTGTTCAGACTGCAGACAACCTAACTTTCAAAGGGAACAACCATAGTTATCCATAAC      290

Qy   388  AACGGTGATGCAGGGACTGTAGCAGGGCTAATCC---TGCGGGAATTAACGTTAACACTGCCGATAAGAT  447
Db   291  GAACGCCAATGCCGGAGCTAATCC---TGCGGGAATTAACGTTAACACTGCCGATAAGAT      347

Qy   448  TACCACGTTTATAGGGTTTTCTTCGCTATCTTTATTGCGTCTCCTGGAAGTTCGATAAC      507
Db   348  TCTTACGCTGACAGATTTTTCTTCAAGTTGAGCTTTAAGGAAATGAGCCCATCTTCTCTAGTGAA      407

Qy   508  TACCGGCAAAGAGAGCCGTTAGCTGCTCTACGGGGTAGCTTGAGTTTGACAAAATGTCAG      567
Db   408  TACTGAAAAAGGGGGC---TATGAAATCCGAGGAGCATTAAACTTAGCGAATAATGCCAG      464

Qy   568  TTTGCTCTTCAGCAAAAACTTTCACGGATAAATGCGGTGCTATCACCCGCAAAAACTCT      627
Db   465  TATTCTGTTTGATCAGACTATTCCGCTGAAATCGGTGGAGCCATTCTCTTCGCAAAGCTTT    524

Qy   628  TTCATTAACAGGGACTACAATGTCAGCTCGTGTTTCTGAAAATACCTCCTCAAAGAAAGG    687
Db   525  TTCTCTAACCGGCTCGAGCAAAGAAATCAGCTTCACCACTAACTTCTACTGCGAAAAAAGG   584

Qy   688  CGGAGCCATTCAGACTTCCGATGCCCCTACCATTACTGGAAAACAAGGGAAGTCTCTTT    747
Db   585  TGGAGCGATTGCTGCTACGGGAATAGCTCATCTTTCGGACAACCAAGGCACAATCAGATT   644

Qy   748  TTCTGACAATACTTCTTCGGAGTTCTGGAGCTGCAATTTTTACAGAAGCCTCCGGTGACTAT  807
Db   645  TTCTGGGACACGCTGTGAATTCTGGGGAGCAGTATATTCAGAAGCTTCATGACGAT       704

Qy   808  TTCTAATAATGCTAAAGTTCCTTATTGACAATAGGTCACAGGAGCTCCTCAAC          867
Db   705  TGCAGGTAACAACCACGTTGCTTTTAGCAACAATGCTGTTTCCGGTCATCT-------     756

Qy   868  AACGGGGGATATGTCAGGAGGTGCTATCGTCCTAAAGGTGGAGCCATAGTCTTATAAAACTAGTACAGATACTAAGGT  927
Db   757  ------GATGGTTGCGGTGGAGCTATCCCTAAGGGTGGAGCTATTGGTATTGCTGCCAATGGAGA    809

Qy   928  CACCCTCACTGGAAATCAGATGTGTTACTCTTCAGCAACAATACATGACGACAGCGGGAGG   987
Db   810  TACTATAAGAGATAACAAAGTCTTGATTTTGAGGAAAATACTTCTTCAGCAAAAGTGG      869

Qy   988  AGTCATCTATGTGAAAAAGCTCGAACTGACTTAGGAACGAGTGCAAAGATGACAGC      1047
Db   870  AGCGATTTACACCGTAAAACTATAATTGACTTCTCGGTGGGCCTACCGGCATTTATCAATAA   929

Qy  1048  TAGTGTCAATGGAGGTACAGCCTCCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGA  1107
Db   930  CAAAGTTACCCCATGCTACA---CCTAAGGGTGGAGCTATTGGTATTGCTGCCAATGGAGA   986

Qy  1108  ATTGAGTTTATCCGCCGATAGTGGTGACAATGTCTTTTTTAGGGAA---TACAGTCACTTC  1164
Db   987  ATGTAGCTTAACCGCTGAACATGGGATATTACTTTTGATAATAACCTGATATGGCCACACA  1046

Qy  1165  TACTACTCCTGGGACGAAGAGTAGTAGTATCGGACTTAGGAACGAGTGCAAAGATGACAGC  1224
Db  1047  AGACAAATGCTACAATAAAAGAAATGGCCATTAACAATGGCAATGGTGTAAATTCGTCAA   1106

Qy  1225  TTTTGCCGTTCGTCGTCTGCTGAGAGCCATCTACTTCTATGATCCCATAACTACCAGGATCATC  1284
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Db  1107  CTTACGTGCAGCGTCTGGAAGACGATTTCTTCTATGATCCTATCACAGTTG------      1159
Qy  1285  CACAACAGTTACAGATGTCTTAAAAGTTAATGAGACTCCGGCAGATTCTGACTACAATA    1344

Db  1160  -----AAGGTAATGCTGCTGATCTTCCACTTGAATAAAGTGAGGGTGATAAAACGTA     1214
Qy  1345  TACAGGGAACATCATCTTCACAGGAGAAAGTTATCAGAGACAGAGGCCGAGATTCTAA    1404

Db  1215  TAATGGAAGAATTATTTTTCAGGAGAAAAGCTCACTGAGAGAACAAGCTGCTGTTGCGGA    1274
Qy  1405  AAATCTTACTTCGAAGCTACTACAGCCTGTAACTCTTCAGGAGTGACTCTTCAGGATATCTTTAAA  1464

Db  1275  TAACCTAAAGACACATTTACACAGCCTATCACTTTAGCTGCTGGTGGTGAACTTGTGTACG    1334
Qy  1465  ACATGGAGTGACTCTGCAGACTCAGGCCATTCAGCCATTCACTCACAGGCAGAGATTCTCGTCTCGAAAT  1524

Db  1335  CAGCGGTGTGGGAAGTAGAAGCAAAAACAGTCGTGCAAACAGCAGGAATCTTTGATTCTGAT   1394
Qy  1525  GGACGTAGGAACTACTCTA---GAACCTGCTGATACTAGCACCATAAACAATTGGTCAT    1581

Db  1395  GGATGCAGGCAGGCACAAAGTTATCCGCAAAAACAGAAGATGCTACACTGCGAATCTGGCTAT   1454
Qy  1582  TAACATCAGTTCTATAGACGGTGCAAGAAGGCAAAATAGAAACCAAAGTACGTCAAA    1641

Db  1455  TAATCCGAATACCTTAGATGGGAAAAAATTCGCGTAGTCCGTTGCGTGCTGGGGAA    1514
Qy  1642  AAATCTGACTTTATCTGGAACCATCACTTTATTGGACCACGACGGCACGTTTTATGAAAA  1701

Db  1515  GAATGTGACTTTATCAGGTGCGTTATTGGCGTTATTGATCCTACCAGGGAAGTTTATGAAAA  1574
Qy  1702  TGATAGTTTAAGAAATCCTCAGTCCTACGACATCTTAGAGCTCCTATAATGGTGAGAATTCCATTACGGCTATCA  1761

Db  1575  CCATAAGCTAAATGATACGTTAGCTTTAGGAGAATTCAACTTCTGGAAAGGTTCGGT    1634
Qy  1762  AACAAGCACCGCAGTGACTCCAGATCCTCCATATGGTGAATAATGGTGTTGGGGGACAGGGGCTTCACGACTGC  1821

Db  1635  GACAACAACCAAGTGCCTAGTCAGTCATGTTGTTGGTGTTGCTGAAAACCCACTATGGTTATCA  1694
Qy  1822  GGGAAC------TTGGGGCCCCAATTGTTGGGGGACAGGGGCTTCACGACTGC      1869

Db  1695  AGGAAAACTGGTCGTCAGTTGGGTCAAAGATAATAACTCTGATCCTAAAACACAAACAGC    1754
Qy  1870  AACCTTCAACTGGACTAAAAACTGGCTATAAATCCTAATCCCAGCGTATCGCGTCTCTTTAGT  1929

Db  1755  AATCTTTACCTGGAATAAAACAGGATATGTTCCAAATCCTGAACGTCGTGCTCCGCTAGT    1814
Qy  1930  CCCTTAGCTTATGGAATGCATTGTTCTTATAAAACTAGTACAGATACTAAGGT      1989

Db  1815  ACTCAATAGCCCTTTGGGGATCCTTTATAGATTTACGTTCTATTCAAGATGTCTTGGAACG    1874
Qy  1990  TGCAAACGAAGGGTTGC---AGGGAGACCGTGCTTTTTGGTTGTGCTGGATTATCATCAACTT  2046

Db  1875  TAGTTGTGATAGTATTCTTGAGACACGTCGTGTTTGTGGTGTTCTCTGGAATTGGGAACTT    1934
Qy  2047  CTTCCATAAGGAGTAGTACAAAAAACACGACGCGGGGTTCGCATTTGAGTGTGGCGGTTATGT  2106

Db  1935  CTTCCATAAAGATGCGGAATGCTGAAAATCGCAAAATCCGTGCAAATCGCATATCAGTTCGGGATATGT  1994
Qy  2107  CATAGGAGGAAACCTACATACTTGTTCAGATAAGAATCTTAGTGCTGCATTTTGTCAGCT    2166

Db  1995  GTTAGGAGCGCCACAACAAATAACTCGAGAGAGGATTCTCTTAGTGTGGCTTCTCAGTT    2054
Qy  2167  CTTTTGGAGAGATAGAGACTACTTTGTAGCTAAGGTACAGTCACGGAGGAAC      2226

Db  2055  ATTTGCAAAAGATAAAGACTACCCTGTAAGCAAGAACGCCGCAAAACGCTATGCGGGTTC    2114
Qy  2227  TCTCTATTACCAGGCA------CAACGAAACCTATAATCTCTTCCTTGCGAAACTACGGCC    2280

Db  2115  TGTATATTATCAGCATGTGAGCATGGCAAGTTTGATGATCCTCACGCGTTAATGGGCTAA    2174
Qy  2281  TTGTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCGTTTTCAGGAAACTTAGCTA    2340
```

PT   polynucleotide having a Chlamydia sequence or at least one Chlamydia
PT   antigen .
XX
PS   Claim 6; Page 167-168; 183pp; English.
XX
CC   The invention relates to a vaccine (I) comprising at least one
CC   polynucleotide (ABQ78008-ABQ78039) having a Chlamydia sequence or at
CC   least one Chlamydia antigen (ABB98203-ABB98234) and a pharmaceutically
CC   acceptable carrier. The antigens are useful for immunising an animal, by
CC   providing at least one chlamydia antigen or its antigenic fragment to the
CC   animal, in an amount effective to induce an immune response in the animal
CC   e.g. mammals including bovine or human. The method is effective to induce
CC   an immune response against C. psittaci, C. pneumoniae or non-Chlamydia
CC   infection. The method further involves administering to the animal an
CC   antigen or an antigenic fragment from Chlamydia species other than
CC   C. psittaci or C. pneumoniae or an antigenic fragment from a
CC   non-chlamydia species.
XX
SQ   Sequence 2781 BP; 818 A; 555 C; 610 G; 798 T; 0 other;

Query Match   18.2%; Score 546.6; DB 24; Length 2781;
Best Local Similarity   53.7%; Pred. No. 4.2e-141;
Matches 1390; Mismatches 1134; Conservative 0; Indels 63; Gaps 10;

```
Qy    328 TTTTAACACACTAAGGGCGATTTGACTTCACAGGTAACGGGAACTCTCTATTGTTCCA 387
          ||||    |||       |   | |    ||||||
Db    231 TTTTGTTCAGACTGCGAGACAACCTAACTTTCAAAGGGAACAACCATAGCTTATCCATAAC 290

Qy    388 AACGGTGGATGCAGGGACTGTAGCAGGGCTGCTTGTTAACAGCAGCGTGGTAGATAAATC 447
          |||     |     | |    |        ||       ||||||||| |  |||||  |
Db    291 GAACCGGAATGCGGAGCTAATCC---TGCGGGAATTAACGTTAACACTGCCGATAAGAT 347

Qy    448 TACCACGTTTATAGGGTTTCTTCGCTATCTTTTATTGCGTCTCCTGGAAGTTCGATAAC 507
          | |  |   |  |        |   |      |||       |   |
Db    348 TCTTACGCTGACAGATTTTTCTAAGTTGGAGCTTTAAGGAATGCCCATCTTCTCTAGTGAA 407

Qy    508 TACCCGCAAAGGAGCCGGTTAGCTGCTCTCACGGGTAGCTTGAGTTTGACAAAAAATGTCAG 567
          |||   | |||       |        | |  |||            |||
Db    408 TACTGGAAAAGGGGC--TATGGAAAATCCCGGAGGAGCCATTAAAAACTTAGGGAATAATGCCCAG 464

Qy    568 TTTGCTCTTCAGCAAAAACTTTCAACGGATAATGGCGGTGCTATCACCGCAAAAACTCT 627
          |||    |  |   |||||   |          |  |||    |||       |    |
Db    465 TATTCTGTTTGATCAGAACTATTCCGCTGAGAATGGTGGAGCCATCTTCTGCAAAGCTT 524

Qy    628 TTCATTAACAGGGACTACAAATGTCAGCTCGTTTCTGAAAATACCTCCTCAAAGAAGAGG 687
          ||| |||| |||| || ||||||    | ||||   |||||| | ||      ||||| |
Db    525 TTCTCTAACCGGCTCGAGCAAGAAATCAGCTTCACCACTAACTCACTGCGAAAAAAGG 584

Qy    688 CGGAGCCATTCAGACTTCCGATGCCCTTACCATTACTGGAAACCAAGGGAGAGTCTCTTT 747
          |||||| |||   ||||  | | | | |||  ||| ||| ||||| ||  ||||  | |||
Db    585 TGGAGCGGATTGCTGCTCACGGAGAATAGCTCATCTTTCGGACAACAACCAAGCCACAATCAGATT 644

Qy    748 TTCTGACAATACTTCTTCGGATTCTGGAGCTGCAATTTTACAGAAGCCTCGGTGACTAT 807
          |||||  || | ||  |  |||||||||||| |     |||||||||  | ||| |||
Db    645 TTCTGGGAACACTGCTGTGAATTCTCGGGGGAGCAGTATATTCAGAAGCTTCTATGACGAT 704

Qy    808 TTCTAATAATGCTAAAGTTTCCTTTATTGACAATAAGGTCACAGGAGCGAGCTCCTCAAC 867
          ||||    |||   |||  | |||||| ||||||  ||| ||| ||||  |||  |
Db    705 TGCAGGTAACAACCACGTTGCTTTTGCTTTGCAACAATGCTGTTTCCGGTTCATCT------ 756

Qy    868 AACGGGGGGATATGTCAGGAGGTGCTCATCGTGCTTATAAAACTAGTACAGATACTAAGGT 927
          || |     |  ||| |||| | |  |||  |||||  |||||  |||  |  |  |||| |
Db    757 ------GATGGTTGCGGTGGAGCTATCCATTGTAGCAAAACACAGGTTCAGCACCGACCCT 809

Qy    928 CACCCTCACTCGAAATCAGATGTTACTCTTCAGCAACAACAATCATCGACACAGCGGGAGG 987
          || | |||| ||||| ||||  |||||   |||| || ||||  |  | |||||  |||||
Db    810 TACTATAAGAGATAACAAAGTCTTGATTTTTGAGGAAAAATACTTCTTCAGCAAAAGGTGG 869

Qy    988 AGCTATCTATGTGAAAAAGTCTGAACTGGCTTCCGGAGGACTTACCCTATTCAGTAGAAA 1047
          ||| ||  | | ||||  ||| ||| ||||| |  |  | || |||  | ||||| |  ||
Db    870 AGCGATTTACACCGATAAACTCATATTGACTTCTGTGGCCTACGGCATTTATCAATAA 929

Qy   1048 TAGTGTCAATGGAGTGAGGTACAGCTCCTAAAGTGGAGCCATAGCTATCGAAGATAGTGGGGA 1107
```

Db   2175 CACGTGTTGTTCAGGGTTTCTAAAGAGATTCCTATTTTCTGGATGCACAAATTACCTA 2234
Qy   2341 CACCCATACGGATAACGATCTGAAAACCAAGTATACACACATATCCTACTGTTAAAGGAAG 2400
Db   2235 TTGCCACACGGCCAACAACATGACAACGTCCTATACAGACTATCCTGAAGTGAAAGGTTC 2294
Qy   2401 CTGGGGGAATGATAGTTTCGCTTTAGAATTCGGTGGAAGAGCTCCGATTTGCTTAGATGA 2460
Db   2295 TTGGGGTAATGATACCCGGGCTTAACTTGTCTACTAGCGTACCTATCCCGGTATTTAG 2354
Qy   2461 AAGTGCTCTATTTGAGCAGTACATGCCCTTCATGAAATTGCAGTTTGTCTATGCACATCA 2520
Db   2355 TTCTTCTATCTTTGATAGTTATGACACCGTTGCAAAATTACAAGTTGTCATGCGCACCA 2414
Qy   2521 GGAAGGTTTTAAAGAACAGGGAACAGAAGCTCGTGAATTGGAAGTAGCCGTCTTGTGAA 2580
Db   2415 AGATGACTTTAAAGAACCAACAGAGAGGCCGGGTCTTTGAAAGCAGCAGCGATCTTCTCAA 2474
Qy   2581 TCTTGCCTTACCTATCGGGATCCGATTTGATAAGGAATCAGACTGCCAAGATGCAACGTA 2640
Db   2475 CGTTTCTGTGTACCTATAGGTATAAAATTTGAGAAACTCTCCATGAGAGAGAAGTGCTTA 2534
Qy   2641 CAATCTAACTCTTGGTTATACTGGGATCTTGTTCGTAGTAACCCCGACTGTACGGACAAC 2700
Db   2535 TGATCTTACACTGATGTATATACCTGATTCTTGGAAAACTTCGGTACGTCATCAATCCAAGCTGTATGACAGG 2594
Qy   2701 ACTGCGAATTAGGCGGTGATTCTTCGGTACGAAAACTTCGGTACCTTCGTCGATCTTCGTCTAGACAACAGCTTT 2760
Db   2595 ATTGGCGATCAATGACGTTCCCTGGTTAACCACAGCTACGAATCTTCTGCTAGACAACAGCTTT 2654
Qy   2761 AGTCCTTCGTGCAGGGAACCATTTTGCTTTAACTCAAAATTTGAAGCCTTTAGCCAATT 2820
Db   2655 CATAGTTCGCGCGGTAACCATATTGCCTTAACCTCTGGTGTTGAGATGTTCAGTCAGTT 2714
Qy   2821 TTCTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTAGACTTAGGAGCAAAATACCA 2880
Db   2715 TGGTTTCGAATTACGAAGCTCTTCAAGAAATTATAACGTAGATCTTCGGCGCTAAGGTCGC 2774
Qy   2881 ATTCTAA 2887
Db   2775 GTTCTAA 2781

RESULT 6
ABQ78033
ID   ABQ78033 standard; DNA; 2781 BP.
AC   ABQ78033;
XX
DT   03-OCT-2002 (first entry)
XX
DE   Chlamydia polynucleotide SEQ ID NO 56.
XX
KW   Chlamydia; antibacterial; vaccine; immune response; infection; gene; ds.
OS   Chlamydia psittaci.
XX
PN   WO200247718-A2.
XX
PD   20-JUN-2002.
XX
PF   17-DEC-2001; 2001WO-US48773.
XX
PR   15-DEC-2000; 2000US-255839P.
XX
PA   (TEXA) UNIV TEXAS SYSTEM.
XX
PI   Johnston SA;
XX
DR   WPI; 2002-583472/62.
DR   P-PSDB; ABB98228.
XX
PT   Vaccine useful for immunizing an animal, comprising at least one

Db 1995 GTTAGGAGCCACAACAAATACCTGAGAGAGGATTCTTAGTGTGGCTTTCTGTCAGTT 2054

Qy 2167 CTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGGAATCAAGAGTACAGTCTACGGAGGAAC 2226
Db 2055 ATTTGCAAAGATAAAGACTACCTTGTAAGCAAGAAGCCGCAAACGTCTATGCGGGTTC 2114

Qy 2227 TCTCTATTACCAGCA------CAACGAAACCTATATCTCTCCTTGCAAACTACGGCC 2280
Db 2115 TGTATATTATTCAGCATGTGAGCAGTTGATGATCTCACGCGGTTATTTAATGGGCCTAA 2174

Qy 2281 TTGTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCTTCTTTCAGGAAAACCTTAGCTA 2340
Db 2175 CACGTGTTGTTCAGGGTTTTCTAAAGAGATTCCTATTTTCTTGGATGCACAAATTACCTA 2234

Qy 2341 CACCCATACCGATAACGACCGATCTGAAAACCAAGTATACAACATATCCACTGTTAAAGGAAG 2400
Db 2235 TTGCCACCGGCCAACAACATGACAACGTCCTATACGTCTGAACGTGAAAGGTTC 2294

Qy 2401 CTGGGGAATGATAGTTTCGCTTTAGAATTCGGTGGAAGAGCTCCGATTTGCTTGAGATGA 2460
Db 2295 TTGGGTAATGATACCCTGGCTTAACTTTGTCTACTAGCGTACCTATCCCGGTATTTAG 2354

Qy 2461 AAGTGCTCTATTTGAGCAGTACATGCCCTTCATGAAATTCAGTTTGTCTATGCACATCA 2520
Db 2355 TTCTTCTATCTTTGATAGTTATGCACCGTTGCAAAATTACAAGTTGTCTATGCGCACCA 2414

Qy 2521 GGAAGGTTTAAAGAACAGGGAACAGAGCTCGTGAATTTGGAAGTAGCCGTCTTGTGAA 2580
Db 2415 AGATGACTTTAAAGAACCAACAACAGAAGGCCGGGTCTTTGAAAGCAGCGATCTTCTCAA 2474

Qy 2581 TCTTGCCTTACCTATCTGGGATCCGATTTGATAAGGAATCAGAACTGCCAAGATGCAACGTA 2640
Db 2475 CGTTTCTGTACCTATAGGTATAAGTTGGATCTTGTTCGTAGTGTAACCCGACTGTACGACAAC 2700

Qy 2641 CAATCTAACTCTTGGTTATACTGTGGATCTTGTTCGTAGTGTAACCCGACTGTACGACAAC 2700
Db 2535 TGATCTTACACTGATGTATATTACCTGATGTGTACCGTCATAATCCAAGCTGTATGACAGG 2594

Qy 2701 ACTGCGAATTAGCCGGTGATTCTGGTGATTCTTCGGAAAACCTTCGGTACGAATTGGCAAGACAAGCTTT 2760
Db 2595 ATTGGCGATCAATGACGTTTCCTGGTTAACCACAGCTACGAATCTGTCTGAGACAAGCTTT 2654

Qy 2761 AGTCCTTCGTCGCAGGGAACCATTTTGCTTTAACTCAAATTTGAAGCCTTAGCCAATT 2820
Db 2655 CATAGTTCGCGCGGGTAACCATATGCCTTAACCTTCGTGTTGTTGAGATGTTCAGTCAGTT 2714

Qy 2821 TTCTTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTAGACTTAGGAGCAAAATACCA 2880
Db 2715 TGGTTTCGAATTACGAAGCTCTTCAAGAAATTATAACGTAGATCTTGGGGCTAAGGTCGC 2774

Qy 2881 ATTCTAA 2887
Db 2775 GTTCTAA 2781

RESULT 7
ABX99200
ID   ABX99200 standard; DNA; 2781 BP.
XX
AC   ABX99200;
XX
DT   20-MAY-2003 (first entry)
XX
DE   C. psittaci genomic DNA sequence CP4 #12 #2.
XX
KW   DNA vaccine; chlamydia infection; blindness; mastitis; infertility;
KW   abortion; sexually transmitted disease; atherosclerotic plaque; ds;
KW   community-acquired pneumonia; coronary heart disease.
XX
OS   Chlamydia psittaci.
XX
PN   US2002183272-A1.
XX

Db 930   CAAAGTTACCCATGCTACA---CCTAAGGGTGGAGCTATTGGTATTGCTGCCAATGGAGA 986

Qy 1108 ATTGAGTTATCCGCCGATAGTGGTGACATTGTCTTTTAGGGA---TACAGTCACTTC 1164
Db 987   ATGTAGCTTAACCGCTGAACATGGGGATATTACTTTTGATAATAACCGATGGCCACACA 1046

Qy 1165 TACTACTCCTGGACGAATAGAAGTAGTATCGACGAGTGCAAAGATGACAGC 1224
Db 1047 AGACAAATGCTACACAATAAAAGAAAATGCCATTAACATTGAAGGCAATGGTAAATTCGTCAA 1106

Qy 1225 TTTGCGTTCTGCTGCTGTGTAGAGCCATCTATGATCCCATAACTACAGGATCATC 1284
Db 1107 CTTACGTGCAGCCGTCTGCGAAAGACGATTTCTTTCTATGATCCTATCACAGTTG------- 1159

Qy 1285 CACAACAGTTACGACGTGCTTAAAAGTTAATGAGACTCCGGCAGATTCTGCACTACAATA 1344
Db 1160 -----AAGGTAATGCTGCTGATCTTCTCACTTTGAATAAAGTCTGAGGGTGATAAAACGTA 1214

Qy 1345 TACAGGGAACATCATCTTCACAGAGGAAAAGTTATCAGAGACAGAGGCCGCAGATTCTAA 1404
Db 1215 TAATGGAAGAATTATTTTTTCAGGAGAGAAAGCTCACTGAAGAACAAGCTGCTGTTGCGGA 1274

Qy 1405 AAATCTTACTTCGAAGCTACTACAGCCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAA 1464
Db 1275 TAACCTAAAGACAAACATTTACACAGCCTATCACTTTAGCTGCTGGTGAACTTGTGTTTACG 1334

Qy 1465 ACATGGAGTGACTCTGCAGCATTCACTCAGGCATTCTCGTCTCGAAAT 1524
Db 1335 CAGCCGGTGTGGGAAGTAGAAGCAAAAACAGTCGTCGTGCAAAACAGCCAGGATCTTTCATTCTCAA 1394

Qy 1525 GGACGTAGGAACTACTCTA---GAACCTGCTGATACTAGCACCATAAACAATTTGGTCAT 1581
Db 1395 GGATGCAGGCACACAAAGTTATCCCGCAAAAACAGAGATGCTACACTGCAGAATCTGGCTAT 1454

Qy 1582 TAACATCAGTTCTATAGACGGTGCAAAGAAGGCAAAAATAGAAGCCAAAGCTACGTCAAA 1641
Db 1455 TAATCCGAATAACCTTAGATGGGAGAAAAAATTCGCCGTAGTCGATTGCTTGCTCTGGGAA 1514

Qy 1642 AAATCTGACTTTATCTGGAACCATCACTTTATTGGACCCGACGGGCACGTTTTATGAAAAA 1701
Db 1515 GAATGTGACTTTATCAGGTGCTATTGGCGTTATTGATCCTACAGGGAAGTTTTATGAAAA 1574

Qy 1702 TCATAGTTTAAGAAATCCTCAGTCCTACGACATCTTAGAGCTTCAAAGCTTCTGGAACTGT 1761
Db 1575 CCATAAGCTAAAATGATACGTTAGCTTTAGGAGGAATTCAACTTTCTCGGGAAAGGTTCGGT 1634

Qy 1762 AACAAGCACCGCAGTGACTCCGCAGATTCCATTACGGCCATCA 1821
Db 1635 GACAACAACCAACGTGCCTAGTCATGTTGTTGTGGTTGCTCAAACCCACTATGGTTATCA 1694

Qy 1822 GGGAAC--------TTGGGGCCCAATTGTTTGGGGGACCAGGGGCTTCTACGACTGC 1869
Db 1695 AGGAAAACTGGTCTGTCGTGGGTCAAAGATAATAACCTCTAAAACAACAAACAGC 1754

Qy 1870 AACCTTCAACTGACTAAAACTGGCTAAAACTGGCTATATCCCGAGCGTATCGGCTCTTTAGT 1929
Db 1755 AATCTTTACCTGGAATAACACGGATATGTTCCAAATCCTGAACGTCGTGCTCCGCTAGT 1814

Qy 1930 CCCTAATAGCTTATGGAATGCATTTATAGATATTAGCTCCATTATCTTATGGAGAC 1989
Db 1815 ACTTCAATAGCCTTTGGGGATCCTTTATGATTTACGTTCTATTCAAGATGTCTTGGAACG 1874

Qy 1990 TGCAAACGAAGGGTTGC---AGGGAGACCGTGCTTTTGGTGTGCGTGGATTATCTAACTT 2046
Db 1875 TAGTTGTGATAGTATTCTTGAGACACGTCGTCGTGTTGGGTCTTGGGGTCTTGTGAATTGGGAACTT 1934

Qy 2047 CTTCCATAAGGATAGTAGTACAAAAACACGACGCGGGTTTCGCCATTTGAGTGGCGGGTTATGT 2106
Db 1935 CTTCCATAAAGATGCTGGAAATGCCGAAAATCGCAAATTCCGTCATATCAGTTCGGGATATGT 1994

Qy 2107 CATAGGAGGAAACCTACATACTTGTTCAGATAAGAGAATTCTTAGTGCTGCATTTGTCAGCT 2166

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PD    05-DEC-2002.
XX
PF    17-DEC-2001; 2001US-0023437.
XX
PR    16-AUG-2000; 2000US-225839P.
XX
PA    (JOHN/) JOHNSTON S A.
PA    (STEM/) STEMKE-HALE K.
PA    (SYKE/) SYKES K F.
PA    (KALT/) KALTENBOECK B.
XX
PI    Johnston SA, Stemke-Hale K, Sykes KF, Kaltenboeck B;
XX
DR    WPI; 2003-328634/31.
DR    P-PSDB; ABU66284.
XX
PT    New vaccine comprising a polynucleotide with a Chlamydia sequence or a
PT    Chlamydia antigen, for inducing an immune response against Chlamydia
PT    psitacci, Chlamydia pneumoniae, other Chlamydia species, or a
PT    non-chlamydia infection -
XX
PS    Claim 6; Page 74-76; 100pp; English.
XX
CC    The invention relates to a vaccine comprising a pharmaceutical carrier
CC    and at least one polynucleotide having a Chlamydia sequence or at least
CC    one Chlamydia antigen. The polynucleotide sequences are obtained
CC    from cloned expression library of fragmented genomic DNA (expressed in
CC    the vector pCMV-UBi(+P3). Also included are immunising an animal
CC    comprising providing to the animal at least one Chlamydia antigen or its
CC    antigenic fragment (expressed from the cloned polynucleotides) to induce
CC    an immune response (the proteins are chosen by transforming a vertebrate
CC    animal with constituents of the library and choosing those which elicit
CC    the best immune response, and then expressing those clones in cell
CC    culture and purifying the protein), preparing antibodies against a
CC    Chlamydia antigen (comprising identifying a Chlamydia antigen that
CC    confers immune resistance against chlamydia bacterial infection when
CC    challenged with the Chlamydia species in which the antigen was prepared,
CC    generating an immune response in a vertebrate animal with the identified
CC    antigen, and obtaining antibodies produced in the animal, the antibodies
CC    are used to assay for the presence of chlamydia infection in a vertebrate
CC    animal) and testing for antigens for a first disease state/infectious
CC    agent (comprising determining an antigenic polypeptide or a nucleic acid
CC    encoding an antigenic polypeptide from a second disease state or
CC    infectious agent, obtaining a homologue of the antigenic polypeptide or
CC    a nucleic acid encoding an antigenic polypeptide from a second disease
CC    state or infectious agent for the first disease state/infectious
CC    agent, and testing the homology to see if it is an antigenic
CC    polypeptide or a nucleic acid encoding an antigenic polypeptide for the
CC    first disease state or infectious agent). The vaccine, antigens and
CC    polynucleotides are useful for inducing a protective immune response in
CC    vertebrate animals against C. psitacci, C. pneumoniae, other species of
CC    Chlamydia, or a non-chlamydia infection. The antigens are also useful for
CC    antibody preparation techniques. Chlamydia species are responsible
CC    for blindness, sexually transmitted disease, community-acquired
CC    pneumonia and act as co-factors in atherosclerotic plaque formation in
CC    coronary heart disease. C. psitacci in particular is a cause of mastitis,
CC    infertility and abortion in cattle. The present sequence is one of the
CC    cloned Chlamydia psittaci genomic DNA fragments of the invention.
XX
SQ    Sequence 2781 BP; 818 A; 555 C; 610 G; 798 T; 0 other;

Query Match     18.2%;    Score 546.6;    DB 25;    Length 2781;
Best Local Similarity   53.7%;
Matches 1390;    Conservative    0;    Mismatches 1134;    Indels    63;    Gaps    10;
         Pred. No. 4.2e-141;
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```
Qy    448 TACCACGTTTATAGGGTTTCTTGCTATCTTTATTGCTCTCCTGGAAGTTCGATAAC 507
              ||||  || |    || || ||||||||   |    |||  |  |||||||  ||
Db    348 TCTTACGCTGACAGATTTTTCTAAGTTGAGCTTTAAGGAATGCCCATCTTCTTAGTGAA 407

Qy    508 TACCGGCAAAGGAGCCGTTAGCTGCTTAGCTGTAGTTGAGTTTGACAAAAATGTCAG 567
              ||| ||| ||||| || |    | ||  |           ||| |  |||| ||
Db    408 TACTCGAAAAGGGGC---TATGAAATCCGGAGGAGGCATTAAACTTAGCGAATAATGCCAG 464

Qy    568 TTTGCTTCAGCAAAACTTTCAACGGATAATGCGTGTCTATCACCGCCAAAAACTCT 627
              |||| | ||| || ||  | ||   ||  ||  | |||    | |||||||| |||
Db    465 TATTCTGTTTGATCAGACATTCCGCTGAACATTCCGAGAAATGGTGGAGCCATCTCTTGCAAAGCTTT 524

Qy    628 TTCATTAACAGGGACTACACATGTCAGCTCTGTTTTCTGAAAATACCTCCTCAAAGAAAGG 687
              |||  |||| ||| || | ||| |||| |  ||  | |||||  |||  |  |||||||||
Db    525 TTCTCTAACCGGCTCGAGCAAAGAAATCAGCTTCACCACTAACTCTACTCGCGAAAAAAGG 584

Qy    688 CGGAGCCATTCAGACTTCCGATGCCCTTACCATTCCGGAAACCAAGGGAGAAGTCTCTT 747
              ||||||  || ||| ||  |    |  |   | | | || | ||||| | |    |||
Db    585 TGGAGCGATTGCTGCTACGGGAATAGCTCATCTTTCGGACAACAACCAAGGCACAATCAGATT 644

Qy    748 TTCTGACAATACTTCTTCGGAGTCTGGAGCTGCAATTTTTACAGAAGCCTCGGTGACTAT 807
              |||||  ||||| | | | |||  |||||| ||| ||||| ||||||| |  || |  |
Db    645 TTCTGGGAACACTGCTGTGAATTCTGGGGAGCAGTATATTCAGAAGCTTCTATGACGAT 704

Qy    808 TTCTAATAATGCTAAAGTTCCTTTATTGACAATAAGGTCACAGGAGCGGAGCTCCTCAAC 867
              | | || |||   || ||||  |  |||| || |  |||| | | || |||| |||  | 
Db    705 TGCAGGTAACAACCACGTTGCTTTTAGCAACAATGCTGTTTCCGGTTCATCT-------  756

Qy    868 AACGGGGATATGTCAGGAGGTGCTATCTGTCTTATAAAACTAGTACAGATACTAAGGT 927
                     || ||   | |||||| ||||   |||||| |||| ||||    | ||| |
Db    757 -------GATGGTTGCGGTGGAGCTATCCATTGGTTCAGCAAAACAGGTTCAGCCACCGACCCT 809

Qy    928 CACCCTCACTGGAAATCACGATGTTACTCTTCAGCAACAATACATCGACAACAGCGGGAGG 987
              || | | | || || | |   ||| ||| ||||||| |||| | | | |||| | |  ||
Db    810 TACTATAAGAGATAACAAAGTCTTGATTTTGAGGAAAAATACTTCTTCAGCAAAAGGTGG 869

Qy    988 AGCTATCTATGTGAAAAAGTCGAACTGGCTTCCGGAGGACTTACCCTATTCAGTAGAAA 1047
              ||| || ||   || |     ||   |  | ||||  | ||| | | ||  ||| |
Db    870 AGCGATTTACACCGATAAACTCATATTGACTTTCGGTGGGCCTACGCATTTATCCAATAA 929

Qy   1048 TAGTGTCAATGGAGGTACAGCTCCTCCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGA 1107
               ||| | |||   || ||| ||       |||||||||||  | |||| |   |||| |||||
Db    930 CAAAGTTACCCATGCTACA---CCTAAGGGTGGAGCCTATTGGTATTGCTGCCAATGGAGA 986

Qy   1108 ATTGAGTTTATCCCGCGATAGTGGTGACATTGTCTTTTTAGGGAA---TACAGTGCACTTC 1164
              ||| ||  ||||  | ||||  ||||   ||| |  || |||||    || |||||| |
Db    987 ATGTAGCTTAACCGCTGAACATGGGGATATTACTTTTGTAATAACCGTGCACGCCACACA 1046

Qy   1165 TACTACTCCTGGGACGAATAGAAGTAGTATCGACTTAGGAACGAGTGCAAAGATGACAGC 1224
              || || | |  ||| || |  ||| || || ||   |||| | || |||| |||||||| 
Db   1047 AGACAATGCTACAATAAAAAGAAATGCCATTAACATTGAAGGCAATGGTAAATTCGTCAA 1106

Qy   1225 TTTGGGTTCTGCTCGGTGTGGTAGAGCCATCATCTCTATGATCCCATAACTACAGGATCATC 1284
               || | |  ||| | ||| ||  |||| ||  |  |||||||| | || | ||||  |
Db   1107 CTTACGTGCAGCGCTCGGAGAGCAAGACGATTTCTTTCTTCTATGATCTCTATCACAGTTG------- 1159

Qy   1285 CACAACAGTTACAGATGTCTTAAAGTTAATGAGACTCCGGCGAGATTCTGCACTACAATA 1344
              ||| |||||||| | ||| || |||||||| | ||| |   |||  || || || |
Db   1160 ----AAGGTAATGCTGCTGATCTTCACTTTGAATAAGCTGAGGGTGATAAAACGTA 1214

Qy   1345 TACAGGGGACACATCATCTTCACAGGAGAAAAGTTATCAGAGACAGCAGAGGCCGCAGATTCTAA 1404
              || ||| || | | || ||||||||||||| || |||  || ||||| | ||| ||| |
Db   1215 TAATGGAAGAATTATTTTTTTCAGGAGAAAAGCTTCACTGGAGAAAGCAAGAACAAGCTGCTGTTGCGGA 1274

Qy   1405 AAATCTTACTTCGGAGCTACTACAGCCTGTAACTCTTCGAGGAGTACTCTATCTTTAAA 1464
               ||  ||| | | || ||  |||||||| |    |   |  || | | | | |||
Db   1275 TAACCTAAAGACAACATTTACAGCCTATCACTCACTTTAGCTGTCTGGTGAACTTGTTACG 1334

Qy   1465 ACATGGAGTGACTCTGCAGACATTCACTCAACAGAGACTTCAACTCGTCTCGAAAT 1524
              || |  |  | |  | ||| |||  || ||||||   || |||  || ||| |||
Db   1335 CAGCGGGTGTGGAAGTAGGAAGCAAAAACAGTCGTGCAAACAGCAGGATCTTTGATTCTGAT 1394

Qy   1525 GGACTAGGAACTACTCTA--GAACCTGCTGATACTAGCACCATAAACAAATTTGGTCAT 1581
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Db 2475 CGTTTCTGTACCTATAGGTATAAAATTTGAGAAACTCTCCTATGGAGAGAGAAGAGTGCTTA 2534
          |||  ||||   ||    ||||||||||||||||||
Qy 2641 CAATCTAACTCTTGGTATACTGTGGATCTGTTCGTAGTAACCCGACTGTACGACAAC 2700
          ||| ||||   ||| |||    ||||
Db 2535 TGATCTTACACTGATGTATATACCTGATGTGTACCGTCATAATCCAAGCTGTATGACAGG 2594
          |||||||      |||||   |||||
Qy 2701 ACTGCGAATTAGCGCGTGATTCTTCGGAAAACCTTCGGTACGAAGCTTTGGCAAGACAAGCTTT 2760
          |||| ||||   |||||||||||
Db 2595 ATTGGCGATCAATGACGTTTCCTGGTTAACCACAGCTACGAATCTTGCTAGACAAGCTTT 2654
          ||| |||  |||   ||||||||||||
Qy 2761 AGTCCTTGCGAGGGAACCATTTTGCTTAACTCAAATTTGAAGGCCTTTAACGTCCAATT 2820
          ||| ||||||| ||  ||||||||||
Db 2655 CATAGTTCGCGCGCGGGTAACCATATTGCCTTAACCTCTCGGTGTTGAGATGTTCAGTCAGTT 2714
          |||| || |  |||  |||||||
Qy 2821 TTCTTTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTAGACTTAGGACTGCAAAATACCA 2880
          ||||  ||||| ||||| ||||
Db 2715 TGGTTTCGAATTACGAAGCTCTTCAAGAAGAATTATAACGTAGATCTTGGCGCTAAGGTCGC 2774
          |||  ||||||
Qy 2881 ATTCTAA 2887
          |||||||
Db 2775 GTTCTAA 2781
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RESULT 8
AAC81914

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ID   AAC81914 standard; DNA; 273254 BP.
XX
AC   AAC81914;
XX
DT   27-FEB-2001   (first entry)
XX
DE   Chlamydia pneumoniae genome DNA.
XX
KW   Genome; diagnosis; vaccine; ds.
XX
OS   Chlamydia pneumoniae.
XX
PN   WO200027994-A2.
XX
PD   18-MAY-2000.
XX
PF   12-NOV-1999;   99WO-US26923.
XX
PR   12-NOV-1998;   98US-0108279.
PR   08-APR-1999;   99US-0128606.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Stephens R,   Mitchell W,   Kalman S,   Davis R;
XX
DR   WPI; 2000-376516/32.
XX
PT   Isolated nucleic acid for use in diagnostic and analytical methods
PT   encodes genomic sequence of Chlamydia pneumoniae -
XX
PS   Claim 2; Page 128-320; 320pp; English.
XX
CC   This invention describes a novel nucleic acid (N1) encoding a Chlamydia
CC   pneumoniae protein (P1), given in the specification. The isolated nucleic
CC   acid is useful for diagnostic and analytical methods, such as,
CC   hybridization-based assays or amplification-based assays. The protein may
CC   be used for diagnostic purposes, for their enzymatic or structural
CC   activity, or as a vaccine. The invention also describes (1) a probe
CC   comprising a hybridizing fragment of N1; (2) an isolated nucleic acid
CC   (N2) that hybridizes under stringent conditions to N1; (3) an expression
CC   cassette comprising N1 under the transcriptional regulation of a
CC   transcriptional initiation region functional in an expression host, and a
CC   transcriptional termination region; (4) a cell comprising an expression
CC   cassette of (3) as part of an extrachromosomal element or integrated into
CC   the genome of a host cell as a result of induction of the expression
CC   cassette into the host cell, and the cellular progeny of the host cell;
CC   (5) a method for producing a P1 comprising growing a cell of (4) where
CC   the protein is expressed and isolating the protein free of other
```

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Db 1395 GGATGCGGAGGCACAAAGTTATCCGCAAAAACAGAAGATGCTACACTGACGAATCTGCTAT 1454
          ||||  ||||   |||      ||||||||||
Qy 1582 TAACATCAGTTCTATAGACGGTGCAAAGAAGGCAAAATAGAAACCAAAGCTACGTCAAA 1641
          ||| ||||   |||  |||   ||||
Db 1455 TAATCCGAATACCTTAGATGGGAAAAAAATTCGCCGTAGTCGATGCCGTGTGCTGGGAA 1514
          |||  ||||||||  |||   ||||
Qy 1642 AAATCTGACTTATCTGAACCATCACTTATTGGACCGACGGCACGTTTTATGAAAA 1701
          ||||||||||  |||||||||||
Db 1515 GAATGTGACTTTATCAGGTGCTTATTGGCGTTATTGATCCTACAGGGAAGTTTTATGAAAA 1574
          |||   ||||   |||   |||||
Qy 1702 TCATAGTTTAAGAAATCCTCAGTCCTACGACATCTTAGAGCTCAAAGCTTCTGGAACTGT 1761
          |||| ||||  ||||   |||||
Db 1575 CCATAAGCTAAATGATACGTTAGCTTTAGGAGGAATTCAACTTTCTGGGAAAGGTTCGGT 1634
          |||  ||| ||   ||||||||
Qy 1762 AACAAGCACCGCAGTGACTCCAGATCCTATAATGGGTGAGAAATTCCATTACGGCTATCA 1821
          ||| |  ||||  |||   |||   ||||
Db 1635 GACAACAACCAACGTGCCTAGTCATGTTGTTGGTGTTGCTGAAACCCACTATGGTTATCA 1694
          |||   |||   ||||||||
Qy 1822 GGGAAC--------TTGGGGCCCAATTGTTGGGGGACAGGGGCTTCTACGACTGC 1869
          ||||||           ||||
Db 1695 AGGAAACTGGTCTGTCGTGGTCAAGATAATAACTCTGATCCTAAAACACAAACAGC 1754
          ||||||  ||||
Qy 1870 AACCTTCAACTGACTAAAACTGGCTATATTCCTAATCCCGAGCGTATCGGCTCTTTAGT 1929
          |||   ||||||   ||||   ||||||||
Db 1755 AATCTTTACCTGGAATAAAACAGGATATGTTCCAAATCCTGAACGTCGTGCTCCGGTAGT 1814
          |||  ||| ||||   ||||   |||||
Qy 1930 CCCTAATAGCTTATGGAATGCATTTATGATATTAGCTCTCCCATTATCTTATGAGAAC 1989
          |||||   ||  ||||   |||||||||
Db 1815 ACTCAATAGCCCTTTGGGGATCCTTTATAGATTTACGTTCTATTCAAGATGTCTTGAAACG 1874
          |||||||||   ||||   ||||
Qy 1990 TGCAAACGAAGGGTTGC---AGGGAGACACGGTGCTTTTGGTGTGCTCGGATTATCTAACTT 2046
          |||||||||   |||||   ||||||||
Db 1875 TAGTGTTGATAGTATTCTTGAGACACGTTCGTGGTTGTTGGGTCTCTGGAAATTGGGAACTT 1934
          |||   ||||   ||||||||||
Qy 2047 CTTCCATAAGGATAGTACAAAAAACACGACGCGGGTTTCGCCATTGAGTGGCGGTTATGT 2106
          |||||||| |||||   |||   |||||||
Db 1935 CTTCCATAAAGATCGGAATGCTGAAAATCGCAAATTCCGTCATATCAGTTCGGGATATGT 1994
          |||||||||   |||||||
Qy 2107 CATAGGAGGAAACCTACATACTTGTTCAGATAAGATTCTTAGTGCTGCTCATTTGTCAGCT 2166
          |||||||   |||   |||||||||||
Db 1995 GTTAGGAGCCAACAACAAATACCTCGAGAGAGGATTCCTCTTAGTGTGGCTTTCTGTCAGTT 2054
          |||||||   ||||||||
Qy 2167 CTTTGGAGAGATAGAGACTACTTTGTAGCTAAGAATCAAGGTACAGTGTTACGAGGGAAC 2226
          |||||||||||   ||||   ||||||||||
Db 2055 ATTTGCAAAAGATAAAGACTACCTTGTAAGCAAGAACGCCCGCAAACGTCTATGCGGGTTC 2114
          |||   |||||||||
Qy 2227 TCTCTATTACCAGCA------CAACGAAACCTATATCTCTCTTCCTTGCAAACTACCGGCC 2280
          ||||||||||||          |||||
Db 2115 TGTATATTATCAGCATGTGAGCAAGTTTGATGATCTCACGCGCGTTATTTAATGGGCCTAA 2174
          ||| |||||||||
Qy 2281 TTGTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCCTTTTCAGGAAACCTTAGCTA 2340
          |||||   |||||||||   |||||
Db 2175 CACGTGTTGTTGTTCAGGGGTTTTCAGGGTTTTCAAAGAGATTCCTATTTTCTTGGATGCACAAATTACCTA 2234
          ||||   ||||||||   ||||
Qy 2341 CACCCATACGGATAACGAATCTGAAAACCAAGTATACAACATATCTACTGTTAAAGGAAG 2400
          |||||||   |||||   |||||||
Db 2235 TTGCCACACGGCCAACAACATGACAACGTCCTATACAGACTATCCTGAAGTGAAAAGGTTC 2294
          |||||||   ||||||||||
Qy 2401 CTGGGGGAATGATGATGTTTCGCTTTAGAATTCGGTGGAAGAGCTCCGATTTGCTTAGATGA 2460
          |||||||   ||||||   ||||
Db 2295 TTGGGGTAATGATACCCTGGCTTAACTTTGTCTACTAGCGTACCTATCCCCGTATTTAG 2354
          |||||||   ||||||||||
Qy 2461 AAGTGCTCTATTTGAGCAGTACATGCCCTTCATGAAATTGCAGTTGTCTATGCACATCA 2520
          |||||||||   |||||   |||||||
Db 2355 TTCTTCTATCTTTGATAGTTATGCACCGTTGCAAAATTACAAGTTGTCTATGCGCCACCA 2414
          |||||||   ||||||||
Qy 2521 GGAAGGTTTAAAGAACAACAGGGAACAGGAGCTCGTGGAAGAGTGCCGTCTTGTGAA 2580
          ||||||||||||   |||   |||||||
Db 2415 AGATGACTTTAAAGAACCAACAACACAGAGAGGCCGGGTCTTTGAAAGCAGCGATCTTCTCAA 2474
          ||||||||||||
Qy 2581 TCTTTGCCTTACCTATCGGGATCCGATTTGATAAGGAATCAGATCAGACTGCCAAGATGCACGTA 2640
          ||||||   |||||||||
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CC   proteins; (6) a purified polypeptide composition comprising at least 50
CC   weight % of P1; and (7) a monoclonal antibody binding specifically to the
CC   peptide of (6).
XX
SQ   Sequence 273254 BP; 76423 A; 51054 C; 61965 G; 83812 T; 0 other;

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Query Match             17.7%;  Score 531.2;  DB 21;  Length 273254;
Best Local Similarity   53.0%;
Matches 1415;  Conservative    0;  Mismatches 1183;  Indels   74;  Gaps   10;
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Qy      247 TGCTGGAACTACCTACCTATTTAAGGAAATGCACTCTAGAAAAATATTCCTGGAACAGG 306
Db    98349 TACTGGAATAGACTATACTCGAGAGATAAACTCTGCAAAACCTTGGGGATTCGG-    98407

Qy      307 CACAGCAATCACACAAAAGCTGTTTAACAACACTAAGGCGATTTGACTTGCACAGTGA  366
Db    98408 --CAGCTTTAACGAAGGTTGTTTTTCTGACACTACGGAATCTTTAAGCTTTGCCGGTAA 98465

Qy      367 CGGGAACTCTCTATTGTTCCAAACGGTGGATGCGAGGGACTGTGAGCAGGGCTGCTGTTAA 426
Db    98466 GGGGTACTTCACTTTCTTCTTTTTTAAATATTAAGTCTAGTGCTGCGGAAGGCCAGCACTTTCGT 98525

Qy      427 CAGCAGCGTGGTGTAGATAAATCTACCACGTTTATAGGGTTTTCTTCGCTATCTTTTATTGC 486
Db    98526 TACAACTGATAAAAATCTGTCGCTAACAGGATTTCGAGTCTTACTTTCTTAGCTGGCGCCCC 98585

Qy      487 GTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGCCGTTAGCTGCTCTACGGGTAGCTT 546
Db    98586 ATCATCGGTAATCACAACCCCCTCAGGAAAAAGGTGCAGTTAAAATGTGGAGGGGGATC---T 98642

Qy      547 GAGTTTGACAAAAAATGTCAGTTTGCTCTTCAGCAAAACTTTCAACGGATAATGCGCGG 606
Db    98643 TACATTTGATAGCGAACATATTTTTATTTTAAACAAGATTACTACTGTGAGGGAAAATGGCGG 98702

Qy      607 TGCTATCACCGCAAAAACTCTTTCATTAACAGGGACTACAATGTCAGCTCTCGTTTTCTGA 666
Db    98703 AGCCATTTCTACCAAGAATCTTTCTTTGTGAAAAAAACAGCACGGGATCGATTTCTTTTTGAAGG 98762

Qy      667 AAAATA------CCTCCTCAAAGAAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTAC 717
Db    98763 GAATAAATCGAGCGCAACAGGGAAAAAAGGTGGGGTATTGGGGCTATTGTGCTACTGGTACTGTAGA 98822

Qy      718 CATTACTGGAAACCAAGGGAAGCTCTCTTTTTTCTGACAATACTCTTCTTCGGATTCTGGAGC 777
Db    98823 TATTACAAATAATAATAATACGGCCTCCTACCCCTTCTCGAACAATATTGCTGAAGCTGCAGTGG 98882

Qy      778 TGCAATTTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTTCCTTTATTGA 837
Db    98883 AGCTATAAATAGCACAGGAAATCGTACAAATTACAGGGAATACGTCTCTTGTATTTTTCTGA 98942

Qy      838 CAATAAGGTCACAGGAGCGAGCTCCTCCTCAACAACGGGGATATGTGTCAGGAGGAGTGCTATCTG 897
Db    98943 AAATAGTGTGAC---AGCGACACCGCAGGGGTATCTCCTTCTGAAATGGGAGATGCCG----    98995

Qy      898 TGCTTATAAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTT 957
Db    98996 --------ATGTTACCATATATCTGGGAATCAGATCAGAGTGTAACTTT 99029

Qy      958 CAGCAACAATACATGCGACAACAGCCGGAGCGCTATCTATGTGAAAAAGCTCGAACTGGC 1017
Db    99030 CTCAGGAAAACCAAGCTGTAGCTATGGCGAGCCATTTATGCTAAGAAGCTTACACTGGC 99089

Qy     1018 TTCCGGAGGACT-----TACCCTACTCAGTAGAAAAATAGTGCAATGGAGAAGCTCCT 1072
Db    99090 TTCCGGGGGGGGGTATCTCCTTTTCAACAATATAGTTCAACAATATAGTCCAAGGTACCACTGCAGGT 99149

Qy     1073 AAAGGTGGAGCCATAGCTATCGAAGATATCGGGAATTGGGGAATTATGAGTTTATCCGCCGATAGTGGT 1132
Db    99150 TTCCGGGGGGGGGTCCGGAAATGCCTGGAGCTGAGAGTGTAGTCTTTCAGCAGGAAGCAGAGG 99209

Qy     1133 GACATTGTCTCTTTTAGGGAATACGTCACTTCTACTACTCCC---TGGGACTACAAATAGAAGT 1189
Db    99210 GACATTACCTTCAATGGAATGCCCATTGTTGCAACTACACACCACAAACTACAACGAAATGT 99269
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Qy     1190 AGTATCGACTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCGTCTGCTGGTGTAGAGCC 1249
Db    99270 TCTATTGACATAGGATCTACTGCAAAGAATCACGAATTTACGTCGCAATATCTGGCGATAGC 99329

Qy     1250 ATCTACTTCTATGATCCATAACTACACAGGATCATCCACAACAGTTACAGATGTCTTAAAA 1309
Db    99330 ATCTTTTCTACGATCCGATTCGCTAATACGGCTGCGGATTCTAATACGCTTACAGATACTTTAAT 99389

Qy     1310 GTTAATGAGACTGCCGGACAGATTCTGCACTACACATACAGGGAACATCATCTTCACAGGA 1369
Db    99390 CTCAATAAGGCTGATGCAGGTAGTAGTACAGAGATTATAGTGGGTCGATTGTTTTTTCTGT 99449

Qy     1370 GAAAAGTTATCAGAGACAGAGGCCGCAGATTCTAAAAATCTTACTTCTGAAGCTACTACAG 1429
Db    99450 GAAAAGCCTCTGAAGATGAAGCAAAAGTGCAGCAAAAGTGTCACTCTCGATAACGAAA 99509

Qy     1430 CCTGTAACTCTTTCAGGAGTGACTCTGATGCGAGGGACTCTGTAGCAGGGCGTCTGCTGTTAA 1489
Db    99510 CCTGTAACTCTAACTGCAGGAAAATTAGTACTTAAACGGTGTCACTCTCGATACGAAA 99569

Qy     1490 GCATTCACTCAACGACAGCAGATTCTCGTCTGAAATGGACTAGGAACTACTCTAGAACC- 1548
Db    99570 GGCTTTACTCAGACCGCGGGGTTCCTCTGTTATTATTGGACTCTTATAGAGCGGTCA 99629

Qy     1549 --TGCTGATACTAGCACCCATAAACAATTGGTCATTAACATCAGTTCTAACGGGGTCA 1606
Db    99630 AGTACAGAGGAGGTCACTTTTTAACGGTCTTTCCATTCCTGTAGACTCTTTAGGCGGAGGT 99689

Qy     1607 AAGAAGGCAAAAATAGAAACCAAAGCTACGTCAAAAATCTGACTTTATCTGGAACCATC 1666
Db    99690 AAGAAAGTTGTAATTGCTCGTTCGCAGCAAGTAAAAATAGTAGCCCCTTAGTGTGTCCGATT 99749

Qy     1667 ACTTTATTGGACCCGACGGGCACGTTTTATGAAAATCAGAATAGTTTAAGAAAATCCTCAGTCC 1726
Db    99750 CTTCTTTTGGATAACCAAGGAAGTGCTTATGAAAATCACGACTTAGGAAAAACTCAAGAC 99809

Qy     1727 TACGACATCTTAGAGCTCAAAGCTTCGCTCTCGGGTAACAAGCACCGGACTCCAGAT 1786
Db    99810 TTTTCATTGTGCGAGCTCGTCCTGGGTACTGGTACTGTAGACTGTTCCAGCCGTT 99869

Qy     1787 CCTATAATGGGTGAGAAATTCCATTCAGGGAACTTGGGCGCCCAATTGTTTTGG 1846
Db    99870 CCTACAGTAGCAACTCCTACGCACTATGGGTATCAAGGTATCAAGGACTTGGGTT 99929

Qy     1847 G---------GGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAAAAACTGGC 1894
Db    99930 GATGATACCGCAAGCACTCCAAAGACTAAGACAGCGACATTAGCTTGGACCAATACAGGC 99989

Qy     1895 TATATTCCTAATCCCGAGCGTATCGGCTTCTTAGTCGCTCTTAGTATAGTCCTTAGGATGCATTT 1954
Db    99990 TACCTTCCGAATCCTGAGCGTGCAAGGATCCTTTAGTTCTTAGTAGCCTTTGGGATCTTTT 100049

Qy     1955 ATAGATATTAGTCTCTCTCCATTATCTTCATTGAAATCAGATGTTACTCTT 2014
Db   100050 TCAGACCATCCAAGCGATTCAAGGTGTCATAGGAGAGTGCTTTGACTCTTTGTTCAGAT 100109

Qy     2015 CGTGCTCTTTTGGTGTGCTGGATTATCTTCTATTGTGGAATAAAGCTGGAAAAAAACACGA 2074
Db   100110 CGAGGCTTCGTGGGCTTGCGGGAGTGCGCGCCAATTTCTTAGATAAGAAAGGGGGAAAAA 100169

Qy     2075 CGCGGGTTCCGCCATTTGAGTGGCCGGTTATGTCAGTGGCGGATCAATATTGTTCA 2134
Db   100170 CGCAAATACCGTCATCAATCTGGTGGATATGTCATCGGAGGTGCAGCGGCCAAACTTGTTCT 100229

Qy     2135 GATAAGAATTCTTAGTTGCTGCATTTGTGCAGTCTTTTGTCAACGTGCAAAGGGTTGCAGGGAGAC 2194
Db   100230 GAAAACTTAATTAGCTTTGCCTTTGCCAACTCTTTGGTTAGCGATAAAGATTTTCTTAGTC 100289

Qy     2195 GCTAAGAAATCATACTGATACCTATGCAGGAGCGCCTTCTATATCCAACACCATTACAGAATGT 2254
Db   100290 GCTAAAAATCATACTGATACCTATGCAGGAGCGCCTTCTATATCCAACACCATTACGAATGT 100349
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Qy    2255  ATCTCTCTTCCTTGCAAACTACGGCCTTGTTCGTTGTTGTCTTATGTTCCTACAGAGATTCCT  2314
                  ||||||                   |||||
Db  100350  AGTGGGTTCATAGGTTGTCTCCTTAGATAAA---CTTCCTGCTCTTGGAGTCATAAACCC  100406

Qy    2315  GTTCTCTTTCAGGAAACCTTAGCTACACCCATACGGATAAGATCTGAAAACCAAGTAT  2374
                  |||||              |||        |||||
Db  100407  CTCGTTTTAGAGAGGGCAGCTCGCTTATAGCCACGTCAGTAATGATCTGAAGACAAAGTAT  100466

Qy    2375  ACACACATATCCTACTGTTGTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTAGAATTCGGT  2434
                  ||| ||||||            |||||||||
Db  100467  ACTGCGTATCCTGAGGTGAAAGGTTCTTGGGGGAATAATGCTTTTAACATGATGTTGGGA  100526

Qy    2435  GGAAGAGCTCCGATTTGCTTAGATGAGAAAGTGCTCTATTTGAGCAGTACATGCCCTTCATG  2494
                  |||||                ||||||
Db  100527  GCTTCTTCTCCATTCTTATCCTGAATACCTGCGATTGTTTGATACCTATGCTCCATACATC  100586

Qy    2495  AAATTGCAGTTTGTCTATGCACATCAGGAAGGTTTAAAGAACAGGGAACAGAAGCTCGT  2554
                  |||              ||| |||||
Db  100587  AAACTGAATCTGACCTATATACGTCAGGACAGCTTCTCGGAGAAAGGTACAGAAGGAAGA  100646

Qy    2555  GAATTGGAAGTAGCCGTCTTGTGAATCTTGCCTACCTATCGGGATCCGATTTGATAAG  2614
                  ||||                 ||||||
Db  100647  TCTTTTGTAGACAGCAACCTCTTCAATTTATCTTGCCTATAGGGGTGAAGTTTGAGAAG  100706

Qy    2615  GAATCAGACTGCCAAGATGCAAGCTACGTACAATCTAACTCTTGGTTATACTGTTGGGATCTTGTT  2674
                  |||||||              ||||||
Db  100707  TTCTCTGATTGTAATGACTTTTCTTATGATCGACTTTATCCTATGTTCCTGATCTTTATC  100766

Qy    2675  CGTAGTAACCCCGACTGTACGACAACACTGCCAATTAGCGGTGATTCTTGGAAAACCTTC  2734
                  ||||               ||  ||||||
Db  100767  CGCAATGATCCCAAATGCACTTGTAATCAGCCGGAGCCCTTGTGGAAACTTAT  100826

Qy    2735  GGTACGAATTTGGCAAGACAAGCTTTAGTCCTTCGGTGCAGGGAACCATTTTTGCTTTAAC  2794
                  |||||                |||| |||
Db  100827  GCCAATAACTTAGCACGACGACAGGCCTTGCAAGTGGCGTCCAGCCAGTCACTACGCCTTTCTCT  100886

Qy    2795  TCAAATTTTGAAGCCTTTAGCCAATTTCTTTTGAATTGCGTGGGTCATCTCGCAATTAC  2854
                  |||||                 |||||
Db  100887  CCTATGTTTGAAGTGCTCGGCCAGTTTGTCTTGTGGATCCTGCGTGGATTTAT  100946

Qy    2855  AATGTAGACTTAGGAGCAAAATAACCAATTCTA  2886
                  |||||||        |||||||||
Db  100947  AATGTAGATCTTGGGGGTAAGTTCCAATTCTA  100978
```

RESULT 9
AAX06817
ID   AAX06817 standard; DNA; 2815 BP.
XX
AC   AAX06817;
XX
DT   26-APR-1999 (first entry)
XX
DE   Chlamydia pneumoniae surface exposed protein Omp5 DNA.
XX
KW   Omp5; outer membrane protein 5; surface exposed protein; antigen;
KW   infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
XX
OS   Chlamydia pneumoniae.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..2787
FT   /*tag= a
XX
PN   WO9858953-A2.
XX
PD   30-DEC-1998.
XX
PF   19-JUN-1998; 98WO-DK00266.
XX
PR   23-JUN-1997; 97DK-0000744.
XX
PA   (BIRK/) BIRKLUND S.

PA   (CHRI/) CHRISTIANSEN G.
XX
PI   Birkelund S, Christiansen G, Knudsen K, Madsen A;
PI   Mygind P;
XX
DR   WPI; 1999-105610/09.
DR   P-PSDB; AAW88418.
XX
PT   Species-specific test for identifying mammals infected with
PT   Chlamydia pneumoniae - comprises detecting antibodies specific for
PT   outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT   these proteins
XX
PS   Claim 6; Page 42-43; 115pp; English.
XX
CC   This DNA sequence codes for the novel 97.2 kDa surface exposed
CC   protein Omp5 (see AAW88418) of the human respiratory pathogen
CC   Chlamydia pneumoniae. By generating antibodies against C.
CC   pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
CC   was obtained which reacted with outer membrane proteins. The
CC   antibody was used to identify the genes (see AAX06816-27) encoding
CC   Omp4-Omp15 proteins (see AAW88417-28) in an expression library of
CC   C. pneumoniae DNA. The genes are situated in 2 gene clusters:
CC   Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
CC   the other, and encode polypeptides of about 89.6-100.3 kDa and
CC   about 56.1 kDa. The invention provides a new species specific test
CC   for identifying mammals (including humans) infected with Chlamydia
CC   pneumoniae. The test comprises detecting antibodies specific for
CC   Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC   membrane proteins, especially by PCR. The proteins are also used
CC   in the diagnosis of C. pneumoniae infection in mammals. The
CC   nucleic acids and proteins can also be used in the immunization of
CC   mammals, the nucleic acids being particularly useful as DNA
CC   vaccines for effecting in vivo expression of antigens. The
CC   vaccines may also prevent atherosclerosis and bronchial asthma,
CC   which are possibly associated with C. pneumoniae.
XX
SQ   Sequence 2815 BP; 790 A; 575 C; 626 G; 824 T; 0 other;

Query Match   17.7%; Score 530.2; DB 20; Length 2815;
Best Local Similarity   52.9%; Pred. No. 1.5e-136;
Matches 1415; Conservative   0; Mismatches 1183; Indels   75; Gaps   10;

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Qy    247  TGCTGGACTACCTACCTATTTAAGGGAAAGTGTCACTCTAGAAAATATTCCTGAACAGG  306
                 |||||                ||||||
Db    156  TACTGGGATAGACTATACTCTGACAGGAGATATAACTCTGCAAAACCTTGGGGATTCGG-  214

Qy    307  CACAGCAATCACAAAAGCTGTTTTAACAACTAAGGGCGGATTTGACTTCACAGGTAA  366
                 |||||||              ||||||
Db    215  --CAGCTTTAACGAAGGGTTGTTTTTCTGACACTACAGGGACTGTAGCAGGGGCTGCTGTTAA  272

Qy    367  CGGGAACTCTCTATTGTTCCAAACGGTGGATGCAGGGACTGTAGCAGGGCGCAGCACTTTCTGT  426
                 |||||               ||||||
Db    273  GGGGTACTTCACTTTCTTTTTTAAATATTAAGTCTAGTGCTGCTGAAGGCGGATC--T-CTGT  332

Qy    427  CAGCAGCGTGGTAGATAAATCTACCACGTTTATAGGGTTTCTTCGCTATCTTTTATTGC  486
                 |||||                ||||||
Db    333  TACAACTGATAAAAATCGTCGCTAACAGATTTTCGAGTCTTACTTTCTTAGCGGCCCC  392

Qy    487  GTCTCCTGGAAGTTGATAACTACCGGCAAAGGAGCCGTTAGCTGCTCTACGGGTAGCTT  546
                 |||||                ||||||
Db    393  ATCATGGTAATCACAACCCCCTCAGGAAAAAGGTGCAGTTAAATGTGGAGGGGGATC---T  449

Qy    547  GAGTTTGACAAGAAAATGTCAGTTTGCTCTTCAGCAAAAACTTTCAACGATAATGGCGG  606
                 |||||               ||||||
Db    450  TACATTTGATAACAATGAACTATTTATTTTAAACAGATTACTGTGAGGAAAATGGCGG  509

Qy    607  TGCTATCACCGCAAAAACTCTTTCAATAACGGGACTACACATGTCAGCTCGTTTTCTGA  666
                 |||||               ||||||
Db    510  AGCCATTTTCACCAAGAATCTTTCTTTGAAAAACAGCACGCGGATCGAATTTCTTTTTGAAGG  569

Qy    667  AAATA-------CCTCCTCAAAGAAGAAGGCGGAGCCCATTCGAGACTTCCGATGCCCTTAC  717
                 |||||                ||||||
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Db   570  GAATAAATCGAGCGCAACAGGGAAAAAGGTGGGCTATTGTGCTACTGGTACTGTAGA         629
Qy   718  CATTACTGGAAACCAAGGGAGAAGTCTCTTTTTCGACAATACTTCTTCGGATTCTTGGAGC  777
          ||||||  |  || |    |||   ||  |||||| | ||||||
Db   630  TATTCAAATAATACGGGCTCCTACACCCTCTTCTCGGAACACAATATGTGCTGAAGCTGCAGGTGG    689

Qy   778  TGCAATTTTTACAGAGAGCCTCGGTGACTATTTCTAATAAATGCTAAAGTTTCCTTTATTGA       837
          ||  || | ||  ||||   || |||  ||||
Db   690  AGCTATAAAATAGCACAGGAAACTGTACAATTACAGGGAATACGTCTCTTGTATTTTCTGA    749

Qy   838  CAATAAGGTCACAGGAGGCAGCTTCCTCAACAACAGCGGGGATATGTCAGGAGGTGCTATCTG      897
          ||      | ||||  |
Db   750  AAAATAGTGTGAC---AGCGACCCAGGAAATGGAGGAGCTCTTTTCTGGGAATGCCG----    802

Qy   898  TGCTTATAAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAAATCAGATGTTACTCTT      957
          ||          || ||||||| |||||
Db   803  ------------AtGTTACCATATATCTGGGAATCAGAGTGTAACTTT    836

Qy   958  CAGCAACAATACATCGACACAGGGAGGAGCTATCTATGTGAAAAAGTCGAACTGGC      1017
          |||   ||| |||    ||||||| ||  |||||||||||
Db   837  CTCAGGAAACCAAGCTGTAGCTAATGGCGGAGCCATTTATGCTAAGAAGCTTACACTGGGC    896

Qy   1018 TTCCGGAGGACT------TACCCTATTCAGTAGAAAATAGTGTCAATGGAGGTACAGCTCC     1071
          ||                ||       ||
Db   897  TTCCCGGGGGGGGGGTATCTCCTTTTCTAACAATAGTCCAAGGTACCACTGCCAGG    956

Qy   1072 TAAAGGTGGAGCCATAGCTATCGAAGATAGTGCGGAATTGAGTTTATCCGCCGATAGTGG     1131
          ||    |    | |||| ||||| ||||  |||||||||||
Db   957  TAATGGTGGAGCTGCAGCGTGGTAGTGTAGTCTTTCAGCAGAAGCAGG    1016

Qy   1132 TGACATTGTCTTTTTAGGGAATACAGTCACTTCTACTCC---TGGGACGAATAGAAG      1188
          |||||       | |||||   |||
Db   1017 GGACATTACCTTCAATGGGAATGGCATTGCATTGTTGCAACTACCACCAAACTACAAAAAGAAA    1076

Qy   1189 TAGTAATCGACTTAGGAACAGAGTGCAAAAGTGCAAAGATGACAGCTTTGCCGTTCTGCTGCGTGGTAGAGC     1248
          ||  |||  |||||  |||| |||||
Db   1077 TTCTATTGACATAGGATCTACTGCAAAGATCACGGAATCACGTTTAGCTGCAATATCTGGGCATAG    1136

Qy   1249 CATCTACTTCTCTATGGATCCCATAACTACACAGGATCATCCACAAACAGTTACAGATGTCTTAAA     1308
          || ||| |||| |  | || |||
Db   1137 CATCTTTTTTCTACGATCCGATTACTTGCTAATACGGCTCGCGGATTCACAGATACTTTAAA    1196

Qy   1309 AGTTAATGAGACTCCGGCAGAATTCTGCACTACAATATACAGGGAACATCATCTTCACACAGG     1368
          ||  ||||     |    ||||| ||    |
Db   1197 TCTCAATAAGGCTGATGCAGTGAATAATGTACAGATTATAGTGGTCGATTGTTTTTTCTGG    1256

Qy   1369 AGAAAAAGTTATCAGAGACGAGGCCCGAGATTCTAAAAATCTTAAAAATCTTACTTCGGAAGCTACTACA     1428
          |||  || |||| ||||| |||   |||
Db   1257 TGAAAAAGCTCTCTGAAGATGAAGCAAAAGTTGCAGACAAGGTTGCAGACACCTCACTTCTACGCTGAAGCA    1316

Qy   1429 GCCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAACATGAGTGACTCTGCCAGACTCA     1488
          |||| |  || |||||||      |   ||  ||||
Db   1317 GCCTGTAACTGTTAACTGCAGAAAATTTAGTACTTAAACGGTGTCCACTCTGCGATACGAA    1376

Qy   1489 GGCAATCAACAGGCCAGCAGATTCCGTCTCGAAAATGGACGTAGGAACTACTCTAGAACC     1548
          ||  || || |||  |  || |||||
Db   1377 AGGCTTTTTACTCAGACGCGCGGGTTCCTCGTGTTATTATGGATGCGGCGCACAACGTTAAAAGC    1436

Qy   1549 ---TGCTGATACTAGCACCATAAACAATTTGGTCATTAACATCAGTTCTATAGACCGGTGC     1605
          ||     ||| || ||
Db   1437 AAGTACAGAGAGGAGGTCACTTTAACAGGTCTCTAGACACTCTTAGGCGAGGG    1496

Qy   1606 AAAGAAGCAAAAATAGAAACCAAAGCTACGTCAGAAAATCTCAAAAAAATCTGAACCAT     1665
          ||| ||||| |||   ||||||  || |  ||||| |||
Db   1497 CCGCAATGATCCCAAATGCACTACACTACAGCACTTGTAATCAGCACTTAGCCCTTAGTGTCCGAT    1556

Qy   1666 CACTTATTGGACCCGACGGGCACGTTTATGAAAATCATTAGTTTAAGAAATCCTCAGTC     1725
          |||  |||  |||||||||
Db   1557 TGCCAATAACTTAGCACCAAGGGAAATGCTTATGAAAATCACGACTTAGGAAAAACTCAGA    1616

Qy   1726 CTACGACATCTTAGAGCTCAAAGCTCTGCTCTGGGTACTGCGGTACTGTTCCAGCGGT     1785
          ||  ||||||       ||||| ||
Db   1617 CTTTTCATTTGTGCAGCTCTGCTCTGGGTACTGCGAACAACTACGAGTGTTCCAGCGGT    1676
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Qy   1786 TCCTATAATGGGTGAGAAATTCCATTACGGCTATCAGGAGAACTGGGGCCCAATTGTTTG     1845
          |||||  |  |  |||||      ||  |||||||  |||  |||||   ||
Db   1677 TCCTACAGTAGCAACCTCCACGCACTATGGGTATCAAGGTACTTGGGAATGACTTGGGT    1736

Qy   1846 GG--------GACAGGGGCTTCTACGACTGCAACCTCAACTGACTAAAACTGG     1893
          ||        | |         ||   ||||| |||||
Db   1737 TGATGATACCGCAAGCACTCCAAAGACTAAGACAGCGACATTAGCTTGGACCAATACAGG    1796

Qy   1894 CTATATTCCTAATCCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCATT     1953
          ||| | |  |||||  ||||||  |   ||||||||| ||||||||| | |||  ||| ||
Db   1797 CTACCTTCGGAATCCTGAGCGTCAAGGACCTTTAGTTCCTAATAGCCTTTGGGGATCTTT    1856

Qy   1954 TATAGATATTAGCTCTCTCCATTATCTTATGGAGCACTGCAAACGAAGGGTTGCAGGGAGA     2013
          || ||||| |   |  |   |||| |||  |||||  |||| | |||| ||| ||||
Db   1857 TTCAGACATCCAAGCGATTCAAGGTGTCATAGAGAGAAGGAAGTGCTTTGACTCTTTGTTCAGA    1916

Qy   2014 CCGTGCTTTTGGTGTGGTCGATTATCTCAACTTCCTGATTAATCTAACTTCTTCCAAGAGGATAGTACTAAAAACACG     2073
          |||| |  |  |   ||     |||  | ||||
Db   1917 TCGAGGCTTCTGGGCTGCGGGAGTCGCCAATTTCTAGAGATAAAGATAAGAAGGGGGAAA    1976

Qy   2074 ACGCGGGGTTCGGCATTGAGTGGCGGTTATGTCAATGGAGGTACAGCTCC     2133
          ||      |  |      ||  |||| | || |  |     |   |   ||
Db   1977 ACGCAAATACCGTCATAAATCTGGTGATATGCTATCGGAGGTGCAGCCAAACTTGTTC    2036

Qy   2134 AGATAAGATTCTTAGTGCTGCTCAGTTTGTCAGCTCTTGGAAGAGAGATAGAGACTACTTTGT     2193
          || |  |||  | || ||    ||  |     |    || ||    ||||||| |||| |
Db   2037 TGAAAACTTAATTAGCTTGCCTTTTGCCAACTCTTGTGGAGGCGATAAAGATTTCTTAGT    2096

Qy   2194 AGCTAAGAATCAAGTACAGTCTACGGACGAACTCTCTTGGAAGAGAGACCTCTATTACCAGCACAACGAAACCTA     2253
          ||| |  |||||    | |||||| |||||| ||||| ||||   |  | |  || ||||||||
Db   2097 CGCTAAAAATCATTACTGATACCTATGCAGAGGCCTTCTACAACACATTACAGATGTC    2156

Qy   2254 TATCTCTTCCTTGCAAACTACGGGCCTTGTTCGTTGTCTATTGTCTTATGTTCCTACGAGATTCC     2313
          || ||| |    | ||||  |||   || ||
Db   2157 TAGTGGGTTCATAGGTTCTCTCCTTAGATAA---CTTCCTGGCTCTTGGAGTCATAAACC    2213

Qy   2314 TGTTCTCTTTTCAGGAAACCTTAGCTAGACACCATAACGGATAACTGAAAAACCAAGTA     2373
          ||  || |  | |||||    ||| ||||| |
Db   2214 CCTCGTTTTAGAGGGGCAGCTCGCTCGCTTATAGCCACGTCAGTCAGTAATGATCTGAAGACAAAGTA    2273

Qy   2374 TACAACATCCTACTGTGTAAAGAGAGCTGGGGAATGAGTAGTTCGCTTTAGAATTCGG     2433
          |   | || |   ||  | |||  ||  |||||||||
Db   2274 TACTGCGTATCCTGAGGTGAAAGGTTCTTGGGGTGAAGAGAATAATGCTTTTAACATGATGGTGGG    2333

Qy   2434 TGGAAGAGCTCCGATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTAACATGCCCTTCAT     2493
          ||  |||  |||||||||||  |||
Db   2334 AGCTTCTTCTCATTCTTATCCTGAATAACCTGCGATTGTTTTGATACTATGTCTCCATACAT    2393

Qy   2494 GAAATTGCAGTTTGTCATGCACATCCAGAGGACACATCAGGGAACAGAAGAGCTCG     2553
          || ||||||||     ||||  |    |||  ||||  || |
Db   2394 CAAACTGAATCTGACCGTAACAGTCAGGACAGCAGCTCAGGAGAGAAAGGTACAGAAGGAG    2453

Qy   2554 TGAATTTGGAAGTAGCCGTGTCTGTGTGAATCTTGCCTTGCGATTTGATAA     2613
          ||    |  |  |||||    |  |  |  |   ||| |  |||| |||||
Db   2454 ATCTTTTGATGACAGCAACCTCCTTCAATTATCTTTGCCTATAGGGGGTGAAGTTTGAGAA    2513

Qy   2614 GGAATCAGACTGCCAAGATGCAACGTACAACGTACAAGATGGATCCTGT     2673
          ||  |||||   |  |||| || | |    |||  |||   |||| ||||
Db   2514 GTTCTCGATTGTAATGACAGTTTCTTTATGACTTTATCCTATGTTCCTGATCTTAT    2573

Qy   2674 TCGTAGTAACCCCGACTGTACAGCAACAACTACAGGGTGAATTAGCGGTGGGAAACCTT     2733
          ||   |  |     | |||| ||||||   |    ||
Db   2574 CCGCAATGATCCCAAATGCACTACACTACAGCACTTGTAATCAGCACTTAGCCCTTAGTGTCCGGAACTTA    2633

Qy   2734 CGGTACGACGAATTTGGCAAGACAAGCTTAGTCCTTCGGTGCAGGGAACGAACCCATTTTGTCTTTAA     2793
          |||  | || ||| | |||  |||    || |
Db   2634 TGCCAATAACTTAGCACCACAGCAGCGCCTTTGCAGTGCGCAGTGCATTACGCCCTTCTC    2693

Qy   2794 CTCAAATTTGAAGCTTAGCCAATTTCTTTTGAGTTGCTTTGTGCTGGGGTCATCTCGCAATTA     2853
          |||  | |  ||||||      ||  ||||| | || ||||
Db   2694 TCCTATGTTTGAAGTGCTCGGCCAGTTTGTGTTTCTTTGAAGTTCTTGAGTTGCTGGATCGATTA    2753
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Qy    2854  CAATGTAGACTTAGGAGCAAAATACCAATTCTA 2886
            ||||||||  ||| ||||| ||  ||||||||||
Db    2754  TAATGTAGATCTTGGGGTAAGTTCCAATTCTA 2786
```

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RESULT 10
ABL91231
ID    ABL91231 standard; DNA; 2787 BP.
XX
AC    ABL91231;
XX
DT    29-JUL-2002  (first entry)
XX
DE    Chlamydia pneumoniae cp0010 ORF DNA, SEQ ID NO:96.
XX
KW    Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KW    human respiratory disease; cardiovascular disease; atherosclerosis;
KW    coronary artery disease; carotid artery stenosis; myocardial infarction;
KW    cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW    strain CWL029; open reading frame; ORF; gene; ds.
XX
OS    Chlamydia pneumoniae.
XX
FH    Key            Location/Qualifiers
FT    CDS            1..2787
FT                   /*tag= a
FT                   /product= "cp0010"
FT    sig_peptide    1..75
FT                   /*tag= b
FT    mat_peptide    76..2784
FT                   /*tag= c
FT                   /product= "Mature protein"
XX
PN    WO20020606-A2.
XX
PD    10-JAN-2002.
XX
PF    03-JUL-2001; 2001WO-IB01445.
XX
PR    03-JUL-2000; 2000GB-0016363.
PR    11-JUL-2000; 2000GB-0017047.
PR    21-JUL-2000; 2000GB-0017983.
PR    07-AUG-2000; 2000GB-0019368.
PR    18-AUG-2000; 2000GB-0020440.
PR    14-SEP-2000; 2000GB-0022583.
PR    10-NOV-2000; 2000GB-0027549.
PR    22-DEC-2000; 2000GB-0031706.
XX
PA    (CHIR-) CHIRON SPA.
XX
PI    Ratti G, Grandi G;
XX
DR    WPI; 2002-154726/20.
DR    N-PSDB; ABB90573.
XX
PT    Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT    medicament for treatment or prevention of infection due to Chlamydia,
PT    preferably Chlamydia pneumoniae, and for diagnostic purposes -
XX
PS    Claim 5; Page 88-89; 364pp; English.
XX
CC    Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
CC    pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
CC    them. The proteins are predicted to be immunogenic and may therefore be
CC    useful in vaccine production and for diagnostic purposes. Chlamydia
CC    pneumoniae is a common cause of respiratory disease in humans, and is
CC    also involved in the development of cardiovascular diseases such as
CC    atherosclerosis, coronary artery disease, carotid artery stenosis,
CC    myocardial infarction, cerebrovascular disease, aortic aneurysm,
CC    claudication and stroke. The proteins and nucleic acids of the invention
CC    may be used in vaccines and pharmaceutical compositions for the
CC    prevention or treatment of chlamydial infections, particularly Chlamydia
CC    pneumoniae infections. The proteins may also be used in the detection of
CC    Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
CC    DNA probe assay or blotting techniques for determining Chlamydia
CC    pneumoniae gene expression. The present sequence represents a
CC    specifically claimed DNA which encodes a Chlamydia pneumoniae protein of
CC    the invention.
XX
SQ    Sequence 2787 BP; 785 A; 568 C; 619 G; 815 T; 0 other;
```

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Query Match             17.6%;  Score 527;  DB 24;  Length 2787;
Best Local Similarity   52.9%;  Pred. No.1.2e-135;
Matches 1413;  Conservative    0;  Mismatches 1185;  Indels   75;  Gaps    10;
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Qy   247  TGCTGGAACTACCTACCTATTTAAGGGAAATGTCACTCTAGAAAATATTCCTGGGACAGG 306
          ||||||||  |||||| ||   || |||||||| ||||| ||||||| ||||||  |||
Db   156  TACTGGAATAGACTATACTCTGACAGAGATATAACCTCTGCAAAACCTTGGGGATTCGG- 214
```

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Qy   307  CACAGCAATCACAAAAAGCTGTTTAACAACACTAAGGGCGATTTGACTTTCACAGTAA 366
          ||||| ||  ||||||  ||  || ||||||  ||| ||| ||||| |||||||||
Db   215  --CAGCTTTAACGAGAGGTTGTTTTCTGACACTACCGAAATCTTAAGCTTTGCCGGTAA 272
```

```
Qy   367  CGGGAACTCTCTATTGTTCCAAACGGTTGGATGCAGGGACTGTAGCACGGGTGCTGTTAA 426
          ||| ||||| ||| ||     |||||| |||| |||||||| | || |||| ||| ||
Db   273  GGGGTACTCACTTTCTTTTTAAATATTAAGTCTAGTGCTGAAGGCGCAGCACTTTCTGT 332
```

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Qy   427  CAGCAGCGTGGTAGATAAATCTACCACGTTTATAGGGTTTCTTCGCTATCTTTATTGC 486
          | ||| |  |||| || ||| |||   |||| ||| ||||  |||| || |||||||
Db   333  TACAACTGATAAAAATCTGTCGCTAACAGGATTTTCGAGTCTTACTTTCTTAGCGGCCCC 392
```

```
Qy   487  GTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGCCGTTAGCTGCTCTACGGGTAGCTT 546
          |   || ||| || |||| ||| || || ||||| || |||||| ||  |||||  ||
Db   393  ATCATCGGTAATCACAACCCCTCCAGGAAAAGGTGCAGTTAAATGTGAGGGGATC---T 449
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Qy   547  GAGTTTGACAAAAAATGTCAGTTGCTCTTCAGCAAAAAACTTTCAACGGATAATGGCGG 606
          || |||||| ||||  || |||| | ||||||  ||| |||||  |||| |||| |||
Db   450  TACATTTGATAACAATGGAACATTTTATTTAAACAAGATTACTGTGAGGAAAATGGCGG 509
```

```
Qy   607  TGCTATCACCGCAAAAACTCTTTCATTAACAGGGACTACAATGTCAGCTCTGTTTTCTGA 666
          || ||| ||||| |||| || || || |||||| ||| |||| |||| ||  |||||||
Db   510  AGCCATTCTACCAAGAATCTTTCTTTGAAAAACAGCACGGGATCGATTTCTTTTTGAAGG 569
```

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Qy   667  AAATA-------CCTCCTCAAAGAAAGGCGAGCCATTCAGACTTCCGATGCCCTTAC 717
          |||||       |||| || |||||||   |||| |||||| ||||| ||| |||||
Db   570  GAATAAATCGAGCCAACAGGGAAAAAGGTGGGGCTATTGTGCTACTGGTACTGTAGA 629
```

```
Qy   718  CATTACTGAAACCAAGGGAAGTCTCTTTTCTGACAATACTTCTTCGGATTCTGGAGC 777
          ||||| ||  ||||| ||||||   |||||||| ||||||| || ||  |||||||
Db   630  TATTACAAATAATACGGCTCCTACCCCTTCTCGAACAATATTCTGAAGCTGCAGGTGG 689
```

```
Qy   778  TGCAATTTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTCCTTTATTGA 837
          ||||||    || || |||||| | |||||| ||| ||||  ||   |||||  ||||
Db   690  AGCTATAAATAGCACAGGAAACTGTACAATTACGGGAATACGTCTCTTCGTATTTTCTGA 749
```

```
Qy   838  CAATAAGGTCACAGGAGCGAGCTCCTCAACAACGGGGATATGTCAGGAGGTGCTATCTG 897
          ||||| ||| |||  || |||||  |||| ||| | ||| |||| ||| |   ||||||
Db   750  AAATAGTGTGAC---AGCGACCGCAGGAAATGGAGGAGCTCTTTCTGGAGATGCCG---- 802
```

```
Qy   898  TGCTTATAAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTT 957
          |||||| || ||||| ||| ||| || | || |||||| |||| |||| || |||| ||
Db   803  ------------------ATGTTACCATATCTGGGAATCAGAGTAGTGTAACTTT 836
```

```
Qy   958  CAGCAACAATACATCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGGC 1017
          ||||| |||  || || ||  || | ||||| || |||    |  |||  ||| || |||
Db   837  CTCAGGAAACCAAGCTGTAGCTAATGGCGGAGCCATTTATGCTAAGAAGCTTACATCGGC 896
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Qy  1018  TTCCGGAGAC-----TTACCCTATTCAGTAGAAAATAGTGTCAATGGAGTGAGGTACAGTCC 1071
          |||||       ||  |||| | || | || | || ||   |   | || ||  |||||
Db   897  TTCCGGGGGGGGGGTATCTCCTTTCTACAATAATAGTCCAAGTACCACTCGCAGG 956
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Qy  1072  TAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGAATTGAGTTATCCGCCGATAGTGG 1131
          ||  ||||||| |||||  |||| ||||||||| |||| |||  ||||||| |||||
Db   957  TAATGGTGGAGCCATTTCTATACTGGCCAGCTGAGAGTGTAGTCTTTTCAGCAGAAGCAGG 1016
```

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Qy  1132  TGACATTGCTCTTTTTAGGGAATACAGTACCACTTCTACTACTCC---TGGGACGAANTAGAAG 1188
```

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RESULT 11
AAZ61509
ID   AAZ61509 standard; DNA; 2957 BP.
XX
AC   AAZ61509;
XX
DT   19-JUN-2000  (first entry)
XX
DE   DNA encoding the CPN100395 polypeptide.
XX
KW   CPN100395; Chlamydia infection; immune response; vaccine; ss.
XX
OS   Chlamydia pneumoniae.
XX
FH   Key            Location/Qualifiers
FT   CDS            101..2857
FT                  /*tag= a
XX
PN   WO20001183-A2.
XX
PD   02-MAR-2000.
XX
PF   18-AUG-1999;    99WO-IB01449.
XX
PR   20-AUG-1998;    98US-0097187.
PR   20-AUG-1998;    98US-0097188.
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Qy 2097 CGCTAAAAAATCATACTGATACCTATGCAGGAGGCCTTCTATATCCAACACATTACAGAAATG 2156
Db 2254 TATCTCTCTTCCTTGCAAACTACGGCCTTGTTCGTTGTCTTATGTTCCTACAGAGATTCC 2313
Db 2157 TAGTGGGTTCATAGGTTGTCTCTTAGATAAA---CTTCCTCGGCTCTTGGAGTCATAAACC 2213
Qy 2314 TGTTCCTCTTTTCAGGAAAACCTTAGCTACACCCATACGGATCAACGATCTGAAAACCAAGTA 2373
Db 2214 CCTCGTTTTAGAAGGGCAGCTCGCTTATAGCCACGTCAGTAATGATCTGAAGACAAAGTA 2273
Qy 2374 TACAACATATCCTACTGTTAAAGGAAGCTCGGGGAATGATAGTTTCGCTTAGAATTCGG 2433
Db 2274 TACTGCGTATCCTGAGGTGAAAGGTTCTTGGGGGAATAATGCTTTTAACATGATGTTGGG 2333
Qy 2434 TGGAAGAGCTCCGATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTACATGCCCTTCAT 2493
Db 2334 AGCTTCTTCTCATTCTTATCCTGAATACCTGCATTGTTTTGATACCTATCGTCCATACAT 2393
Qy 2494 GAAATTGCAGTTTGTCTATGCAGCTCAGGAAGGTTTAAAGAACCAGGAACAGAAGCTCG 2553
Db 2394 CAAACTGAATCTGACCTATATACGTCAGGACAGCCTTCTCGGAGAAGGTACAGAAGGAAG 2453
Qy 2554 TGAATTGGAAGTAGCCGTCTTGTGAATCTTGCCTTACCTATCGGGATCCGATTTGATAA 2613
Db 2454 ATCTTTTGATGACAGCACAACCTCTTCAATTTATCTTTGCCTATAGGGGTGAAGTTTGAGAA 2513
Qy 2614 GGAATCAGACTGCCAAGATGCAACGTACAATCTAACTCTTGGTTATACTCTTGGATCTTGT 2673
Db 2514 GTTCTCTGATTGTAATGACTTTCTTATGATCTGACTTTATCCTATGTTCCTGATCTTAT 2573
Qy 2674 TCGTAGTAACCCGACTGTACGACACACTGCGAATTAGCGTGGTGATTCTTGGAAAACCTT 2733
Db 2574 CCGCAATGATCCCAAATGCAACTACACGCACTTGTAATCAGCGGAGCCTCTTGGGAAACTTA 2633
Qy 2734 CGGTACGACAATTGGCAAGACAAGCTTTAGTTCCTTCGTCGTGCGAGGGAACCCATTTTTGCTTAA 2793
Db 2634 TGCCAATAACTTAGCACGACAGAGCCCTTGCAAGTGCGTGCCAAGTCAGTACGACGCCTTCTC 2693
Qy 2794 CTCAAARTTTGAAGCCTTAGCCAATTTCTTTTGAATTGCGTCGTGGGTCATCTCCGCAATTA 2853
Db 2694 TCCTATGTTTGAAGTGCTCCGGCCAGTTTGTCTTTGAGTTCGTGGATCCTCACCGGATTTA 2753
Qy 2854 CAATGTAGACTTAGGAGCAAAATACCAATTCTA 2886
Db 2754 TAATGTAGATCTTGGGGGTAAGTTCCAATTCTA 2786
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Db  1017 GGACATTACCTTCAATGGGAATGCCATTGTTGCAACTACACCACCACAAAACTACAAAAAGAAA 1076
Qy  1189 TAGTATCGACTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTGCTGGTAGAGC 1248
Db  1077 TTCTATTGACATAGACTACTGCAAAGATCACGAATTTACGTGCAATATCTGGGCATAG 1136
Qy  1249 CATCTCACTTCTATGATCCCATAACTACACAGTTACAGATGTCTTAAA 1308
Qy  1137 CATCTTTTCTACGATCCGATTACTGCTAATACGGCTCGCGGATTCTACAGATACTTTAAA 1196
Db  1309 AGTTAATGAGACTCCGGCAGATTCGCACTACAATATACAGGGAACATCATCTTCACAGG 1368
Qy  1197 TCTCAATAAGGCTGATGCAGGTAATAGTACAGATTATATGTGGGTCGATTGTTTTTTCGG 1256
Db  1369 AGAAAAAGTTATCAGAGACAGAGGCCGCAGAATTCTAAAAATCTTACTTCGAAGCTACTACA 1428
Qy  1257 TGAAAAGCTCTCTGAAGATGAAGCAAAAGTTGCAGACAACCTTCACCTTCACCGCTGAAGCA 1316
Db  1429 GCCTGTAACTCTTTCAGGAGAGTACTCTATCTTTTAAAACATGGAGTGGACTCTGCAGACTCA 1488
Qy  1317 GCCTGTAACTCTAACTGCAGGGAAATTTAGTACTTAAACGTGGTCACCTCTCGATACGAA 1376
Db  1489 GGCATTCACTCAACACAGGCAGATTCGTCTCGAAATGGACGTAGGGAACTACTCTAGAACC 1548
Qy  1377 AGGCTTTACTTCAGACCGCGGGTTCCTCTGTTATTATGGATGCGGGCACAACGTTAAAAGC 1436
Db  1549 ---TGCTGATACTAGCAGCACCATAAACAATTTGGTCATTACCAGTCTTATAGACGGTGC 1605
Qy  1437 AAGTACAGAGGAGGTCACTTTAACAGGTCTTTACAGGTCTTTAACACCTTCCTGTGTAGACTCTTTAGGCGAGGG 1496
Db  1606 AAAGAAGGCAAAAATAGAAACCAAAGCTACGTCAAAAAATCTGACTTTATCTGGAACCAT 1665
Qy  1497 TAAGAAAGTTGTAATTGCTCTTCGCAGCAAGTAAAAATGTAGCCCTTAGTGGTCCGAT 1556
Db  1666 CACTTTTATTGGGACCCGACGGGCACGTTATGAAATCATAGTTAAGAAAATCCTCAGTC 1725
Qy  1557 TCTTCTTTGATAACCAAGGAATGCTTTGCTCTCTGGGTACTGACTTAGGAAAAAACTCAAGA 1616
Db  1726 CTACGACATCTTAGAGCTCAAAGCTTCTGGAACTGTAACAAGCACCGCAGTGACTCCAGA 1785
Qy  1617 CTTTTCATTTGTCAGCTCTCGCTCGTCTGCGGTACTGGGTATCAAGGTACTTGGGGAATGACTTGGGT 1676
Db  1786 TCCTATAATGGGTGAGAAATTCCATTACGGCTATCAGGGAACTTGGGGCCCAATTGTTTG 1845
Db  1677 TCCTACAGTAGCAACTCCTACGCACTATGGGTATCAAGGTACTTGGGGAATGACTTGGGT 1736
Qy  1846 GG--------GGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAAAACTGG 1893
Db  1737 TGATGATACCGGCAACTCCAAAGACTCAAGACTACAGCGACATTAGCTTGGACCAATACAGG 1796
Qy  1894 CTATATTCCTAATCCCGAGCGTATCGGCCTTCGGCCTCTTTAGTCCTTAGTAGCTTATGAATGCATT 1953
Db  1797 CTACCTTCCGAATCCTGAGCGTCAAGGAACCTTTAGTTCCTAATAGCCTTGGGGATCTTT 1856
Qy  1954 TATAGATAATTAGCTCTCTCCATTATCTTCATTGTTCCTCAGCGTTGAAGGGTTGCAGGAGA 2013
Db  1857 TTCAGACATCCAAGCGATTCAAGTGTCATAGAGAAGTGCTTTGACTCTTTGTTCAGA 1916
Qy  2014 CCGTGCTGTTTTTGGTGTGCTGGATTATCTCAACTGGGCCCATTGTTTG 2073
Db  1917 TCGAGGCTTCTCTGGGCTTCGGCGGAGTCGCCAATTTCTTAGTAGGAGGAAAGATAAGAGAAGGGGGGGAAAA 1976
Qy  2074 ACGCGGGTTTCGGCATTGAGTGGCGGTTATGTCATAGGAGGAGAAACCTTACATACTTGTTC 2133
Db  1977 ACGCAAAATACCGTCATAAATCTGGTGGATATGCTATCGGAGGGTGCAGCGCCAAACTTGTTC 2036
Qy  2134 AGATAAGAGATTCTTAGTGCTGCTTGACTTTGCAGCTCTTTGGAAGAGACTGACTACTTTGT 2193
Db  2037 TGAAAACTTAATTAGCTTTGCCAACTCTTTGTTGGTAGCCGATAAAGAGATTTCTTAGT 2096
Qy  2194 AGCTAAGAATCAAGGTACAGTCTCTATTACCAGCACGAGAACTCTCTATTACCAGCACGAACCTA 2253
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PR   20-AUG-1998;   98US-0097189.
PR   20-AUG-1998;   98US-0097190.
PR   20-AUG-1998;   98US-0097195.
PR   20-AUG-1998;   98US-0097196.
PR   20-AUG-1998;   98US-0097197.
PR   27-AUG-1998;   98US-0097191.
PR   17-AUG-1999;   99US-0376770.
XX
PA   (CONN-) CONNAUGHT LAB LTD.
XX
PI   Murdin AD, Oomen RP;
XX
DR   WPI; 2000-224703/19.
DR   P-PSDB; AAY69369.
XX
PT   Novel antigens and corresponding DNA molecules that can be used to
PT   prevent, treat and diagnose disease caused by Chlamydia infection in
PT   mammals, especially humans -
XX
PS   Claim 1; Fig 15-E; 201pp; English.
XX
CC   AAZ61502-09 encode Chlamydia pneumoniae polypeptides. The polypeptides
CC   are present in the bacterial membrane structure, in the external
CC   vicinity of the membrane structure, in the inclusion membrane
CC   structure, in the external vicinity of the inclusion membrane structure,
CC   and in the cytoplasm of the infected cell. The polypeptides may be
CC   used to prevent, treat and detect the presence of Chlamydia infection
CC   and/or the presence of Chlamydia in a sample. The polypeptides may
CC   also be used to induce an immune response in a mammal. The vaccine
CC   vector comprising the polynucleotides is used to induce an immune
CC   response in a mammal. Antibodies directed against the polypeptides
CC   may also be used therapeutically to treat and/or prevent a Chlamydia
CC   infection.
XX
SQ   Sequence 2957 BP; 818 A; 598 C; 683 G; 858 T; 0 other;

Query Match   17.5%;   Score 524.6; DB 21; Length 2957;
Best Local Similarity   53.4%;   Pred. No. 5.7e-135;
Matches 1424; Conservative   0; Mismatches 1159; Indels   84; Gaps   12;

Qy   242 GAAGATGCTGAACTACCTACCTATTTAAGGGAAATGTCACTCTAGAAAATATTCCTGA 301
Db   260 GATGCTAGTGGCACGACCTATATTCTCGATGGGGATGTCTCGATA---AGCCAAGCAGGG 316

Qy   302 ACAGGCACAGCACAATCACAAAAGCTGTGTTAACACACTAAGGGGGATTTGACTTTCACA 361
Db   317 AAACAAACGAGCTTAACACAAGTTGTTTTCTAACACTGCAGAGAAATCTTACCTTCTTA 376

Qy   362 GGTAACGGGAACTCTCTATTGTTCCAAACGGTGGATGCAGGGACTGTAGCAGGGGCTGCT 421
Db   377 GGGAACGGATTTTCTCTTCTTCATTTGACAATATTATTCGTCTACTGTTGCAGGTGTTGTT 436

Qy   422 GTTAACAGCAGGGTGGTAGATAAATCTACCACGGTTTTTCGTCTATCTTTT 481
Db   437 GTTAGCAATACAGCAGCTTCGGGAATCTTGGGAATTCTCAGGATTTTCAACTCTTCGGATG 496

Qy   482 ATTGCGTCTCCTGGAAGTTCGATAACTACCACCGGCAAAGGAGCCGTTAGCTCCTTACGGGGT 541
Db   497 -------AGGACCACAGTAAAGGAGCGTAAAGAGCCATTAAAATTACCCATGGT 547

Qy   542 AGCTTGAGTTTGACAAAAATGTCAGTTTGCTCTTCAGCAAAAAACTTTCAACGGATAAT 601
Db   548 --CTGGGTGTTTGAGAGTATAGGGAAATCTTGATCTT-AATGAAAAATGCCCTCTAGTGAAAAAT 604

Qy   602 GGCGGTGCTATCACCGGCAAAAATCTCTTCATTCAATACAGGGACTACAATGTCAGCTCTGTTT 661
Db   605 GGGGGAGCCATCAATACGAAGCATCTTGTCTTTGACTTGGAGTACGCGCGTTTGTAGCGTTC 664

Qy   662 TCTGAAAATACCTCCTCAAAGAAAGGGGAGCCATTCAGACTTCCGGATGCCCTTACCATT 721
Db   665 CTTTGGCAATAGCTCGTCGCAACAAGGGGAGCCGATCTATCGTTCTTGGTGACTCTGTGATT 724

Qy   722 ACTGGAAACCAAGGAGGGGAAGTCTCTTTTTCTGACAATACTCTTCCGGATTCGGAGCTGCA 781

Db   725 TCTGAGAAATGCAGGAATCTTGAGCTTCGGAAACAACAGTGCGACAACATCAGGAGGCGGCG 784

Qy   782 ATTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTCCTTTATTGACAAT 841
Db   785 ATCTCTGCTGAAGGGAACCTTGTGATCTCCAATAACCAAAATAATCTTTTCGATGGCTGC 844

Qy   842 AAGGTCACAGAGCGAGCTCCTCAACAACGGGGATATGTCGAGGAGGTGCTATCTGTGCT 901
Db   845 AAAGCAACTACAAATGGCGGAGCTATTGATTGTAACAAAGCAGGGG------------ 890

Qy   902 TATAAAACTAGTACAGATACTAAGGTCACCCTCACTGGGAAATCAGATGTTACTCTTCAGC 961
Db   891 ------CGAACCCAGACCCTATCTTGACTCTTTCAGGAAATGAGAGCCTGCATTTTCTG 943

Qy   962 AACAATACATCGACAACAGCGGGAGGAGCTATCATCGTGTCTATGTGAAAAAGCTCGAACTGGCTTCC 1021
Db   944 AATAAACACAGCAGGAAATAGTGGAGGTGCGATTTATACCAAAAAATTGGTGTTATCCTCA 1003

Qy   1022 GGAGGACTTACCCTATTCAGTAGAAATAGTGTCAAATGAGTACAGCTCCTAAAGGTGGA 1081
Db   1004 GGACGAGGAGGAGTGTGTATTTTCTAACAACAAAGCTGCGAATGCTACTCCTAAAGGAGGG 1063

Qy   1082 GCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGTGACATTGTC 1141
Db   1064 GCAATTGCGATTCTAGATTCTGGAGAGATTAGCATTTCTGCGATCTCGGCAATATCATT 1123

Qy   1142 TTTTTAGGGAATACAGTGCACTTCTAC-------TACTCCTGGGACGAATAGAAGTAGTATC 1195
Db   1124 TTCGAGGGCCAATACTACAGGACACTACAGGAGAGTCCTGCGAGTGTGACCAGAAATGCTATA 1183

Qy   1196 GACTTAGGAACCAGTGCAAAGATGACAGCAGTTTGCGTTCGTCGCTGGTGGGAAATAAAGTTATT 1255
Db   1184 GATCTTGCATCGAATGCAAAATTTTTAAATCCGACGACGCGGGAAATAAAGTTATT 1243

Qy   1256 TTCTATGATCCCATAACTACACAGGATCATCCACAACAGTTACAGATGTCTTAAAAGTTAAT 1315
Db   1244 TTCTATGATCCTATCACGA--------GCTCAGGAGCTACTGATAAGCTCTCTTTGAAT 1294

Qy   1316 GAGACTCCGGCAGATTCTGCACTACAATATCAGGGAACATCATCTTCACAGGAGAAAG 1375
Db   1295 AAAGCTGACGCAGGATCTGGAAATACCTATGAAGCTACATCGTTTTCTCTGGAGAGAAA 1354

Qy   1376 TTATCAGAGACAGAGGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAGCCTGTA 1435
Db   1355 CTCTTCAGAAGAGAGAACTTAAGAAACCTGACAATCTGAAGTCTACATTTACACAGCCTGTA 1414

Qy   1436 ACTCTTTCGAGGAGGTACTCTATCTTTAAAACATGGAGTGACTCTCGCAGGACTCAGGCATTC 1495
Db   1415 GAGCTTGCTGCAGGTGCCTTAGTATTGAAAGATGGTGACTGAGTGACTACTACTATA 1474

Qy   1496 ACTCAACAGGCAGCGAGATTCTCGTCTGCGAAATGACGTAGGAGAACTACTCTAGA--ACCTGCT 1552
Db   1475 ACGGCAGGTGCGAGGGATCGAAAGTCGTTATGATGAGGAGGACTACTTTTGAGGCAAGCGCT 1534

Qy   1553 GATACTAGCTACCATTGGTCATTAATAAACAATTTGGTCATTAACTACCATTATATAGATTCCTTAGATGGGACAAATAAA 1594

Db   1535 GAGGGGGTCACTCTCAATGGCCTAGCCATTAATATAGAGATCCTTAGATGGGACAAATAAA 1594

Qy   1613 GCAAAAATAGAAACCAAAGCTACGTCAAAAAACTTTCAACGGATAAT 1672
Db   1595 GCTATCATTAAGGCGACGGCAGCCAAGTAAGGATGGTGCCTTATCAGGGCCTATCATGTGCTT 1654

Qy   1673 TTGGACCCGACCGGCACGTTTTATGAAAAGACATAGTTTAAGAAAATCCTCACGGAC 1732
Db   1655 GTAGATGCTTCAGGGGAACTTATTATGAGCATCATCAGTCAATCATCAGTCACAGAGCAGTCTTTCCT 1714

Qy   1733 ATCTTAGAGCTCAAAGCTTCTGCACAAGGCTCTCCGATGGCCCTTACCATT 1792
Db   1715 TTAATAGAGCTTTTCTGCACAAGGAACGATGACTACTACAGATATCCCCGATACCCCAATT 1774

Qy   1793 ATGGGGTGAGAAATTCCATTACGGCTATCAGGGAACTTGG-------GGCCCAATTGTTTTGG 1846

RESULT 12
ABL91192
ID   ABL91192 standard; DNA; 534 BP.
XX
AC   ABL91192;
XX
DT   29-JUL-2002 (first entry)
XX
DE   Chlamydia pneumoniae cp0014 ORF DNA, SEQ ID NO:18.
XX
KW   Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KW   human respiratory disease; cardiovascular disease; atherosclerosis;
KW   coronary artery disease; carotid artery stenosis; myocardial infarction;
KW   cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW   strain CWL029; open reading frame; ORF; gene; ds.
XX
OS   Chlamydia pneumoniae.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..534
FT   /*tag= a
FT   /product= "cp0014"
XX
PN   WO200202606-A2.
XX
PD   10-JAN-2002.
XX
PF   03-JUL-2001; 2001WO-IB01445.
XX
PR   03-JUL-2000; 2000GB-0016363.
PR   11-JUL-2000; 2000GB-0017047.
PR   21-JUL-2000; 2000GB-0017983.
PR   07-AUG-2000; 2000GB-0019368.
PR   18-AUG-2000; 2000GB-0020440.
PR   14-SEP-2000; 2000GB-0022583.
PR   10-NOV-2000; 2000GB-0027549.
PR   22-DEC-2000; 2000GB-0031706.
XX
PA   (CHIR-) CHIRON SPA.
XX
PI   Ratti G, Grandi G;
XX
DR   WPI; 2002-154726/20.
DR   N-PSDB; ABB90534.
XX
PT   Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT   medicament for treatment or prevention of infection due to Chlamydia,
PT   preferably Chlamydia pneumoniae, and for diagnostic purposes -
XX
PS   Claim 5; Page 49; 364pp; English.
XX
CC   Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
CC   pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
CC   them. The proteins are predicted to be immunogenic and may therefore be
CC   useful in vaccine production and for diagnostic purposes. Chlamydia
CC   pneumoniae is a common cause of respiratory disease in humans, and is
CC   also involved in the development of cardiovascular diseases such as
CC   atherosclerosis, coronary artery disease, carotid artery stenosis,
CC   myocardial infarction, cerebrovascular disease, aortic aneurysm,
CC   claudication and stroke. The proteins and nucleic acids of the invention
CC   may be used in vaccines and pharmaceutical compositions for the
CC   prevention or treatment of chlamydial infections, particularly Chlamydia
CC   pneumoniae infections. The proteins may also be used in the detection of
CC   Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
CC   DNA probe assay or blotting techniques for determining Chlamydia
CC   pneumoniae gene expression. The present sequence represents a
CC   specifically claimed DNA which encodes a Chlamydia pneumoniae protein of
CC   the invention.
XX
SQ   Sequence 534 BP; 147 A; 105 C; 117 G; 165 T; 0 other;

Qy   1775 CTAAATACTACGAATCACTATGGTATCAAGGGAACTGGAATATTGTTTGGGTCGACGAT 1834
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1847 GGGACAGGGGCGTTCTACCACTGCAACCTTCAACTGGACTAAAACTGGCTATATTCCTAAT 1906

Db   1835 GCAACTGCGAAAAACAAAAAATGCTACCTTAACTTGGACTAAAACAGGATCAAGCCGAAT 1894
            ||||||| ||| |||||||||| ||||| |||||||| ||| |||||||| || ||
Qy   1907 CCCGAGCCGTATCGGCTCTTAGTCCCTAATAGCTTATGGAATGCATTTATAGATATTAGC 1966

Db   1895 CCAGAACGTCAGGGACCTTTGGTTCCTAATAGCCTGTGGGGTTCTTTTGTCGATGTCCGC 1954
                   ||||| ||||||| ||||||||||| |||||| |||||||
Qy   1967 TCCTCCATTATCTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGACCGTGCTTTTTGG 2026

Qy   1955 TCCATTCAGAGCCTCATGGACCGGAGCACAAGTTCGTTATCTTCGTCAACAAATTTGTGG 2014
                  |||||||||
Db   2027 TGTGCTGGATTATCTAACTCTTCCATAAGGATAGTACAAAAAACGACGCGGGTTTCGC 2086

Db   2015 GTATCAGGAATCGCGGACTTTTTGCATGAAGATCAGAAAGGAAACCAACGTAGTTATCGT 2074
            |||||| || || |||||| ||||||
Qy   2087 CATTTGAGTGCGGCCGTTATGTCAATAGGAGGAAAACCTACATACTTGTTCAGATAAGATTCTT 2146

Qy   2075 CATTCTAGCGCGGGTGTATGCATTAGGAGGAGGAGATTCTTCACGGCTTCTGAAAATTTCTTT 2134
            |||||| ||||||| ||||| || || |||| | ||
Db   2147 AGTGCTGCATTTGTCAGCTCTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAATCAA 2206

Db   2135 AATTTTGCTTTTTGTCAGCTTTTTGGCTACAGCAAGGACCATCTTGTGGCTAAGAACCAT 2194
            |||||| |||| ||||| || |||||||| ||||||
Qy   2207 GGTACAGTCTACGGAGAACTCTCTATTACCAGCACAACGAAACCTATATCTCTCTTCCT 2266

Qy   2195 ACCCATGTATATGCAGGGGCAATGAGTTACCGACACCTCGGAGAGTCTAAGACCCTTCGCT 2254
                 ||||| |||| | ||| || || ||| ||| || ||||
Db   2267 TGCAAACTACGGCCTTGTTCGTTCGTGTCTATGTTCCTACAGAGATTCCTGTTCTCTTTTCA 2326

Db   2255 AAGAT--------TTTGTCAGGAAAATTCTGACTCCCTACCTTTTGTCTTCAAT 2299
            ||||| |||||||| |||||||| || ||||| ||||||||||
Qy   2327 GGAAACCTTAGCTACACCCATACGGATAACGATCTGAAAACCAAGTATACAACATATCCT 2386

Qy   2300 GCTCGGTTTGCTTATGGCCATACCGACCACAATAACAAAGTACACTGGCTATTCT 2359
                 |||||| || || |||| || || ||
Db   2387 ACTGTTAAAGGAAGCTGGGGGAATGAGTTTCGCTTTAGAATTCGTGTGGAAGAGCTTCCG 2446

Db   2360 CCTCGTTAAGGAAGCTGGGGGAAATGATGCCCTTCGTATAGAATGTGGAGGAGCTATCCCG 2419
                  |||| ||||| | ||||| ||| ||||||| ||| |||| ||||
Qy   2447 A---TTTGCTTAGATGAAGAAGTGCTCTATTTGAGCAGTACATGCCCTTCATGAAATTGCAG 2503

Qy   2420 GTAGTTGCTTCAGACGTCGGGTCTTGGGTGGATACCCACACGCCATTTCTAAACCTTAGAG 2479
            | | ||||||||||| |||||||||||
Db   2480 ATGATCTATGCACATCAGAATGACTTTAAGGAAACCGCACAGAAGGCCGTTCTTTTCCAA 2539

Qy   2504 TTTGTCTATGCACATCAGGAAGGTTTTAAAGAACAGGGAACAGAGAAGCTCGTGAATTTTGGA 2563
            ||||||||||||| ||| ||| |||| |||||| ||| || ||||| ||||||
Db   2564 AGTAGCCGTCTTGTGAATCTTGCCTACTTGCCTTACCTATCCGATTTGATAAGGAATCAGAC 2623

Db   2540 AGTGAAGACCTCTTCAATCTAGCGGTTCCTGTAGGGATTAAAATTTGAA-----ATTC 2593
                 |||||||||||||||||||||||||||||||||||||||||||||
Qy   2624 TGCCAAGATGCAACGTACAAATCTAACTCTTGGTTATACTGGATCTTCGTTCGTAGTAAC 2683

Qy   2594 TCCGATAAGTCTACGTATGATCTCTCCATAGCTTACGTTCCCGATGTGATTCGTAATGAT 2653
            ||||| | ||||||| |||||||||| |||||| ||||||| |||||| ||||||||
Db   2684 CCCGACTGTACGGACAACACTGCGAATTAGCCGGTGATTCTTGGAAAACCTTCGGTACGAAT 2743

Db   2654 CCAGGCTGCACGGACGACAACTCTTTATGGTTTCTGGGGATTCTTGGGTGCACATGTGTACAAGC 2713
                 || ||||||| |||| || || ||||| || ||
Qy   2744 TTGGCAAGACAAGCTTAGTAGTCCTTCCGTCGTGCAGGGAACCCATTTTGCTTTAAACTCAAATTTT 2803

Qy   2714 TTGTCTAGACAAGCTCTTTCGTACGTGCTGAAATCATCATGCCTTTGCTTCAAACTTTT 2773
             | ||||| ||||||| ||| ||||||| ||||||| |||||| ||||| ||
Db   2804 GAAGCCTTTAGCCAATTTCTTTGAATTGCTGGGTCATCTCGCAATTACAAATGTAGAC 2863

Db   2774 GAAGTTTCAGTCAGTTTGAAGTCGCAGTTGCGAGTTCTTCGTCGTAGCTATCGAT 2833
            ||||| ||||| ||||||||||| ||||||| ||| ||||||||| ||
Qy   2804 GAAGCCTTTAGCCAATTTCTTTGAATTGCTGGGTCATCTCGCAATTACAAATGTAGAC 2863

Qy   2864 TTAGGAGCAAAATACCAATTCTAATGC 2890
            |||||||||||||| ||||| ||||
Db   2834 CTTGGAGGAAGAGATTCGGATTTTAATCC 2860

PT Species-specific test for identifying mammals infected with
PT Chlamydia pneumoniae - comprises detecting antibodies specific for
PT outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT these proteins
XX
PS Claim 6; Page 55-56; 115pp; English.
XX
CC This DNA sequence codes for the novel 96.7 kDa surface exposed
CC protein Omp9 (see AAW88422) of the human respiratory pathogen
CC Chlamydia pneumoniae. By generating antibodies against C.
CC pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
CC was obtained which reacted with outer membrane proteins. The
CC antibody was used to identify the genes (see AAX06816-27) encoding
CC Omp4-Omp15 proteins (see AAW88417-28) in an expression library of
CC C. pneumoniae DNA. The genes are situated in 2 gene clusters:
CC Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
CC the other, and encode polypeptides of about 89.6-100.3 kDa and
CC about 56.1 kDa. The invention provides a new species specific test
CC for identifying mammals (including humans) infected with Chlamydia
CC pneumoniae. The test comprises detecting antibodies specific for
CC Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC membrane proteins, especially by PCR. The proteins are also used
CC in the diagnosis of C. pneumoniae infection in mammals. The
CC nucleic acids and proteins can also be used in the immunization of
CC mammals, the nucleic acids being particularly useful as DNA
CC vaccines for effecting in vivo expression of antigens. The
CC vaccines may also prevent atherosclerosis and bronchial asthma,
CC which are possibly associated with C. pneumoniae.
XX
SQ Sequence 2757 BP; 770 A; 564 C; 642 G; 781 T; 0 other;

Query Match   17.4%;   Score 522.2;   DB 20;   Length 2757;
Best Local Similarity   53.4%;   Pred. No. 2.5e-134;
Matches 1424;   Conservative   0;   Mismatches 1153;   Indels 90;   Gaps 12;

```
Qy  242 GAAGATGCTGGAACTACCTACCTATTTAAGGAAATGTCACTCTAGAAAAATATTCCTGGA 301
            ||||||  |||  | ||| ||||  || | ||||| |||||||| |       || ||
Db  160 GATGCTAGTGGCACGACCTATATTCCTGATGGGGATGTCTCGATA---AGCCAAGCAGGG 216

Qy  302 ACAGGCACAGCAATCACAAAAAGCTGTTTAACAACACTAAGGGCGATTTGACTTTCACA 361
           | |  | ||| | ||| | ||| ||||| | ||||||  |||  | ||| || ||
Db  217 AAACAAACGAGCTTAACCACAAGTGTTTTCTAACACTGCAGGAAATCTTACCTTCTTA 276

Qy  362 GGTAACGGGAACTCTCTATTGTTCCAAACGGTGGATGCAGGGACTGTAGCAGGGGTGCT 421
            | ||||||| ||| ||| || |  | |  |  | ||  |||  ||| |||| |||| ||
Db  277 GGGAACGGGATTTTCTCTTCATTTGACATATATATTTCGTCTACTGTTGCAGGTGTGTT 336

Qy  422 GTTAACAGCAGGCGTGGTAGAATAAATCTACCACGTTTATAGGGGAGCTTGGGGGT 481
           |||| |||| ||||  |   ||| |  || | ||  || |
Db  337 GTTAGCAATACAGCAGCTTCTGGATTACGAAATTCTCAGGATTTCAACTCTTCGGATG 396

Qy  482 ATTGCGTCTCCTGGAAGTTCAGTTTGCTCTTCAGCCAAAAAACTTTCAACGGATAAT 541
           |||| |||||| |       || ||| | |   |      ||||  ||||  ||||
Db  397 CTTGCAGCTCCT------AGGACCCACAGGTAAAGGAGCCATTA--AAATTACCGAT 444

Qy  542 AGCTTGAGTTGACAAAAAATGTCAGTTTGCTCTTCAGCAAAAACTTTCAACGGATAAT 601
            | ||  ||| ||  || |||  |  || | |  | ||  |  ||||  ||||  ||||
Db  445 GGTCTCGGTGTTTGAGAGTATAGGGAATCTTGACCAAAATGAAAATGCCTCAGTGAAAAT 504

Qy  602 GGCGGTGCTATCACCGCCAAAAACTCTTCATTAACGGGACTACAATGTCAGTCTCTGTT 661
           ||  ||| |||||| |||||||  ||| |  |    | || |  | || |    ||||
Db  505 GGGGGAGCCATCAATCAATACGAAGACTTTGTCTTTGACTCGGAGTACGCCGGTTTGAGCGTTC 564

Qy  662 TCTGAAAATACCTCCTCAAAGAAGAAGGCCGAGCCATTCAGACTTCCGATGCCCTTACCATT 721
           ||||| ||| ||| | |||| | |  | | || | || ||  |  | ||| |   | ||||
Db  565 CTTTGCAATAGCTCGTCGCAACAAGGGGAGCGATCTATGCTTCTCGGTGACTCGTGATT 624

Qy  722 ACTGGAAACCAAGGGAAGGGAAGTCTCTTTTCTGACAATACTTCTTCGGATTCTGGAGCTGCA 781
           ||||  ||| || ||  ||   || |  || ||| ||| | |  | | || |  || | | ||
Db  625 TCTGAGAATGCAGGAATCTTGAGCTTCCGGAAACAACAGTGCGACAACATCAGGAGGGCGCG 684

Qy  782 ATTTTTACAGAAGCCTCGGGTGACTATTTCTAAATGCTAAAGTTCCTTTATTGACAAT 841
           ||||| ||| | ||| |||| |||| |||||    | |||||||||  | |||  ||||
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Query Match   17.4%;   Score 523;   DB 24;   Length 534;
Best Local Similarity   99.8%;   Pred. No. 6.8e-135;
Matches 534;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps 1;

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Qy  101 ATGAAGTCTTCTTCCCAAGTTGTATTTTGTATTTCTACATTGCTATTTGCCTTTGTCTATG 160
        ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db    1 ATGAAGTCTTCTTCCCAAGTTGTATTTTGTATTTCTACATTGCTATTTGCCCTTTGTCTATG 60

Qy  161 ATTGCTACCGAGACAGTTTGGATTCAAGTGCGAGTTCGATGGGAATAAAAATGGTAAT 220
        |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   61 ATTGCTACCGAGACAGTTTGATTCAAGTGCGAGTTCGATGGGAATAAAAATGGTAAT 120

Qy  221 TTTTCAGTTCGTGAGAGTCAGGAAGATGCTGGAACTACCTATTTAAGGGAAATGTC 280
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 TTTTCAGTTCGTGAGAGTCAGGAAGATGCTGGAACTACCTATTTAAGGGAAATGTC 180

Qy  281 ACTCTAGAAAATATTCCTGGAACAGGCACAGCAATCACAAAAAGCTGTTTTAACAACACT 340
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ACTCTAGAAAATATTCCTGGAACAGGCACAGCAATCACAAAAAGCTGTTTTAACAACACT 240

Qy  341 AAGGGCGATTTGACTTTCACAGGGTAACGGGAACTCTCTATTGTTCCAAACGGTGGATGCA 400
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 AAGGGCGATTTGACTTTCACAGGGTAACGGGAACTCTCTATTGTTCCAAACGGTGGATGCA 300

Qy  401 GGGACTGTAGCAGGGGCGTGCGTGTTAACAGCAGCCGTGGTAGAATAAATCTACCACGTTTATA 460
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GGGACTGTAGCAGGGGCGTGCGTGTTAACAGCAGCCGTGGTAGAATAAATCTACCACGTTTATA 360

Qy  461 GGGTTTCTTCGCTATCTTTATTGCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGGA 520
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GGGTTTCTTCGCTATCTTTATTGCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGGA 420

Qy  521 GCCGTTAGCTGCTCCTACGGGTAGCTTGAGTTTGACAAAAAATGTCAGTTTGCTCTTCAGC 580
        ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  421 GCCGTTAGCTGCTCCTACGGGTAGCTTGAGTTTGAC-AAAAATGTCAGTTTGCTCTTCAGC 479

Qy  581 AAAAACTTTTCAACGGATAAATGCGGTGCTATCACCCGCAAAAACTCTTTCATTAA 635
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  480 AAAAACTTTTCAACGGATAAATGCGGTGCTATCACCCGCCAAAAACTCTTTCATTAA 534
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RESULT 13
AAX06821
ID AAX06821 standard; DNA; 2757 BP.
XX
AC AAX06821;
XX
DT 26-APR-1999 (first entry)
XX
DE Chlamydia pneumoniae surface exposed protein Omp9 DNA.
XX
KW Omp9; outer membrane protein 9; surface exposed protein; antigen;
KW infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
XX
OS Chlamydia pneumoniae.
XX
PN WO9858953-A2.
XX
PD 30-DEC-1998.
XX
PF 19-JUN-1998; 98WO-DK00266.
XX
PR 23-JUN-1997; 97DK-0000744.
XX
PA (BIRK/) BIRKELUND S.
PA (CHRI/) CHRISTIANSEN G.
XX
PI Birkelund S, Christiansen G, Knudsen K, Madsen A;
PI Mygind P;
XX
DR WPI; 1999-105610/09.
DR P-PSDB; AAW06822.
XX

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Qy  1904  AATCCCGAGCGTATCGCTCTTAGTCCCAATAGCTTATGGAATGCATTTATAGATATT  1963
          ||||| |||| |||||||||||  |||||||||| |||||| || |||||||| |||
Db  1792  AATCCAGAACGTCAGGGACCTTTGGTTCCTAATAGCCTGTGGGGTTCTTTTGTCGATGTC  1851

Qy  1964  AGCTCTCCATTATCTTATGGAGACTGCAAACGAAAGGGTTGCAGGGAGGACCGTGCTTTT  2023
          |||||       ||||                               |||
Db  1852  CGCTCCATTCAGAGCCTCATGGACCCATGACCGGACCAAGTTCGTTATCTTCGTCAACAAATTTG  1911

Qy  2024  TGGTGTGCTGGATTATCTAACTTCTTCCATAAGGATAGTAGTACAAAAACACCACGCGGTTT  2083
          |||||                  ||||||| || |||||||||| ||  ||||||||
Db  1912  TGGGTATCAGGAATCGCGGACCTTTTGCATGAAGATCAGAAGGAAACCAACGTAGTTAT  1971

Qy  2084  CGCCATTGAGTGGCGGTTATGTCATAGGAGGAAACCTACATACTTGTTCAGATAAGAATT  2143
          ||||||    ||||||   || ||||| ||||||||| || |||| ||||||| |||
Db  1972  CGTCATTCTCAGCGCGGTTATGCATTAGGAGGAGGAATTCTTCACGGCTTCTGAAAATTTC  2031

Qy  2144  CTTAGTGCTGCATTTTGTCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAAT  2203
          ||||||||   | ||| ||  ||||||   |  | ||||||||||||||| ||||||
Db  2032  TTTAATTTGTGCTTTTTGTCAGCTTTTTGGGCTACGACAAGGACCATCTGTGGCTAAGAAC  2091

Qy  2204  CAAGGTACAGTCTACCGAGGAACTCTATTACCAGCACAACGAAACCTATATCTCTCTT  2263
          |||||           |  ||||| ||| |||||||||| ||||  ||||||||| | |
Db  2092  CATACCCATGTATATGCAGGGGCAATGAGTTACCGAGAGTCTAAGACCCTCTAAGAGATTCCTGTTCTCTTT  2151

Qy  2264  CCTTGCAAACTACGGCCTTGTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCTCTTT  2323
                                 |||||||||||| |||||| |||  |||| |
Db  2152  GCTAAGA---------------------TTTTGTCAGGAAAATTCTGACTCCCTACCTTTGTCTTC  2196

Qy  2324  TCAGGAAACCTTAGCTACACCCATACGATAACGATCTGAAAACCAAGTATACAACACATAT  2383
                   |||| || |||||  || |||| || ||||||| || ||| ||||||||||
Db  2197  AATGCTCGGTTTGCTTATGGCCATACCAGCAATAACATGACCCACAAAGTACACTGGCTAT  2256

Qy  2384  CCTACTGTAAAGAGAGCTGGGGAGATGATAGTTTGCTTAGAATTCGGTGGAAGAGAGCT  2443
          |||  ||||||| || ||||| |||||| ||| |||| ||| || ||| |||||||||
Db  2257  TCTCCCTGTTAAGGAAGGCTGGGGAAATGATGCGCTTCGGGTATAGAATGTGAGGAGCTATC  2316

Qy  2444  CCGA----TTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTACATGCCCCTCATGAAATTG  2500
          ||||       |||  |||||||||| |||| ||||  || | |||| |||||| ||
Db  2317  CCGGTAGTTGCTTCAGGACGTCGGTCTTGGGGTGGATAACCCACACGCCATTTCTAAACCTA  2376

Qy  2501  CAGTTGTCTATGCACATCAGGAGAGGTTTAAAGAACAGGAACACAGAAGCTCGTGAATTT  2560
          |||||| ||||| ||| ||||  ||||| ||||| || ||||||  |||| | |  |||||
Db  2377  GAGATGATTCTATGCACATCAGAATGACTTTAAGGAAAAACGGCACAGAGAGGCCGTTCTTTC  2436

Qy  2561  GGAAGTAGCCGTCTTGTGAATCTTGCCTTACCTATCGGATCTGATTTGATAAGGAATCA  2620
          |||||||||||||||||||||||||| |||||||  |||| ||||||||  |||| |
Db  2437  CAAAGTGAAGACCTCTTCAATCTCAATCTAGCCGGTCCGGTTCCTGTAGGGATAAAAATTTGAGAA------A  2490

Qy  2621  GACTGCGAAGATGCAACGTACAATCTAACTCTTGGTTTATACTGTGGATCTTGTTCGTAGT  2680
          ||| |||||||| |||| ||||  ||||| |||||||| | || |||| |||||||  ||
Db  2491  TTCTCCGTATAGTCTACGTATGATCTCTCCATAGCTTTACGTGTCGATTGATTCGTAAT  2550

Qy  2681  AACCCCGACTGTACGACACACTCGGGGTGATTCTTGGAAAACCTTCGGTACG  2740
          ||||||||||||| ||||||||||||| ||||| ||||||| ||||||| ||
Db  2551  GATCCAGCGTCGACGACACAACTCTTATGGTTTCTGGGGATTCTTCGGTGGTCGACATGTGGTACA  2610

Qy  2741  AATTTGGCAAGACAAGCTTAGTCCTTCGTGCGAGGGAACCATTTTGCTTTAACTCAAAT  2800
          |||| || |||| ||||| |||||  || || ||||||||  |||| |  |||||| |
Db  2611  AGCTGTGTCAGCAAGCTCTTCTGTACGTGCTGGAAATCATCATGCTTTGCTTCAAAC  2670

Qy  2801  TTTGAAGCCTTAGCCAATTTCTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTA  2860
          ||||||      |||||||||  ||||| ||||  |||| || | |||||  |||||
Db  2671  TTTGAAGTTTCAGTTCAGTTGAAGTCAGAGTTCTGTCTCTCTGTAGCTATGCTATC  2730

Qy  2861  GACTTAGGAGCAAAATACCAATTCTAA  2887
          |||| || |||||  ||||||||| ||
Db  2731  GATCTTGGAGGAGATTCGGATTTTAA  2757
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RESULT 14
AAA30851
ID   AAA30851 standard; DNA; 2950 BP.
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Db   685  ATCTCTGCTGTGAAGGGAACCTTGTGATCTCCAATAACCAAAATATCTTTTCGATGGCTGC  744
          ||||        || |||| ||||||||||||||  ||||   ||||||| |||||||||
Qy   842  AAGTCACAGGAGCGAGCTCCTCAACACGGGGATATGTCAGGAGGTGCTATCTGTGCT  901

Db   745  AAAGCAACTACAAATGGCGGAGCTATTGATTGTAACAAAGCAGGGG----------  790
          |||  ||||  |||||||  |||||||| |||||  |||||||||
Qy   902  TATAAAACTAGTACAGATACTAAGGTCACCCTCACTGACGATGTTACTCTTCAGC  961

Db   791  ------CGAACCCAGACCCTATCTTCAGGAAATGAGAGCCTGCATTTCTG  843
                | |||||| || |||| |||  || ||||| ||||||||||
Qy   962  AACATACATGCGACACAGCGGGAGGGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTCC  1021

Db   844  AATAACACAGCAGGAAATAGTGAGGAAATGGATTTATACCAAAAAAATTGGTGTGTTATCCTCA  903
          ||  |||||| |||||| || || |||   ||||||||||||||  ||||||||||||
Qy  1022  GGAGGACTTACCCTATTCAGTAGAAAATAGTGTCAATGAGGTACAGCTCCTAAAGGTTGGA  1081

Db   904  GGACGAGGAGGAGGTGTTATTTTCTAACAACAAAGCTGCGAATGCTACTCGTAAAGGAGGG  963
          ||   || |||||||  | || ||| ||||||| |||||||| || |||||||||
Qy  1082  GCCATAGCTATCGAAGAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGTC  1141

Db   964  GCAATTGCCATTCTAGATTCTGAGAGATTAGCATTCTGCAGATCTCGGCAATATCATT  1023
                    ||||||||| ||||||||| |||||   ||||  || ||||||||| |
Qy  1142  TTTTAGGGAATACAGTCACTTCTAC------TACTCCTGGGACGAATAGAAGTAGTATC  1195

Db  1024  TTCGAGGGCAATACTACAGGAACGTCCTGCGAGTGTGACCAGAATGCTATA  1083
          ||  ||| |||  |||| |||| |||| ||||  ||||| |||||||||
Qy  1196  GACTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTTGCTTGCTCTGGTTGAGAGCCATCTAC  1255

Db  1084  GATCTTGCATCGAATGCAAAATTTTTAAATCTCCCAGCGACTCCGGGGAAATAAAGTTATT  1143
          |||| ||||   |||| |||   | ||||| ||| | ||||||
Qy  1256  TTCTATGATCCCATAACTACAGGATCATCCACACAGTTACAGATGTCTTAAAGTTAAT  1315

Db  1144  TTCTATGAATCCTATCACGA-------GCTCAGAGCTACTGATAAGCTCTCTTTGAAT  1194
          |||||||| || |||||||        || ||||||| || |||| || |||||||
Qy  1316  GAGACTCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAGAGAAAAG  1375

Db  1195  AAAGTGACGGCAGGATCTGAAATACCTTATGAAGGCTACAGTGAGAGGCAACATA  1254
          |||| ||   ||| |||| ||| ||| |||||||||| || |||||  ||
Qy  1376  TTATCAGAGACCAGAGAGGCCGGAGATTCTAAAAATCTTACTTGAGACTACAGCCCTGTA  1435

Db  1255  CTCTCAGAGAGGAACTTAAGAAACCTGACAATCTGAAGTCTACATTTACACAGGCTGTA  1314
          |||||||||||||||||||||||||| |  ||| ||||   |||||   |||||
Qy  1436  ACTCTTTCAGGAGGTACTCTATCTTTAAAACATGGAACTCTGCAGACTCCAGCTCATTC  1495

Db  1315  GAGATGATCTATGCACATCAGGGAGATGAGAGTGAGATGACTGTGAGTTGCAAATAATACTATA  1374
          || ||| ||||| |||||||  |||  ||  ||||||| ||   |||||| || |  |
Qy  1496  ACTCAACAGGCAGATTCTCGTCTCGAAAATGGACGTAGAGAACTACTCTAGA---ACCTGCT  1552

Db  1375  ACGCAGGTCGAGGGATCGAAAGTCGTTATGCTGATGAGGGGACTACTTTGTAGGCAAGCGCT  1434
          ||||||||  ||||||   || ||||| |||| ||||||||||| || | |||| ||
Qy  1553  GATACTAGCACCATAAACAATTGGTCAATCAGTTGTCATTGTTATGATGACCGGTGCAAAGAAG  1612

Db  1435  GAGGGGGTCACTCTCAATGGCCTAGCCATTAATAATAGATTCCTTAGATGGACAAATAA  1494
          || |  | |||  |||||  |||  ||||||||||||   || || ||||| ||||
Qy  1613  GCAAAAATAGAAACCAAAGCTACGTCAAAGACATTTTATCTGGAACCATCACTTTA  1672

Db  1495  GCTATCATTAGGGCAGCAAGTAAGGAATGTGTTGCCTTATCAGGGCCTATCATGCTT  1554
          |||| ||||  || |||  ||| ||||  |||||||||| |||||||||| ||||
Qy  1673  TTGGACCCGACGGCACGTTTATGGAAAATCATAGTTTAAGAAATCCTCAGTCCTTACGAC  1732

Db  1555  GTAGATGCTCAGGGGGAACTATTATGGACATCAGAATCTCAGTCAACAGCCAGGGTCTTTCCT  1614
          || ||||| ||||   |||| ||||| || |  ||||  || || |||||| |||||
Qy  1733  ATCTTAGAGCTCAAAGCTTCTGGAACTGTAACAAGCACCGGCAGTGACTCCAGATCCTATA  1792

Db  1615  GCAAAAATAGAAACCAAAGCCTGTCAAAAAATCTGACTTTATCTGGAACCACCACTTTA  1674
                    || |||||||| || ||||| || |||| || ||| ||||  |||||
Qy  1793  ATGGGTGAGAAATTCCATTACGGCTATCAGGGGAACTGGGCCCCAATTGTTGGGGGACA  1852

Db  1675  CTAAATATTACGCAATCACTATGGGTATCAAGGAACT--GGAATAATTGTTCGGTCGAC  1731
          ||   || |||||||  |  |||||  |||||||  |  | || ||||  ||||||||
Qy  1853  GGGGCTTCT-------ACGACTGCAACCTTCAACTGAACTGGCTATATTCCT  1903

Db  1732  GATGCAACTGCAAAAAGCAAAAAAATGCTACCTTAACTTGGACTAAAACAGGATACAAGCCG  1791
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XX
AC   AAA30851;
XX
DT   29-AUG-2000  (first entry)
XX
DE   Chlamydia antigen CPN100638 full length coding sequence.
XX
KW   Chlamydia antigen; diagnosis; infection; community acquired pneumonia;
KW   therapy; upper respiratory tract disease; bronchitis; sinusitis;
KW   asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma;
KW   ds.
XX
OS   Chlamydia pneumoniae.
XX
FH   Key             Location/Qualifiers
FT   CDS             101..2887
FT                   /*tag= a
FT                   /product= Chlamydia antigen CPN100638
XX
PN   WO200032794-A2.
XX
PD   08-JUN-2000.
XX
PP   01-DEC-1999;  99WO-CA01147.
XX
PR   01-DEC-1998;  98US-0110339.
PR   01-DEC-1998;  98US-0110340.
PR   01-DEC-1998;  98US-0110427.
PR   01-DEC-1998;  98US-0110428.
PR   01-DEC-1998;  98US-0110438.
XX
PA   (CONN-) CONNAUGHT LAB LTD.
XX
PI   Murdin AD, Oomen RP, Wang J;
XX
DR   WPI; 2000-412339/35.
DR   P-PSDB; AAY90239.
XX
PT   Nucleic acids encoding polypeptide antigens from Chlamydia useful for
PT   preventing, diagnosing and treating diseases such as community acquired
PT   pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
PT   asthma --
XX
PS   Claim 2; Fig 5; 174pp; English.
XX
CC   This sequence encodes a Chlamydia antigen of the invention, designated
CC   CPN100638. The nucleic acids (and their complementary sequences) may be
CC   used as diagnostic agents for detecting the presence of nucleic acids
CC   encoding Chlamydia antigens in samples according to standard methods,
CC   and therefore, for diagnosing Chlamydia infections. For example, they may
CC   be used as primers and probes for diagnostic polymerase chain reaction
CC   (PCR) assays. Antisense sequences may be used to down regulate
CC   expression of the proteins and may be used to treat infections. The
CC   nucleic acids may also be used to produce the protein antigens they
CC   encode according to standard recombinant DNA methodologies. The
CC   proteins may then be used as antigens for the production of antibodies
CC   (i.e. as vaccines) for preventing infection by Chlamydia. The
CC   antibodies may also be used as diagnostic reagents for detecting
CC   infections. Chlamydia is a pathogen implicated in the development of
CC   (for example) community acquired pneumonia, upper respiratory tract
CC   disease (especially bronchitis and sinusitis, asthmatic bronchitis,
CC   adult-onset asthma and acute exacerbations of asthma in adults.
XX
SQ   Sequence 2950 BP; 855 A; 724 C; 562 G; 809 T; 0 other;

Query Match             17.3%;  Score 518.2;  DB 21;  Length 2950;
Best Local Similarity   53.3%;  Pred. No. 3.4e-133;
Matches  1427;  Conservative    0;  Mismatches  1173;  Indels   75;  Gaps   13;

Qy        243 AAGATGCTGGAACTACCTATTTAAGGGAAATGCACTCTAGAAAAATATTCCTGGAA 302
                ||||| |||||||  | |||||||  || |  |||| | ||| |  |||| ||
Db        258 ATGCAGAATGGAACTATCATATAATCTAACAGGGGATGTCTC---AATCACCACCAGGAT 314
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Qy   303  CAGGCACAGCAATCACAAAAAGCTGTTTTAACACACTAAGGGCGATTGACTTTCACAG  362
          | ||| ||||| || |  |  ||| ||| ||  |      | | |  |||| || ||
Db   315  CTCCGACAGCTCTAACCGCTCCTGCTTTAAAGAAACTACTGGGAATCTTCTTTCCAAG  374

Qy   363  GTAACGGGAACTCTCTATTGTTCCAAACGGTGGATGCAGGGACTGTAGCAGGGGCTGCTG  422
          | ||| |  |||| | |  | || || |  | | |||    |  |||    | || ||
Db   375  GCCACGGCTACCAATTTCTCCTACAAAAATCGATGCGGG------AGCGAACTGTACCT  428

Qy   423  TTAACAGCAGCGTGGTAGATAAATCTACCACGTTTATAGGGTTTCTCGCTATCTTTTA  482
          || ||| | ||   | |  | ||  |  |  | || ||  | |||| | |||| |||| |
Db   429  TTACCAATACAGCTGCAAATAAGCTTCTCTCCTTTCAGGATTCTCCATTGTCACTAA  488

Qy   483  TTGCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGCCGTTAGCTGCTCACGGGGTA  542
          |  |  ||  |  | |   ||| ||  | | ||| ||| || | | ||  || | ||
Db   489  TACAAACCACGAATGCT------ACCACAGGAACAGGAGCCATCAAGTCCACAGGAGCTT  542

Qy   543  GCTTGAGTTTGACAAAAAATGTCAGTTTGCTCTTCAGCAAAAACTTTCAACGCATAATG  602
          |  | | |  | |  |  | || |||||| | |||  | ||||||||| | | ||| ||
Db   543  GTTCTATTCAGTCGAACTAT---AGTTGCTACTTTGGCCAAAACTTTCTAATGACAATG  599

Qy   603  GCGGTGCTATCACCGCCAAAAACTCTTCATTAACAGGGACTACAAATGTCAGCTCTGTTTT  662
          | || || | | | ||||  ||||  ||||  ||| | |  | | |  | |   || |||
Db   600  GAGGCGCCCTCCAAGGCAGCTCTATCTATCGTATCGTCTAAACCCCAACCTAAC---GTTTG  656

Qy   663  CTGAAAAATACCTTCCTCAAAGAAAGGCGGAGCCGGAGCCATTCAGAATTCGATGCCCTTACCATTA  722
          | ||||| |||| | |  ||| |||| |  | | |||   |||||||  | |  |  |||||| ||||
Db   657  CCAAAAACAAAGCACCGCAAAAAGGGGGTGCCCTCTATTCCACGGGAGGGATTACAATTA  716

Qy   723  CTGGAAACCAAGGGGAGAGTCTCTTTTCTGACAATACTTCTTCCGGATTCTGGAGCTGCAA  782
          | ||||||| || |  | |||| | | ||| |||||||| |  | ||| | |||| || ||
Db   717  ACAATACGTTAAACTCAGCATCATTTTCTGAAAATACCGGCGGCGAACAATGGCGGAGCCA  776

Qy   783  TTTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTTCCTTTATTGACAATA  842
          ||| |||| | | ||| | |||| |  || | | ||  |||  |  ||||| || ||| |
Db   777  TTTACACGGAGCTAGCAGTTTATTAGCAGCACAAAAGCAATTAGCTTTATAAACAATA  836

Qy   843  AGGTCACAGAGGAGCGAGCTCCTCAACAACGGGGATAATGTCAGGGGAGCCATTTACTGTAGTA  902
                                   ||  | |||| | | ||| |||| |||||| | | |||| | |
Db   837  GTGTGACCG----------CAACCTCAGCTACAGGGGGAGCCATTACTGTAGTA  881

Qy   903  ATAAAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAGCA  962
          | | ||| ||| ||||| |  || | |   || ||  | |||| |   |  | ||| | |
Db   882  GTACATCAGCCCCCAACCAGTCTAAACTCTATCAGACACAGGGGAACTGAACTTTATAG  941

Qy   963  ACAATACATGACAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTGAACTGCTTCCG  1022
           |||| |||||||| ||||| |  |  |||  | | || ||| ||| |  ||  ||||
Db   942  GAAATACAGCAATTACTAGTGGTGGGGCGATTTATACTGACAATCTAGTTCTTCTTCTG  1001

Qy  1023  GAGGACTTACCCTATTCAGTAGAAATAGTGCAATGAGCTCAAGGTGGAG  1082
          |||||  ||||| ||||| ||| ||||| | ||  |||  |  |||| || |||| ||
Db  1002  GAGGACCTACGCTTTTAAAACAACTCTGGCTATGATACTGCAGCTCCCCTTAGGAGAG  1061

Qy  1083  CCATAGCTATCGAAGATAGTGGGAATTGAGTTTATCCGGCGATAGTGTGACATTGTCT  1142
          ||  | || ||||| || | | |||| ||| | | ||| |||| | ||| | |||||
Db  1062  CAATTGCGATTGCTGACTCTGGATCTTTGAGTCTTTCGGCTCTTGGTGGAGACATCACTT  1121

Qy  1143  TTTTAGGGAATACAGT-------CACTTCTACTCCTGGACGAATGAAGAAGTAGTA  1193
          |||| | | ||| | ||  |  |||||||| || |||| ||| ||| ||| |||
Db  1122  TTGAGGAAACACAGTAGTCAAAGAGCTTCTTCGAGTCAAAGACCACTACCAGAATTCTA  1181

Qy  1194  TCGACTTAGGA---ACGAGTGCAAAGATGACAGCGCTTGCGTTCTGCGTCTGGTAGAGCCA  1250
          |  | | || |    ||| || | |||||| || |  | |  ||   |||| ||||| |||
Db  1182  TTAACACTGGAAACACCAATGCTAAGATTGTACAGCTGCAGCTGCGAGCCTCTCAAGGACAATACTA  1241

Qy  1251  TCTACTTCTTATGATCCCATAACTACAGGATCATCCACACAGTTACAGATGTCTTAAAAG  1310
          |||| | || | ||| | ||| ||  || |||  | |  |  ||  ||| | | | |||
Db  1242  TCTACTTCTATGATCCTATAACAATCTATAACAACTAGCATCACTGCAGCTGCTCTAAACT  1301

Qy  1311  TTAATGAGACTCCGGCAGATTCTGCACTACTACAATAAGAGGAACATCATCTTCACAGGAG  1370
          | |||| ||| || ||  |||||  |||| | || |||| | | || | ||||| ||||||
Db  1302  TAAATGGTCCTGACCTTGCAGGGAATCCTGCATATCAAGGAACCATCGTATTTTCTGGAG  1361

Qy  1371  AAAAGTTATCAGAGACAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAGC  1430
          ||||| ||| |||  | ||||| |  ||||| ||| | |||| | |||||| || |  |
Db        (continued)
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Db 2433 CCTTACCACCACTGCTTTAAGCCATGAGGTCTCTTCCACGCGTATTTCCTTTCATCA 2492
         |||| |||||||||||| || ||||| |||| ||
Qy 2496 AATTGCAGTTGTCTATGCACATCAGGAGAGGTTTAAAGAAC---AGGGAACAGAAGCTC 2552

Db 2493 AAGTAGAAGCTTCGTACATACACCAAGATAGCTTCAAAGAACGTATATACACCTTGGTAC 2552
         ||||||||| |||| | ||| ||||| ||||||||||||
Qy 2553 GTGAATTGGAAGTAGCCGTCTTGTGAATCTTGCCTTACCTATCGGGATCCGATTTGATA 2612

Db 2553 GATCTTTCGATAGCGGTGATTTAATTAACGTCTCTGTGCCTATTGGAATTACCTTCGAGA 2612
         || ||| | ||||||| ||| || || ||||||||||||
Qy 2613 AGGAATCAGACTGCCAAGATGCAAGTACAAATCTAACTCTTGGTTATACTGTGGATCTTG 2672

Db 2613 GATTCTCGAGAAACAGAGCGTGCGTCTTACGAAGCTACTACGTCATCTGCCGATGTCT 2672
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Qy 2673 TTCGTAGTAACCCGACTGTACGACAACACTGCGAATTAGCGGTGATTCTTGGAAAACCT 2732

Db 2673 ATGTAAGAATCCTGACTGACGACAGCTCTCCTAATCAACAATACCGTGGAAAACTA 2732
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Qy 2733 TCGGTACGAATTGGCAAGACAAGCTTAGTCCTTCGTGCAGGGAACCATTTTGCTTTA 2792

Db 2733 CAGGAACGAATCCTCAAGACAAGCTGGTATCGGAAGAGCAGGGATCTTTTATGCCTTCT 2792
         | || ||||| || |||||||||| || |||| || ||| ||||| ||| ||| |
Qy 2793 ACTCAAATTTGAAGCCTTTAGCCAATTTCTTTGAATTGCGTGGGTCATCTCGCCAATT 2852

Db 2793 CTCCAAATCTTGAGGTCACAGTAACCTATCTATGGAAATTCGTGGATCTTCACGCAGCT 2852
         | | ||| | ||| |||| | || | | || ||| || | || |||| |||||||
Qy 2853 ACAATGTAGACTTAGGAGCAAAATACCAATCTAA 2887

Db 2853 ACAATGCAGATCTTGGAGGTAAGTTCCAGTTCTAA 2887
         |||||| || || |||| || || ||| ||||

RESULT 15
ABL91200
ID   ABL91200 standard; DNA; 2787 BP.
XX
AC   ABL91200;
XX
DT   29-JUL-2002 (first entry)
XX
DE   Chlamydia pneumoniae cp6731 ORF DNA, SEQ ID NO:34.
XX
KW   Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KW   human respiratory disease; cardiovascular disease; atherosclerosis;
KW   coronary artery disease; carotid artery stenosis; myocardial infarction;
KW   cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW   strain CWL029; open reading frame; ORF; gene; ds.
XX
OS   Chlamydia pneumoniae.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..2787
FT   /*tag= a
FT   /product= "cp6731"
FT   sig_peptide   1..78
FT   /*tag= b
FT   mat_peptide   79..2784
FT   /*tag= c
FT   /product= "Mature protein"
XX
PN   WO20020202606-A2.
XX
PD   10-JAN-2002.
XX
PF   03-JUL-2001; 2001WO-IB01445.
XX
PR   03-JUL-2000; 2000GB-0016363.
PR   11-JUL-2000; 2000GB-0017047.
PR   21-JUL-2000; 2000GB-0017983.
PR   07-AUG-2000; 2000GB-0019368.
PR   18-AUG-2000; 2000GB-0020440.
PR   14-SEP-2000; 2000GB-0022583.
PR   10-NOV-2000; 2000GB-0027549.
PR   22-DEC-2000; 2000GB-0031706.

Db 1362 AGAAGCTCTCGGAAGCAGAAGCTGCAGAACTCAAATCTACAAATTCAGCAAC 1421
         ||||| ||| |||| | |||||| ||||| ||||| || | |||||
Qy 1431 CTGTAACTCTTTCAGGAGGTACTCTATCTTAAAACATGGAGTGACTCTGCGACTCAGG 1490

Db 1422 CCTCTAACTCTTGCGGGAGGGCAACTCTCTCTTAAATCAGGAGTCACTCAGTTGCTAGT 1481
         || | ||||| ||||||||| |||||| |||||| |||| || || ||||||| |
Qy 1491 CATTCACTCAACAGGCAGATTCTCGTCTCGAAATGAGACGTAGGAACTACTCTAGAAACTG 1550

Db 1482 CCCTTTTCGCAATCTCCGGGCTCACCCTCCTCATGGATGCAGGGACCCACATTAGAAACCG 1541
         | || | |||| || || || || | | ||||| ||| | | | ||| |||||||||
Qy 1551 CTGATACTAGCACCATAAACAATTGGTCATTAACATCAGTTCTATAGACGTGCAAAGA 1610

Db 1542 CTGATGGGGATCACTATCAATAAATCTGTTCTTCATGTAGATTCCTTAAAAGAGACCAAGA 1601
         |||| ||| |||| ||||| |||| |||| | |||| ||| || |||||| | |||
Qy 1611 AGGCAAAAATAGAAACCAAAGCTACGTCAAAAAAATCTGACTTTATCTGACCATCACTT 1670

Db 1602 AGGGCACGCTAAAAGCAACACAAGCAAGTCAGCAAGTCACTTTATCTGGATCGCTCTCTC 1661
         ||| || | ||| || ||| ||||| | || | | ||| ||| || || || |||| |
Qy 1671 TATTGGACCCGACGGGCACGTTTATGAAAATCATAGTTAAGAAATCCAGTCCTACG 1730

Db 1662 TTGTAGAATCCTTCTGGAAATGTCTACGAAGATGTCTTGGAATAACCCTCAAGTCTTTT 1721
         || || ||| | |||||||| | | |||| | ||| ||||| || |||| ||| |
Qy 1731 ACATCTTAGAGCTCAAAGCTT-----CTGGAACTGTAACAAGCACCCGCAGTGACTCCAG 1784

Db 1722 CTTGTCTCACTCTTACTGCTGCAGCGACGACCCCGGAATATTCACATCACAGACTTAGCTGCTG 1781
         |||| || |||| ||| | || | | | |||| ||| | ||| |||| || |||| ||
Qy 1785 ATCCTATAATGGGTGAGAAATTCATTCGGCTGTATCAGGGAACTGGGGCCCCAATTGTTT 1844

Db 1782 ATCCCCTAGAAAAAAAAATCCTATCCATTGGGGATACCAAGGGGAATTGGCATTATCTTGGC 1841
         |||| |||| ||||| || | |||| ||| |||| |||||| || ||| ||| ||||

Qy 1845 GGGGACCAGGGGC-----TTCTACGACTGCAACCTTCAACTGGACTAAAACTGGCTATA 1898

Db 1842 AAGAGGATACTGCGACTAAATCCAAAGCAGGCGACTCTTACCTGACGACAAAAACAGGATACA 1901
         |||| |||| | | ||||| ||||||| | ||||| |||| | ||| ||||| ||||

Qy 1899 TTCCTAATCCCGAGCGTATCGGCTTCTTTGAGTCCCTAATAGCTTATGGAATGCATTTATAG 1958

Db 1902 ATCCGAATCCTGAGCGTCGTGAACGCGTAGGTCTGTCTAACACGCTATGGGGATCCTTGTTG 1961
         || || ||||| |||| | || | | ||| || |||| || | |||||| ||| |||||

Qy 1959 ATATTAGCTCTCTCCATTATCTTATGGGACGACTGCAAACGAAGGGTTGCAGGGACCGTG 2018

Db 1962 ATGTGCGGCTCCATACACAGCAGCTTGTGTAGCCACTAAAGTACGCCAATCTCAAGAAACTCGCGCG 2021
         |||| ||||| || ||| || || | |||| | ||||| || ||| || || | | |

Qy 2019 CTTTTTGGTGTGCTGATTATCTAACTTCTTCCATAAGGATAGTATCAACGATGTTACACGACGCG 2078

Db 2022 GCATCTGGTGTGAAGGGATCTCGAACTTCTTCCATAAAGATAGCACGAAGATAAATAAAG 2081
         || || |||||| || ||||| | ||| ||||| ||||||| || | || | |||||

Qy 2079 GGTTTCGCCATTTGAGTGGCGGTTATGTCATAGGAGGAAACCTACATTACTTGTTCAGATA 2138

Db 2082 GTTTTCGCCACATAAGTGCAGGTTATGTTGTAGGAGCGACTACAACAACCATTAGCTTCTGATA 2141
         |||| ||||| || |||| ||||||||| |||| |||| || | ||| || ||| ||||

Qy 2139 AGATTCTTAGTGTGCTGCATTTTGTCAGCTCTTTGGAAGAGATAGAGACTACTTGTAGCTA 2198

Db 2142 ATCTTATCACTGCAGCCTTCTGCCAATTATTCGGGAAGATCACTTTATAAAATA 2201
         | |||| | | |||| || || || ||||| | ||| || || | || ||

Qy 2199 AGAATCAAGGTACAGTCTACGGAGGAAGACTCTCTATTACCAGCACAACGAAACCTATATCT 2258

Db 2202 AAAATAGAGTTCTGCCATGCAGCTTCTCTCCAGCATCTCCAGCATCTCAGCCGCACCTTGTCTT 2261
         |||| |||| || || | || ||| ||| ||| || |||| || || | | | ||||

Qy 2259 CTCTTCCTTGCAAACTATTACGGCCTTGTCTTTCGTGTCTTATAGTCCTACAGAGATTCCTGTTCC 2318

Db 2262 CTCCAAGCTTGTAC------GCTACCTTCCTGGATCTGAAGTGAAGAGTGAGCAGCCTGTCC 2312
         ||| | ||| || || || || || ||| | || ||| |||| ||||| ||||

Qy 2319 TCTTTTCAGGAAACCTTAGCTACACCCATACAGCTAACGATCTGAAAAACCAAGTATACAA 2378

Db 2313 TCTTGATGCTCAGATCAGCTTATCTATAGTAAAAATACTATGAAAAATCTATTACACCC 2372
         |||| | ||| ||| | || ||| || ||||| | | || | |||| || ||||||

Qy 2379 CATATCCTACTGTTAAAGGAAGCTGGGGAAGTAGTGTTCGCTTTTAGAATTCG---GTG 2435

Db 2373 AAGCACCAAAGGGAGAGAGTCGTGTGTATAATGACGGTTGCGTCTCTGGAACTTGCGAGCT 2432
         ||| || ||| || || ||| | || || || ||||| | | |||| || |||

Qy 2436 GAAGAGCTCCGATTTGCTTAGTAGAGAAGTGCTCTATTGGAGTGAAGAGTACATGCCCTTCATGA 2495

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XX
PA   (CHIR-) CHIRON SPA.
XX
PI   Ratti G, Grandi G;
XX
DR   WPI; 2002-154726/20.
DR   N-PSDB; ABB90542.
XX
PT   Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT   medicament for treatment or prevention of infection due to Chlamydia,
PT   preferably Chlamydia pneumoniae, and for diagnostic purposes -
XX
PS   Claim 5; Page 57-58; 364pp; English.
XX
CC   Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
CC   pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
CC   them. The proteins are predicted to be immunogenic and may therefore be
CC   useful in vaccine production and for diagnostic purposes. Chlamydia
CC   pneumoniae is a common cause of respiratory disease in humans, and is
CC   also involved in the development of cardiovascular diseases such as
CC   atherosclerosis, coronary artery disease, carotid artery stenosis,
CC   myocardial infarction, cerebrovascular disease, aortic aneurysm,
CC   claudication and stroke. The proteins and nucleic acids of the invention
CC   may be used in vaccines and pharmaceutical compositions for the
CC   prevention or treatment of chlamydial infections, particularly Chlamydia
CC   pneumoniae infections. The proteins may also be used in the detection of
CC   Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
CC   DNA probe assay or blotting techniques for determining Chlamydia
CC   pneumoniae gene expression. The present sequence represents a
CC   specifically claimed DNA which encodes a Chlamydia pneumoniae protein of
CC   the invention.
XX
SQ   Sequence 2787 BP; 814 A; 689 C; 535 G; 749 T; 0 other;

Query Match             17.2%;  Score 516.6;  DB 24;  Length 2787;
Best Local Similarity   53.3%;
                        Pred. No. 9.2e-133;
Matches  1426;  Conservative   0;  Mismatches 1174;  Indels  75;  Gaps  13;
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Qy    243 AAGATGCTGGAACTACCTACCTATTTAAGGGAAATGTCACTCTAGAAAATATTCCTGGAA 302
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Db    158 ATGCAGATGGAACTATCTATAATCTAACAGGGGATGTCTC--AATCACCAATGCAGGAT 214

Qy    303 CAGGGACAGCAGCAATCACAAAAAGTGTTTTAACAACACTAAGGGCGATTTGACTTTCACAG 362
              ||| |||||||| ||||   |||||  ||||| ||  ||| ||    |||||||| ||||
Db    215 CTCCGACAGCTCTAACCGCTTCCGCTTTAAAGAAACTACTGGGAATCTTTCTTTCCAAG 274

Qy    363 GTAACGGAGAACTCTCTATTGTTCCAAACGGTGGATGCAGGGACTGTAGCAGGGGCTGTCTG 422
             ||| ||| ||| |  | ||| |  ||  | |||| |||||
Db    275 GCCACGGCTACCAATTTCTCCTACAAAAATATCGATGCGGG------AGCGAACTGTACCT 328

Qy    423 TTAACAGCAGCGTGGTGTAGATAAATCTACCACGTTTATAGGGTTTCTTCGCTCATCTTTTA 482
             |||  ||| || |||  |  ||||  |||| | ||||   |||| |||||
Db    329 TTACCAATACAGCTGCAAATAAGCTTCTCTCCTTTTCAGGATTCTCCTATTTGTCACTAA 388

Qy    483 TTGCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGCCGTTAGCTGCTCTACGGGTA 542
             | | || |||||||  ||| ||| ||| |||||||||  | | ||| |||||
Db    389 TACAAACCACGAATGCT-----ACCACAGGAACCAGGACCAGGAGCCATCAAGTCCACAGGAGCTT 442

Qy    543 GCTTGAGTTGACAAAAAATGTCAGTTTGCTCTTCAGCAAAAAACTTTTCAACGGGATAATG 602
              ||| | | |||||||||  | || |||| || ||| ||||||||||||  || ||| |||
Db    443 GTTCTATTCAGTCGAACTAT--AGTTGCTACTTTGGCCCAAAACTTTTCTAATGACAATG 499

Qy    603 GCGGTGCTATCACCGCGCAAAAATCTTCATTACAGGGACTACAAATGTCAGCTCTGTTTT 662
             |  | ||   |||| |||| ||| | | | |  |||| | |||||  | ||  | |||
Db    500 GAGGCGGCCCCTCCAAGGCAGCTCTCATATCATGCGGGTGCCCCTCTATTCCACGGGGATTACAATTA 556

Qy    663 CTGAAAATACCTCCTCAAAGAAAGGCGAGCCCATTCAGACTTCCGATGCCCTTACCATTA 722
               ||||| | | | |||| |||  |||  |   ||||| |||||| |||   |||||||||
Db    557 CCAAAAACAAAGCAACGCAAAAAGGGGTGCCCCTCTATTCCACGGGGATTACAATTA 616

Qy    723 CTGGAAACCAAGGGGAGAAGTCTCTTTTTCTGACAATACTTCTCGGATTCTGGAGCTGCAA 782
             || |||| | ||| |||| |||||||||| |||| ||| |||| || |||||||| | ||
Db    617 ACAATACGTTAAACTCAGCATCATTTTTCTGAAAATACCGGCGGCAACAATGGCGGAGCCA 676
```

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Qy    783 TTTTTACAGAAGCCTCGGTGACTATTCTTAATATGCTAAAGTTTCCTTTATGACAATA 842
              ||| ||||||| || |||| |||||  |||||| | |||   | |||  |||  ||||
Db    677 TTTACACGGAAGCTAGCAGTTTTATTAGCAGCAACAAAGCATTAGCTTTATAAACAATA 736

Qy    843 AGGTCACAGAGACGAGCGAGCTCCTCAACAACGGGGATATGTCAGGAGGTGCTATCGTGCTT 902
                      ||   |||    ||||  |||
Db    737 ------------GTGTGACCG----------CAACCTCAGCTACAGGGGACCG 781

Qy    903 ATAAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAGCA 962
              | | | ||| |  || ||  | ||| |  |||||| |||  |||||| || ||||| |
Db    782 GTACATCAGCCCCCAAACCAGTCTTAACTCTATCAGACACAGGGGAACTGAACTTTATAG 841

Qy    963 ACAATACATGACACAGCGGAGGAGCTATCTATGTGAAAAAGTCGAACTGGCTTCCG 1022
              |||| | | || | |  |||| || |    |||| || |||||| |||| |||||
Db    842 GAAATACAGCAATTACTAGTGGTGGGCCGATTTATACTGACAATCTAGTTCTTTCTTCTG 901

Qy   1023 GAGGACTTACCCTATTCAGTAGAAATAGTGTCAATGGAGTAGCTCCTAAAGGTGGAG 1082
             ||||| | ||| | |||  |  ||  |||| || |||| |||| ||||  |||||||
Db    902 GAGGAGCCTACGCTTTTAAAAACAACTCTGTATAGATACTGCAGTCTCCCTTAGGAGGAG 961

Qy   1083 CCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATGTGTGACATTGTCT 1142
             | || || || ||  | | |||  | ||||| ||    ||||||   |||| ||||
Db    962 CAATTGCGATTGCTGACTCTGGATCTTTGAGTCTTGGTGGACGAATAGAAGTAGTA 1021

Qy   1143 TTTTAGGGAATACAGT--------CACTTCTACTACTCCTGGGACGAATATCAGAAGTAGTA 1193
             || ||| |||||| ||        ||| | | |  |||   ||| || || |||||  |
Db   1022 TTGACGAAACACAGTAGTCAAAGGAGCTTCTTCGAGTCAGACCACTACCAGAAATTCTA 1081

Qy   1194 TCGACTTAGGA---ACGAGTGCAAAGATGACAGCTTTGGCGTTCTGCTGCTGGTAGAGCCA 1250
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Db   1082 TTAACATCGGAAACACCAATGCTAAGATTGTACAGCTGCAGCCTCTGCCGCCTCCAAGGCAATACTA 1141

Qy   1251 TCTACTTCTATGATCCCATAACTACTACAGGATCATCCACACAGTTACAGATGTCTTAAAAG 1310
             | |||||||||||||| ||||||||| || ||||||| | | | || ||| || ||||||
Db   1142 TCTACTTCTATGATCCTATGATCCTATAACAACTAGCATCAACTCACTGCCAGCTCTCTCAGATGCTCTCTAAACT 1201

Qy   1311 TTAATGAGACTCCGGCAGATTCTGCACTACACAAATACAGGGAACATCATCTTCACAGGAG 1370
             | |||| | | |  |||| || |||| | || ||||| |||| | |  | ||| | |||||
Db   1202 TAAATGGTCCTGACCTTGCAGGGAATCCTGCATAGCAGGGATCTGCATATCGTATTTTCTGGAG 1261

Qy   1371 AAAAGTTATCAGAGACAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAGC 1430
             | ||  | || ||||||| ||| || || |   ||| ||  ||| | ||| ||| | | |
Db   1262 AGAAGCTCTCGGAAGCAGAAGCTGCGAAGCTGTGATAATCTACAATTCAGCAAC 1321

Qy   1431 CTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAACATGGAGTGACTCTGCAGACTCAGG 1490
             || |||||||  | ||||| | | || |  |||| ||||||    |||  |||| |||
Db   1322 CTCTAACTCTTGCGGGAGGAGGCAACCTCTCTCTAAATCAGGGG------AGCGAACTGTACCT 1381

Qy   1491 CATTCACTCAACAGGCAGATTCTCGTCTGCAAGTGGACGTAGGAGAACTACTCTAGAACCTG 1550
             | |||  |||| |  |   | |||  |||  |  |||| | ||| | || | | |||| | |
Db   1382 CCTTTTCGCAATCTCCCGGGCTTCACCCTCCCATGGATGCAGGGGACCACCATTAGAAACCG 1441

Qy   1551 CTGATACTAGCACCATAAACAATTGGTCATTAACATCAGTTCATAGACGGTGCAAAGA 1610
             |||||  | |||| ||||| |||| |||  || |  | ||| | || |  |||||||
Db   1442 CTGATGGGATCACTATCAATCAATTATCTGTTCTCAATGTAGATTCCTTCAAAGACCAAGA 1501

Qy   1611 AGGCAAAAATAGAAACCAAAGCTACGTCAAAAAATCTGACTTTATCTGGAACCATCACTT 1670
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Db   1502 AGGCTACGCTAAAAGCAACAACAAGCAAGTCAGACGTCACTTTATCTGGATCGCGTCTCTC 1561

Qy   1671 TATTGGACCCGACGGGCACGTTTTATGAAAATCATAGTTTAAGAAATCCTCAGTCCTACG 1730
             | || ||| | |  ||| | | | | ||||| |   | | ||||||||||| || | |
Db   1562 TTGTTAGATCCTTCTGGAAATGTCACGAGAGATGTCTTGGAATAACCCTCAAGTCTTTT 1621

Qy   1731 ACATCTTAGAGCTCAAAGCTT-------CTGAACTGTAACAAGCACCGCAGTGACTCCAG 1784
             || |||  | |||  |||| |       ||||| ||  | || |||  || | | | |
Db   1622 CTTGTCTCACTCTTACTGCTGCGACCCCGGAATATTCACATCACCAGATTAGCTGCTG 1681

Qy   1785 ATCCTATAAATGGGTGAGAAAATCCTATCCATTGGGGATACCAAGGAACTTGGGCCCCAATTGTTT 1844
             ||||  || |   |  |||||||| |||||||||||||||||||| | ||  || |  | || | |
Db   1682 ATCCCCTAGAAAAAATCTATCCATTGGGGATACCAAGGGATAGCGGGCAACAATGGGGCATTATTCCTTGGC 1741
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Qy 1845 GGGGGACAGGGGC------TTCTAGACTGCAACCTTCAACTGGACTAAAACTGCTATA 1898
                     |||| ||||  || |||||||| ||| |||||||
Db 1742 AAGAGGATACTGCGACTAAATCCAAAGCAGCGACTCTTACCTGGACAAAAACAGGATACA 1801

Qy 1899 TTCCTAATCCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCATTTATAG 1958
            ||||| ||||||||| ||| ||| ||||||| |||||| ||||||  |||| |||| |
Db 1802 ATCCGAATCCTGAGCGTCGTGGAACCTTAGTTGCTAACACGCTATGGGGATCCTTTGTTG 1861

Qy 1959 ATATTAGCTCTCTCCATTATCTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGACCGTG 2018
            ||| ||| ||| ||| |  ||| |||||    |||| |||| | |  |||||||||  |
Db 1862 ATGTTGCGCTCCATACAACAGCTTGTGAGCCACTAAAGTACGCCAATCTCAAGAAACTCGCG 1921

Qy 2019 CTTTTTGGTGTGCTGGATTATCTAACTTCTTCCATAAGGATAGTACAAAAACACGACGCG 2078
            ||| ||||||| | |||| ||| | |||||||||||| |||| ||  || | |  | |
Db 1922 GCATCTGGTGTGAAGGGGATCTCGAACTTCTTCCATAAAGATAGCACGAAGATAAATAAAG 1981

Qy 2079 GGTTTCGCCATTTGAGTGGCGGTTATGTCATAGGAGGAAACCTACATACTTGTTCAGATA 2138
            |||||||||| | |||| | |||||||  ||||||| || ||| ||| |  ||| ||||
Db 1982 GTTTTCGCCACATAAGTGCCAGGTTATGTTGTAGGAGCGACTAACACATTAGCTTCTGATA 2041

Qy 2139 AGATTCTTAGTGCTGCATTTGTCAGCTCTTGGAAGAGATAGAGACTACTTTGTTAGCTA 2198
              | | | | ||| |||| | |   | |||||| ||||||||| | |||||   || ||
Db 2042 ATCTTATCACTGAGGCCTTCTGCCAATTATTCGGGAAAGATAGAGATCACTTTATAAATA 2101

Qy 2199 AGAATCAAGTACAGTCTACGGAGGAAACTCTCTATTACCAGCACAACGAAACCTATATCT 2258
              ||| |||  | || ||  |||  | |||| |||| ||| |||||| || |||| |||
Db 2102 AAAATAGAGCTTCTGCCTATGCAGCTTCTCTCCCATCTCCAGCATCTAGCGACCTTGTCTT 2161

Qy 2259 CTCTTCCTTGCAAACTACGGCCGCCTTGTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTC 2318
           ||    || | ||                 ||  ||| || |||| |||||||| |||||
Db 2162 CTCCAAGCTTGTTAC--------GCTACCTTCCTGGATCTGAAAGTGAGCAGCCTGTCC 2212

Qy 2319 TCTTTTCAGGAAACCTTAGCTACCACCCATAGCTAGCTAGGTTAACCTCGGTCTTCCAGATAACGATCTGAAAACCAAGTATACAA 2378
          |||||  | ||  |||| |  | |||  || |||| |||| |    ||||| |||||||||||||
Db 2213 TCTTTGATGCTCAGATCAGCTATATCTAGTAGGAATGATAGTTTGCTTTAGAATTCG---GTG 2272

Qy 2379 CATATCCTACTGTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTAGAATTCG---GTG 2435
            | | |  | |  || || || ||| | ||| | ||| | ||| || ||||||   |||
Db 2273 AAGCACCAAAGGAGGAGAGAGCGCTTCGTGTGGTATAAATGACGGTTGCGCTCTGGAACTTGCGAGCT 2332

Qy 2436 GAAGAGCTCCGATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTAACATGCCCTTCATGA 2495
            ||  | || |  | |||||  || || |  |||||||| |||| || |||| |||||| |
Db 2333 CCCTACCACACACTGCTTTAAGCCATGAGAGGTCTTCCACGCGTATTTTCCTTTCATCA 2392

Qy 2496 AATTGCAGTTGTCTATGCATCAGATCAGGAAGGTTTAAAGAAC---AGGGAACAGAAGCTC 2552
            |  || || ||||||||  || ||||| ||  ||||||||||   ||| ||||| | ||
Db 2393 AAGTAGAAGCTTCGTACAATACACCAAGATAGCTTCAAAGAACGTAAATACTACCTTGGTAC 2452

Qy 2553 GTGAATTGGAAGTAGCCGTCTGTGAATCTTGCCTTACCATCGGATCCGATTTGATA 2612
           ||| || || ||||||| |  |  | ||| ||||  || | ||| | ||| |||||
Db 2453 GATCTTTCGATAGCCGGTGATTTAATTAACGTCTCTGTGCCTATTGGAATTACCTTCGAGA 2512

Qy 2613 AGGAATCAGACTGCCAAGATGCAAGTACAAATCTAACTCTTGGTTATACTGTGGATCTTG 2672
            ||||||| || ||  |||||| | | || | |||| |||| |||||| ||| |||| ||
Db 2513 GATTCTCCGAGAAACGAGCGGTGCGTCCTTACGAAGCTACTGTCATCTACGTGCCGATGTCT 2572

Qy 2673 TTCGTAGTAACCCCGACTTACGCAACACACTGCGAATTAGCGGTGATTCTTGGAAAACCT 2732
            ||||| |  || | |||| ||| ||||||| || |  ||  || ||| | ||||||| |
Db 2573 ATCGTAAGAATCCTGACTGCACGCACGACAGCTCTCCTAATCAACAATACCTCGTGAAAACTA 2632

Qy 2733 TCGGTACGAATTGGCAAGACAAGCTTTAGTCTTCGTGCAGGGAACCATTTTGCTTTA 2792
            | ||| ||||| | ||||||||||| | | || | | ||||||| ||| |||| |||
Db 2633 CAGGAACGAATCCTCAAGACAAGCTGGTATCGGAAGAGCAGGGATCTTTTATGCCTTCT 2692

Qy 2793 ACTCAAATTTGAAGCCTTTAGCCAATTTCTTTTTGAATTGCGTGGTGTATACTGTGGATCTTG 2852
            || ||||| ||||  | || |  | ||| |||| ||| ||||||| || | |||| | ||||
Db 2693 CTCCAAATCTTGAGGTCACAAGTAACCTATCTATGGAAATTCGTGGATCTTCACGCAGCT 2752

Qy 2853 ACAATGTAGACTTAGGAGCAAAATACCAATTCTAA 2887
            ||||||  || |||||| |  ||  |||||||||
Db 2753 ACAATGCAGATCTTGGAGGTAAGTTCCAGTTCTAA 2787
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OM nucleic - nucleic search, using sw model

              GenCore version 5.1.6
              Copyright (c) 1993 - 2003 Compugen Ltd.

Run on:    December 16, 2003, 12:15:22 ; Search time 167 Seconds
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Scoring table:  IDENTITY_NUC
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Searched:       569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters:   1139956

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2975.4	99.2	1230025	4	US-09-198-452A-1	Sequence 1, Appli
c 2	509.8	17.0	1230025	4	US-09-198-452A-1	Sequence 1, Appli
c 3	132.2	4.4	3021	4	US-09-556-877-182	Sequence 182, App
4	132.2	4.4	3021	4	US-09-620-412C-182	Sequence 182, App
5	132.2	4.4	3021	4	US-09-556-877-170	Sequence 170, App
6	131.4	4.4	2949	4	US-09-620-412C-170	Sequence 170, App
7	131.4	4.4	2949	4	US-09-598-419-170	Sequence 170, App
8	131.4	4.4	2949	4	US-09-556-877-169	Sequence 169, App
9	50.6	1.7	2643	4	US-09-620-412C-169	Sequence 169, App
10	50.6	1.7	2643	4	US-09-598-419-169	Sequence 169, App
11	50.6	1.7	2643	4	US-09-556-877-181	Sequence 181, App
12	50.2	1.7	2601	4	US-09-620-412C-181	Sequence 181, App
13	50.2	1.7	2601	4	US-09-598-419-181	Sequence 181, App
14	50.2	1.7	2601	4	US-08-213-419B-3	Sequence 3, Appli
15	42.4	1.4	6124	4	US-08-545-528D-1	Sequence 1, Appli
c 16	39.6	1.3	580073	4	US-09-620-412C-324	Sequence 324, App
c 17	39	1.3	1896	4	US-09-598-419-324	Sequence 324, App
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20	37.6	1.3	1965	4	US-09-620-412C-312	Sequence 312, App
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c 45	35.8	1.2	1951	3	US-08-474-671-112	Sequence 112, App

ALIGNMENTS

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RESULT 1
US-09-198-452A-1
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmen
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pre
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
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; LENGTH: 1230025
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; ORGANISM: Chlamydia pneumoniae
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Qy    481  TATTGCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGCCGTTAGCTGCTCTACGGG   540
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; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmer
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pre
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
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US-09-198-452A-1/c
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Db   518045 TACTGGAATAGACTATACTCTGACAGGAGATATAACCTGCAAAACCTTGGGGATTCGG- 517987

Qy      307 CACAGCAATCACAAAAAGCTGTTTAACACACTAAGGGCGCGATTTGACTTTCACAGGTAA 366
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Db   517986 --CAGCTTAACGAAGGGTGTTTTTTCTGACACTACGAAGTCTTTAAGCTTTGCCGGTAA 517929

Qy      367 CGGGAACTCTCTATTGTTCCAAACGGTGGATGCAGGGACTGTAGCAGGGGCTGCTGTTAA 426
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Db   517928 GGGGTACTCACTCACTTTCTTTTTTAAATNAAGTCTAGTGCTGAAGCGCANACTTTCTGTT 517869

Qy      427 CAGCAGCGTGTAGATAAAATCTGTCGCTAACAGATAAAAATCTGCTCATCTTTATTGC 486
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Db   517868 ------ACAACTGATAAAAATCTGTCGCTAACAGATTTTCGAGTCTTAACGCTTACTTTCTTAGC 517816
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Qy    487 GTTCCTCGGAAGTTCGATAACTACCGGCAAAGAGGAGCCGTTAGCT--GCTCTACGGGTAG  543
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Db 517815 GGCCCATCATCGGTAAATCACAACCCCCTCAGGAAAAGGTGCAGTTAAATGTGGAGGGGA 517756

Qy    544 CTTGAGTTTGACAAAAATGTCAGTTGCTCTTCAGCAAAAACTTTCAACGGATAATG      603
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Db 517755 TCTTACATTTGATAACAATGGAACTATTTTATTTAAACAAGATTACTGTGAGGAAAATG 517696

Qy    604 CGGTGCTATCATCCGCAAAAACTCTTCATTACAACGGGACTACACATGTCAGCTCTGTTTC  663
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Db 517695 CGGACATTTCTACCAAGAATCTTTCTTCTTTGAAAAAACAGCACGCGGATCGATTTCTTTG 517636

Qy    664 TGAAAATA-------CCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCTTA    716
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Db 517635 GGAATAAATCGAGCGCAACAGGGAAAAAAGGTGGGCTATTTGTGCTATTGGTACTGGTAG 517576

Qy    717 CCATTACTGGTGGAAACCAAGGAGGAAGTCTCTTTTCTGACACATATTCTTCGGATTCTGGAG  776
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Db 517575 ATATTACAAATAATACGGCTCCTACCCCTCTTCTGGAACAATATTGCTGAAGCTGCAGGTG 517516

Qy    777 CTGCAATTTTTACAGAAGCTCGGTGACTATTCTTAATAATGCTAAAGTTCCTTTATTG    836
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Db 517515 GAGCTATAAAATAGCACAGGAAAACTGTACAATTACACGTCTCTTTGTATTTTTCTG 517456

Qy    837 ACAATAAGGTACACAGGAGCGGAGCTCCTCAACACGGGGATAATGTTCAGGAGGTGCTATCT  896
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Db 517455 AAAATAGTGTGAC---AGCGACCGGAGAAATGGAGAGGAGCTCTTTTCTGG---------- 517410

Qy    897 GTGCTTATAAAACTAGTACAGATACTACTAAGGTCACCCTCACTGGAAATCAGAATGTTACTCT  956
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Db 517409 -------------AGATGCCGATGTGTACCATATCTACCCATATCTGGGAATCAGAGTGTAACTT 517369

Qy    957 TCAGCAACAATACATGACTCGGATCGCGGAGGAGCTATCTCATGTGAAGAAAGCTGAAACTGG 1016
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Db 517368 TCTTCAGGAAAACCAAGCTGTAGCTAAATGGCGGCAGCCATTTGAAGGAGCTTACACTCG 517309

Qy   1017 CTTCCGGAGGA------CTTACCCTATTCAGTAGAAATAGTGTCAATGGAGTGTACAGCT 1069
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Db 517308 CTTCCGGGGGGGGGGGGTATCTCTTTTCTAACAATATAGTCCAAGGTGTATCGGAAGCA 517249

Qy   1070 CCTAAAGGTGGAGCCATAGCTATCGGAAGACGCGGAGATAGTAGTGGGGAATTGAGTT 1129
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Db 517248 GGTAATGGTGGAGCGCCATTTCTACTATCTGCAGTGTAGTCTTTCAGCAGAAGCA 517189

Qy   1130 GGTGACATTGTCTTTTTAGGGAATACAGTTCACTCTCTACTCC---TGGGACGAATAGA 1186
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Db 517188 GGGACATTACCTTCAATGGGAATGGATGCTCATTGTTGCAACTACACCACCAAACTACGAAAAGA 517129

Qy   1187 AGTAGTACTGACTTAGGAACGAGTGCAAAGATGACAGCAGCAGCAACGA 1246
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Qy   1307 AAAGTTAATGAGACTCCGGCAGAGTCGACTCTCGGAGGAATATACATAGGGAACATCATCTTCACA 1366
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Db 517008 AATCTGAATCTGCAATCTCGAGATCGCTAAATGGCTGAATTTGTTTCT 516949

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Qy   1427 CAGGCCGTAACTCTTCTTCGGAGGACTACTCTTAAAAACATGACTGACTCTGCAGACT 1486
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Qy   1487 CAGGCATTCACTCAACAGCCAGATTCTCGTCTGGAAATGAGACGTAGGAACTACTCTGAA 1546
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Qy   1547 CC---TGCTGATACTAGCACCATAAACAATCATTGGTCATTAACATCCTGTAGACTCTTTAAGCT  1603
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Qy   1604 GCAAAGAAGGCAAAATAGAAACCAAAGTCACGTCAAGCAGTAAAAATCTGACTTTATCTGAACC  1663
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Qy   1724 TCCTACGACATCTTAGAGCTCAAAGCTTCTGGAACTTCTCTGGACTACGTCGAACTGACTCCA  1783
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Db 516588 GACTTTTCATTTGTGCAGCTCTCTCGTCTGGGTACTGCATCATCTACAGATGTTCCAGCG 516529

Qy   1784 GATCCTATAAATGGTGAGAAATTCCATCACGGCTATCACCGGCCATCATCCCCAATTGTT  1843
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Qy   1844 TGGG------GGACAGGGGCTTCTACGACTGCAACTCAACCTTCAAAAACT 1891
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Qy   2072 CGACGCGGGTTCGCCATTGAGTGCGGTTATGTCATTTGTGCATTGATATGCAAACTTGT 2131
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Db 516228 AAACGCAAATACCGTCATAAATCGGTGATGTCATCGGAAATGTCTATCGGGCAACTTGT 516169

Qy   2132 TCAGATAAGATTCTTAGTGTCTGCATTTTGTCATTTGTCAGCTCTCTTTGGAAGAGAGAGTACTTT 2191
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Qy   2432 GGTGGAAGCTTCGGAGTCTGTTAGAGTAAAGTGCTCTATTTGCTTAGTGAAGTTGATCCCTTC 2491
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Qy   2492 ATGAAATTGCAGTTGTCTCTATGCAACATCAGGAGGTTTTAAAGAACAGGGAACAGAAGCT 2551
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Qy   2552 CGTGAATTTGGAAGAGCTCCGATTCGTGTGATCCTACCTATCGGATCCGATTTGAT 2611
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Db 515751 AGATCTTTTGATGACAGCACAACCTCTTCAATTTATCTTTGTGGTGTGAAGTTGAG 515692

Qy   2612 AAGGAATCAGACTGCCAAGATGCAACGGTCAAATTATACTCTTCGGTTATACTGGGATCTT 2671
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Db  515691 AAGTTCCTGATTGTAATGACTTTTCTTATGATCTAATCCTATGTTCCTGATCTT 515632
Qy    2672 GTTCGTAGTAGTAACCCCGACTGTACGACAACACTGCGGAATTAGCGGTGATTCTTGGAAAACC 2731
Db  515631 ATCCGCAATGATCCCAAATGCACTACAGCACTTGTAATCGCGGAGGCCTCTTGGGAAACT 515572
Qy    2732 TTCGGTACGAATTGGAAGACAAGCTTTAGTCCTTCGTGCAGGGAACCATTTTTGCTTT 2791
Db  515571 TATGCCAATAACTTAGCTACGACGACAGGCGTGCAGGCCAGTCACTACGGCCTTC 515512
Qy    2792 AACTCAAATTTTGAAGCTTTAGCCAATTTCTCTTTGAATTGCGTGGGTCATCTCGCAAT 2851
Db  515511 TCTCCTATGTTTGTTGGAAGTGCTCCGGCCAGTTTGTCTTTGAAGTTCGTGGATCCTCACGGATT 515452
Qy    2852 TACAATGTAGACTTAGGAGCAAAATACCAATTCTA 2886
Db  515451 TATAAGTAGATCTTGGGGGTAAGTCCAATTCTA 515417
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RESULT 3
US-09-556-877-182
; Sequence 182, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 182
; LENGTH: 3021
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-556-877-182

Query Match   4.4%; Score 132.2; DB 4; Length 3021;
Best Local Similarity 48.8%; Pred. No. 2.6e-28;
Matches 544; Conservative 0; Mismatches 523; Indels 48; Gaps 5;

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Qy  1776 TGACTCCAGATCCTATAATGGGTGAGAAATTCCATTACGGCTATCAGGGAACTGGGGGCC 1835
Db  1952 TGACTCTAGGGATGAGATGAGCCTAAGTATGGCTATCAAGGAAGCTGCAAGCTTGCCGTGGG 2011
Qy  1836 CAATTGTTTGGGGGACAGGGCTTCTACGACTGCAACCTTCAACTGGACTAAAACTGGCT 1895
Db  2012 ATCCTAATACAGCAAATAATGGTCCTTATACTCCTTATATACTTGTGAAGACTGACTAAAACTGGGT 2071
Qy  1896 ATATTCCTAATCCCGAGCGTATCGGCTTCTTTAGTCCTTAATAGCTTATTGGAATGCATTTA 1955
Db  2072 ATAATCTCGGGCCTGAGCGAGTAGCTTCTTCTTTGGTTCCAAATAGTTTATGGGGATCCATTT 2131
Qy  1956 TAGATATTAGCTCTCCATTATCTTATGATGAGACTGCAAACGAAGGGTTGCAGGGAGACC 2015
Db  2132 TAGATATACGATCGCGCATTCAGCAATTCAGCAAGTGTGGATGGGCGCTCTTATTGTC 2191
Qy  2016 GTGCTTTTTGGTGTGCTGGATTGCTGGATTATCAACTTCTTCCATAAGGATAGTACAAAAACACGAC 2075
Db  2192 GAGGATTATGGGTTTCTGAGTTTCGAATTTCTCTCATCATCATGACCGCGATGTTTAGGTC 2251
Qy  2076 GCGGGTTCTTGCCATTTGAGTGGCGGTTATGTCATGAGGGTTATTCCTTAGGAGCAAACTCCTACATTGTTCAG 2135
Db  2252 AGGGATATCCGGTATATTAGTGGGGGTTATTCCTTAGGAGCAAACTCCTACTTTGATCA- 2310
Qy  2136 ATAAGATTCTTAGTGCTCGCAGCTCTTGTCAGCTCTTGTGGAGAGATAGAGACTACTTTGTAG 2195
Db  2311 --TCGATGTTTGGTCTAGCATTTACCGAAGTATTGGTAGATCTAAAGATTATGTGTAGTGT 2368
Qy  2196 CTAAGAATCAAGTACAGTCTACGGAGGAACTCTCTATTACCAGCACAACGAAACCTATA 2255
Db  2369 GTCGTTCCAATCATCATCGTTGCATAGGATC------------------------CGTTTA 2405
Qy  2256 TCTCTTCCTTGCAAACTACGGCCTTGTGCTTGTCGTTCGTTCCTACAGAGATTCCTG 2315
Db  2406 TCTATCTACCCAACAAGCT--------TTATGTGGATCCTATTTGTTCGGGAGATGCGTT 2456
Qy  2316 TTCTCTTTCAGGAAACCTTAGCTACACCCATACGGATAACGATCTGAAAACCAAGTATA 2375
Db  2457 TATCCGT------------GCTAGCTACGGGTTTGGGAATCAGCATATGAAAAACCTCATATA 2506
Qy  2376 CAACATATCCTACTGTTAAAGGAAGCTCGGGGGAATGATAGTTTCGCTTTAGAATTCGGTG 2435
Db  2507 CATTTGCAGAGGAGGCGATGTTCGTTGGGATAATAAACTGTCTCGGCTGGAGAGATTGGAG 2566
Qy  2436 GAAGAGCTCCGATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTACATG---CCCTTCA 2492
Db  2567 CGGGATTACCGATTGTGATTACTCCATAAGCTCTCATTTGAATGAGTTGCGTCCTTTCG 2626
Qy  2493 TGAAATTGCAGTTGTCATGCACATCAGGAAGGTTTAAAGAACAGGGAACAGAAGCTC 2552
Db  2627 TGCAAGCTGAGTTTTTCTTATGCCGATCATGAATCTTTTACAGAGGAAGGCGATCAAGCTC 2686
Qy  2553 GTGAAATTGGAAGTAGCCGTCTTGTGAATCTTGCCTTACCTATCGGGATCCGATTTGATA 2612
Db  2687 GGGCATTCAAGAGCGGACACATCTCCTAAATCTATCAGTTCCTGTTGGAGTGAAGTTTGATC 2746
Qy  2613 AGGAATCAGACTGCCAAGATGCAACGTACAATCTAACTCTTGGTTATACTGTGGATCTTG 2672
Db  2747 GATGTTCGTAGTACACATCCTAATAAATATAGCTTTATGGCGGCTTATATCTGTGGATGCTT 2806
Qy  2673 TTCGTAGTAACCCCGACTGTACGACAACACTGCGAATTAGCGGTGATTCTTGGAAAACCT 2732
Db  2807 ATCGCACCATCTCTGGTACTGAGACAACCGCTCCTATCCCATCAAGAGACATGGACAACAG 2866
Qy  2733 TCGGTACGAATTTGCCAAGATTTGGCAAGACAAGCTTAGTCCTTCGTGCAGGGAACCATTTTTGCTTTA 2792
Db  2867 ATGCCTTTCATTTAGCAAGACACATGGAGTTGTGGTTAGAGGATCTATGTATGCTCTCTCTAA 2926
Qy  2793 ACTCAAATTTTGAAGCTTTAGCCAATTTCTTTGAATTGCGTGGGTCATCTCGCAATT 2852
Db  2927 CAAGTAATATAGAAGTATATGGCCATGGAAGATATGAGTAATGAGTATCAGAGATGCTTCTCGAGGCT 2986
Qy  2853 ACAATGTAGACTTAGGAGCAAAATACCAATTCTAA 2887
Db  2987 ATGGTTTGAGTGCAGGAGAAGTAAAGTCCGGTTCTAA 3021
```

RESULT 4
US-09-620-412C-182
; Sequence 182, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 182
; LENGTH: 3021
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-182

Query Match   4.4%; Score 132.2; DB 4; Length 3021;
Best Local Similarity 48.8%; Pred. No. 2.6e-28;
Matches 544; Conservative 0; Mismatches 523; Indels 48; Gaps 5;
```

Qy    2853  ACAATGTAGACTTAGGAGCAAAATACCAATTCTAA 2887
            |||||||||||||||||||||||||
Db    2987  ATGGTTTGAGTGCAGGAGGAGTAAAGTCCGGTTCTAA 3021

RESULT 5
US-09-598-419-182
; Sequence 182, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 182
; LENGTH: 3021
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-598-419-182

Query Match             4.4%;  Score 132.2;  DB 4;  Length 3021;
Best Local Similarity   48.8%;  Pred. No. 2.6e-28;
Matches  544;  Conservative   0;  Mismatches 523;  Indels   48;  Gaps   5;

Qy    1776  TGACTCCAGATCCTATAATGGGTGAGAAATTCATTACGGCTATCAGGGAACTTGGGGCC 1835
            ||||||||||||||||||||||||||||
Db    1952  TGACTCTAGGGAATGAGATGCCTAAGTATGGGCTATCAAGGAAGCTGGAAGCTTGCGTGGG 2011

Qy    1836  CAATTGTTTGGGGACAGGGGCTTCTACGACCTTCAACCTTCAACTGGACTAAAACTGGCT 1895
            |||||||||  ||||
Db    2012  ATCCTAATACAGCAAATAATGGTCCTATACTCTGAAAGCTACATGGACTAAAACTGGGT 2071

Qy    1896  ATATTCCTAATCCCGAGGCTATCGGCTCTTAGTCCCTAATAGCTTATGGAATGCATTTA 1955
            ||| ||||| |||||     ||
Db    2072  ATAATCCTGGGCCTGAGCCAGTAGCTCTTCTTTGGTCCAAATAGTTTATGGGATCCATTT 2131

Qy    1956  TAGATATTAGCTCTCTCCATTATCTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGACC 2015
            ||||||| ||||
Db    2132  TAGATATACGATCTGCGCATTCAGCAATTCAAGCAAGTGTGGATGGGCCTCTTATTGTC 2191

Qy    2016  GTGCTTTTTGGTGCTGCTGGAATTATCTAACTTCTTCCATAAGGATAGTAGTACAAAAACACGAC 2075
            |  |||||||   |||||||
Db    2192  GAGGATATGGGTTCTGGAGTTTCGAATTTCTTCTATCATGACGACGATGCTTTAGGTC 2251

Qy    2076  GCGGGTTTCGCCATTTGAGTGGCCGGTTATGTCATTTGAGTCCTTAGTCCCTAATAGCTTCAG 2135
            |||| ||||
Db    2252  AGGGATATGGTTATTTCTTATGCGGATAACATGAAGGAAGGCGATCAAGCTC 2310

Qy    2136  ATAAGAATCTTAGTGCTGCAGTCTCTTTGTCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAG 2195
            ||| ||
Db    2311  --TCGATGTTTGGTCTAGCATTTACCGAAGTATTTGGTAGATCTAAAGATTATGTAGTGT 2368

Qy    2196  CTAAGAATCAAGGTACAGTCTACGGCAGTACATG---CCCTTCA 2255
            |||| ||
Db    2369  GTCGTTCCAATCATCATGCTTGCATAGGATC--------CGTTTA 2405

Qy    2256  TCTCTCTTCCTTGCAAACTACGGCCTTGTTCGTCTTATGTTCCTACAGAGATTCCTG 2315
            ||| |||| |||
Db    2406  TCTATCTACCCAACAAGCT----------TTATGTGGATCCTATTTGTTCGGAGATGCGTT 2456

Qy    2316  TTCTCTTTTCAGGAAAACCTTAGCTACACCCATAACGGATAACGATCGGAAAAACCAAGTATA 2375
            ||| |||||
Db    2457  TATCCGT-----------GCTAGCTACGGGTTTGGGAATGATCAGCATATGAAAAACCTCATATA 2506

Qy    2376  ACTCAAATTTTGAAGCCTTTAGCCAATTTTTCTTTTGAATTGCGTGGGTCATCTCGCAATT 2435
            |||| |
Db    2507  CAACATATCCTACTGTTTAAAGGAAGCTGGGGAATGATAGTTTCGCTTTAGAATTCCGTG 2566

Qy　2436　GAAGAGCTCCGATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTACATG---CCCTTCA 2492
　　　　　　　　||||||　|　||||||||||||||||||||||||||||||||||　　　|||||||
Db　2567　CGGGATTACCGATTGTGTGATTGTGTCTATGCAAGTGGTTTCTATTTGAATGAGTTGCGTCCTTTCG 2626

Qy　2493　TGAAATTGCAGTTTGTCTCTATGCCGATCATCAGGAAGGTTTAAAGAACACAGGGAACAGAAGCTC 2552
　　　　　　　||||||||||||　||||||||||||||||||||||||||||||||||||||||||
Db　2627　TGCAAGCTGAGTTTTCTTATGCCGATCATGAATCTTTTACAGAGGAAGGCGATCAAGCTC 2686

Qy　2553　GTGAAATTTGGAAGTAGCCGTCTGTGAATCTTGCCTTACCTATCGGGATCCGATTTGATA 2612
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2687　GGGCATTCAAGAGCGGACATCTCCTAAATCATCAGTTCCTGTTGGAGTGAAGTTTGATC 2746

Qy　2613　AGGAATCAGACTGCCAAGATGCAACGTACAATCTAACTCTTGGTTATACTGTGGATCTTG 2672
　　　　　|||||||||||||||||||||||||||||||||||||　　||||||||||||||||||
Db　2747　GATGTTCTAGTACATCCTAATAAATATAGCTTTATGGCGGCTTATATCTGTGATGCTT 2806

Qy　2673　TTCGTAGTAACCCCGACTGTACGACAACACTGCGAATTAGCCGGTGATTCTTGGAAAACCT 2732
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2807　ATCGCACCATCTCGGTACTGAGACAACGCTCCTATCCCATCAAGAGACATGGACACACAG 2866

Qy　2733　TCGGTACGAATTTGGCAAGACAAGCTTTAGTCCTCGTGCAGGGAACCATTTTTGCTTTA 2792
　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2867　ATGCCCTTTCATTTAGCAAGACATGGAGTTGTGGTTAGAGGATCTATGTATGCTTCTCTAA 2926

Qy　2793　ACTCAAATTTGAAGCCTTTAGCCAATTTTCTTTGAATTGCGTGGGTCATCTCGCAATT 2852
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2927　CAAGTAATATAGAAGTGCAGAGAAGTAATATGAGTATCGCAAGATATGTTCTCGGTTCAA 2986

Qy　2853　ACAATGTAGACTTAGGAGCAAAATACCAATTCTAA 2887
　　　　　|||||||||||||||||||||||||||||||||
Db　2987　ATGGTTTGAGTGCAGGAGTAAAGTCCGGTTCTAA 3021

RESULT 6
US-09-556-877-170
; Sequence 170, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
;　APPLICANT: Probst, Peter
;　APPLICANT: Bhatia, Ajay
;　APPLICANT: Skeiky, Yasir
;　APPLICANT: Fling, Steve
;　APPLICANT: Maisonneuve, Jeff
;　TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
;　TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
;　FILE REFERENCE: 210121.469C5
;　CURRENT APPLICATION NUMBER: US/09/556,877
;　CURRENT FILING DATE: 2000-04-19
;　NUMBER OF SEQ ID NOS: 305
;　SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 170
;　LENGTH: 2949
;　TYPE: DNA
;　ORGANISM: Chlamydia
US-09-556-877-170

Query Match　　　4.4%;　　Score 131.4;　DB 4;　Length 2949;
Best Local Similarity　48.6%;　Pred. No. 4.5e-28;
Matches　542;　Conservative　2;　Mismatches　523;　Indels　48;　Gaps　5;

Qy　1776　TGACTCCAGATCCTATAAATGGGTGAGAAATTCCATTACGGCTATCAGGGAACTTGGGCC 1835
　　　　　||||||||||||||　|||||||||||||||||||||||||||||||||||||||||
Db　1880　TGACTCTAGGGAATGAGATGATGCCTAAGTGATGTGCTAAGCTTGAAAGCTGGGATCCGGG 1939

Qy　1836　CAATTGTTTGGGGGACCAGGGGCTTCTACGACTGCAACCTTCAACCTGGACTAAAACTGGCT 1895
　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1940　ATCCTAATACAGCAAATAATGGTCCTTATACTCCTGAAAGCTACATGGACTAAAACTGGGT 1999

Qy　1896　ATATTCCTAATCCCGAGCGTATCGGCTATCGGTCTTTTAGTCCTAATAGCTTATGATGAATGCATTTA 1955
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2000　ATAAATCCTGGGCCTGAGCGAGTAGCTTCTTCTTTGGTTCCAAATAGTTTATGGGATCCATTT 2059

Qy　1956　TAGATATTAGCTCTCTCCATTATATCTTATGGAGACTGCAAACGAAGGGTTGCAGGAGACC 2015
　　　　　|||||||||||||

Db　2060　TAGATATACGATCTGCCATTCAGCAATTCAAGCAAGTGTGGATGGGCCGCTCTTATTGTC 2119

Qy　2016　GTGCTTTTGTGGTGCTGATATTCTAACTCTTCCATAAGGATAGTACAAAAACACGAC 2075
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2120　GAGGATTATGGGTTTCTGGAGTTTCGAATTTCTTCATCATGACCGGCATGCTTTAGTC 2179

Qy　2076　GCGGGTTCGCCATTTGAGTGGCCGTTATGTCATAGGAGCGAAAACCTACATACTGTTCAG 2135
　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2180　AGGGATATCGGTATATTAGTGGGGTTATTCCTGGAGGAGCAAACTCCTACTTTGGATCA- 2238

Qy　2136　ATAAGATTCTTAGTGCTGCGATTTTGTCAGCTCTTTGGAAGAGATAGACTACTTTGTAG 2195
　　　　　|||||||||||||||||||||||||||||||||||||||||||||
Db　2239　--TCGATGTTTGGTCTTAGCATTTACCGAAGTATTTGGTAGATCTAAAGATTATGTAGTGT 2296

Qy　2196　CTAAGAATCAAGGTACAGTCTACGGAGGAACTCTCTATTACCACGACACAACGAAACCTATA 2255
　　　　　||||||||||||||||||||||||||||||||||||||
Db　2297　GTGGTTCCAATCATCATGCTTGCATAGGATC--------------CGTTTA 2333

Qy　2256　TCTCTCTTCCTTGCAAACTACGGCCTTGTTGTCGTTGGTAGTTCCTACAGAGATTCCTG 2315
　　　　　||||||||||||||||||||||||||||||||　　　　　　||||||||||||
Db　2334　TCTATCTACCCACCAAGCT--------TTAATGTGGATCCTATTTGTTCGGAGATGCGTT 2384

Qy　2316　TTCTCTTTTCAGGAAAACCTTAGCTACACCCATAGGATAACGATCTGAAAACCAAGTATA 2375
　　　　　||||||||||||||||||　　　　　||||||||||||||||||||
Db　2385　TATCCGT---------GCTAGCTACGGGTTTGGGAATCAGCATATGAAAAACCTCATATA 2434

Qy　2376　CAACATATCCTACTGTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTAGAATTCGGTG 2435
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2435　CATTTGCAGAGGAGAGCCGATGTTCGTTCGTGGATATATAACTGTCTGGCTGGAGAGTTGGAG 2494

Qy　2436　GAAGAGCTCCGATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTACATG---CCCTTCA 2492
　　　　　||||||　|　||||||||||||||||||||||||||||||||||　　　|||||||
Db　2495　CGGGATTACCGATTGTGTGATTGTGTCTATGCAAGTGGTTTCTATTTGAATGAGTTGCGTCCTTTCG 2554

Qy　2493　TGAAATTGCAGTTTGTCTCTATGCCGATCATCAGGAAGGTTTAAAGAACACAGGGAACAGAGCTC 2552
　　　　　||||||||||||　||||||||||||||||||||||||||||||||||||||||||
Db　2555　TGCAAGCTGAGTTTTCTTATGCCGATCATGAATCTTTTACAGAGGAAGGCGATCAAGCTC 2614

Qy　2553　GTGAAATTTGGAAGTAGCCGTCTGTGAATCTTGCCTTACCTATCGGGATCCGATTTGATA 2612
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2615　GGGCATTCAAGAGCGGACATCTCCTAAATCATCAGTTCCTGTTGGAGTGAAGTTTGATC 2674

Qy　2613　AGGAATCAGACTGCCAAGATGCAACGTACAATCTAACTCTTGGTTATACTGTGGATCTTG 2672
　　　　　|||||||||||||||||||||||||||||||||||||　　||||||||||||||||||
Db　2675　GATGTTCTAGTACATCCTAATAAATATAGCTTTATGGCGGCTTATATCTGTGATGCTT 2734

Qy　2673　TTCGTAGTAACCCCGACTGTACGACAACACTGCGAATTAGCCGGTGATTCTTGGAAAACCT 2732
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Db　2735　ATCGCACCATCTCGGTACTGAGACAACGCTCCTATCCCATCAAGAGACATGGACACACAG 2794

Qy　2733　TCGGTACGAATTTGGCAAGACAAGCTTTAGTCCTCGTGCAGGGAACCATTTTTGCTTTA 2792
　　　　　|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2795　ATGCCCTTTCATTTAGCAAGACATGGAGTTGTGGTTAGAGGATCTATGTATGCTTCTCTAA 2854

Qy　2793　ACTCAAATTTGAAGCCTTTAGCCAATTTTCTTTGAATTGCGTGGGTCATCTCGCAATT 2852
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　2855　CAAGTAATATAGAAGTGCAGAGAAGTAATATGAGTATCGCAAGATATGTTCTCGGTTCAA 2914

Qy　2853　ACAATGTAGACTTAGGAGCAAAATACCAATTCTAA 2887
　　　　　|||||||||||||||||||||||||||||||||
Db　2915　ATGGTTTGAGTGCAGGAGTAAAGTCCGGTTCTAA 2949

RESULT 7
US-09-620-412C-170
; Sequence 170, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
;　APPLICANT: Steven P. Fling
;　TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
;　TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
;　FILE REFERENCE: 210121.469C7

; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 170
;   LENGTH: 2949
;   TYPE: DNA
;   ORGANISM: Chlamydia
US-09-620-412C-170

Query Match       4.4%;    Score 131.4;  DB 4;   Length 2949;
Best Local Similarity  48.6%;   Pred. No. 4.5e-28;
Matches 542;   Conservative   2;   Mismatches 523;   Indels  48;   Gaps   5;

Qy 1776 TGACTCCAGATCCTATAAATGGGTGAGAAATTCCATTACGGCTATCAGGGAACTTGGGGCC 1835
Db 1880 TGACTCTAGGGAATGAGATGCCTAAGTATGGCTATCAAGGAAGCTGGAAGCTTGCGTGGG 1939

Qy 1836 CAATTGTTTGGGGACAGGGGCTTCTACGACTGCAACCTTCAACTGACTAAAACTGGCT 1895
Db 1940 ATCCTAATACAGACAAATAATGGTCCTTATACTCTGAAAGCTACATGGACTAAAACTGGGT 1999

Qy 1896 ATATTCCTAATCCCGAGCGTATCGGCTCTTTAGTCCTAATAGCTTATGGAATGCATTTA 1955
Db 2000 ATAATCCTGGGCCTGAGCGAGTAGCTTCTTTGGTTCCAAATAGTTTATGGGGATCCATTT 2059

Qy 1956 TAGATATTAGCTCTCTCCATTATCTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGACC 2015
Db 2060 TAGATATACGATCTGCGCATTCAGCAATCTAACTCTTCTTCCATAAGGAATCAGCAAGTGTG 2119

Qy 2016 GTGCTTTTTGGTGTGTCTGGATTATCTAACTCTTCTTCTCTCATAAGGATAGTACCAAAAACACGAC 2075
Db 2120 GAGGATTATGGGTTTCGGAGTTTCGAATTTCTTCTATCATGACCGCGATGCTTTAGGTC 2179

Qy 2076 GCGGGTTTGCCATTTGAGTGGCGGTTATGTCAATGGAGAAAACCTACACTTGTTCAG 2135
Db 2180 AGGGATATCGGTATATTAGTGGGGGTTATTCCTTAGGAGTAGTCTAAAGATTAATGTGAGTGT 2238

Qy 2136 ATAAGAATTCCTTAGTGCTGCAGATCCATTTTGTCAGCTCTTTGGAAGATAGACTACTTTGTAG 2195
Db 2239 --TCGATGTTTGGTCTAGACATTACCGAAGTATTTGGTGATCTAAAGATTAATGTGAGTGT 2296

Qy 2196 CTAAGAATCAAGGTACAGTCACGGAGGAGACTCTCTATTACCAGCACACGAAACCTATA 2255
Db 2297 GTCGTTCCAATCATCATGCTTGCATAGGATC------------------------CGTTTA 2333

Qy 2256 TCTCTCTTCCTTGCAAACTACGGCCCTTGTTCGTTCGTCTTATGTTCCTACAGAGATTCCTG 2315
Db 2334 TCTATCTACCCAACAAGCT--------TTATGTGGATCCATTAGTTCGGAGATGCGTT 2384

Qy 2316 TTCTCTTTTCAGGAAACCTTAGCTACACCCATACGGATAACGATCTGAAAACCAAGTATA 2375
Db 2385 TATCCGT---------GCTAGCTACGGGTTGGGAATCAGCATATGAAAACCTCATATA 2434

Qy 2376 CAACATATCCTACTGTTAAAGGAAGCTGGGGGATGATGATAGTTTCGCTTTAGAATTCGGTG 2435
Db 2435 CATTTGCAGAGGAGGAGCGATTGTCTTAGATGAAAGTGCTCTATTTGAGCAGTACATG---CCCTTCA 2492

Qy 2436 GAAGAGCTCCGATTTGCTTAGATGAAAGTGCTCTATTTGAAGTGCTTGCGTCCTTTCG 2492
Db 2495 CGGGATTACCGAGTTGTGATTGATTACTGCTTCAAGCTCATTGATTGCGTGCGTCCTTTCG 2554

Qy 2493 TGAAATTGCAGTTGTCTATGCACATCAGGAACAGCAGGAACAGAAGCTC 2552
Db 2555 TGCAAGCTGAGTTTTCTTATGCGGTTGGAGTGGCAATGTTTACAGAGGAAGGCGATCAAGCTC 2614

Qy 2553 GTGAATTTGGAAGTAGCCGTCTTGTGAATCTTGCCTTACCTACTCATGGGGATCCGATTGATA 2612
Db 2615 GGGCATTCAAGAGCTCAAGAGAGTCGACACATCTCATCAGTTCCTGTTGGAGTTTGATC 2674

Qy 2613 AGGAATCAGACTGCCAAAGATGCAACGTACAATCTAACTCTTGTTATACTGTGGATCTTG 2672
Db 2675 GATGTTTCGTAGTACAACATCCTAATAAATAGAGCTTTTATGCGGCGGCCTTATCTCGTGTGATGCTT 2734


; RESULT 8
US-09-598-419-170
; Sequence 170, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
;   APPLICANT: Skeiky, Yasir A.W.
;   APPLICANT: Scholler, John
;   TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
;   TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
;   FILE REFERENCE: 210121.469C6
;   CURRENT APPLICATION NUMBER: US/09/598,419
;   CURRENT FILING DATE: 2000-06-20
;   NUMBER OF SEQ ID NOS: 357
;   SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 170
;   LENGTH: 2949
;   TYPE: DNA
;   ORGANISM: Chlamydia
US-09-598-419-170

Query Match       4.4%;    Score 131.4;  DB 4;   Length 2949;
Best Local Similarity  48.6%;   Pred. No. 4.5e-28;
Matches 542;   Conservative   2;   Mismatches 523;   Indels  48;   Gaps   5;

Qy 1776 TGACTCCAGATCCTATAAATGGGTGAGAAATTCCATTACGGCTATCAGGGAACTTGGGGCC 1835
Db 1880 TGACTCTAGGGAATGAGATGCCTAAGTATGGCTATCAAGGAAGCTGGAAGCTTGCGTGGG 1939

Qy 1836 CAATTGTTTGGGGACAGGGGCTTCTACGACTGCAACCTTCAACTGACTAAAACTGGCT 1895
Db 1940 ATCCTAATACAGCAAATAATGGTCCTTATACTCTGAAAGCTACATGGACTAAAACTGGGT 1999

Qy 1896 ATATTCCTAATCCCGAGCGTATCGGCTCTTTAGTCCTTATATCTCTGAAAGCTAAATCTGGGT 1955
Db 2000 ATAATCCTGGGCCTGAGCGAGTAGCTCTTATATCTCTGAAAGCTAAATCTGGGT 2059

Qy 1956 ATATTCCTAATCCGAGCGTATCCGAGCTCCTTAGTCGCCTAATAGCCATTTATGGAATGCATTTA 2015
Db 2060 ATAATCCTGGGCCTGAGCGAGTAGCTCTTATATCTCTTAGTCGCCATTTATGGGGATCCATTT 2119

Qy 2016 TAGATATTAGCTCTCTCCATTATCTTATGGAGAGCTGCAAACGAAGGGTTGCAGGGACC 2075
Db 2120 TAGATATACGATCTGCGCATTCAGCAATCTAACTCTTCTTCTCTCATAAGGAATCAGCAAGTGTC 2179

Qy 2076 GCGGGTTTGCCATTTGAGTGGCGGTATGTCAATGATATCTCTTGTTATACTGTTGTAG 2135
Db 2180 AGGGATATCGGTATATTAGTGGGGGTTATTCCTTAGGAGTAGTCTAAAATAGTTATGGGGATCCATTT 2238

Qy 2136 ATAAGAATTCCTTAGTGCTGCAATCCATTTTGTCAGCTCTTTGGAAGATAGACTACTTGTTCAG 2195
Db 2239 --TCGATGTTGGTCTAGACATTACCGAAGTATTTGGTGATCA- 2296

Qy 2196 GCGGGTTTCGCCATTTGAGTGGCGGTATGTCGTTATGGTTTCAGTTGTTCTTATTGTTCTTAGTTCTCAG 2255
Db 2297 GTCGTTCCAATCATCATGCTTGCATAGGATC----------------------CGTTTA 2333

Qy 2256 CAATTGTTTGGGGACAGGGGCTTCTTTATGTTCGTTCTTATGTTCCTACAGAACTCGGG 2315
Db 2334 ATCCTAATACAGCAAATAATGGTCCTTATACTCTGAAAGCTACATGGACTAAAACTGGGT 2384

Qy 2316 ATATTCCTAATCCGAGCGTATCCGAGCGATAACGATCCCTCTTAGTCTCCTATAAGCTATTATGGAATGCATTTA 2375
Db 2385 ATAATCCTGGGCCTGAGCGAGTAGCTCTTATATCTCTGAAATAGTTTATGGGGATCCATTT 2434

Qy 2376 TAGATATTAGCTCTCTCCATTATCTTATGGAGACGAGTGCAAACGCAGGTTGTCAGGGAGACC 2435
Db 2435 TAGATATACGATCTGCGCATTCAGCAATCTAACTCTTCTCCATAAGGAATCAGCAAGTGTC 2494

Qy 2436 GTGCTTTTTGGTGTGTCTGGATTATCTAACTTCTCCATAAGTAGTACAAAAACACGAC 2492
Db 2495 GAGGATTATGGGTTTCGGAGTTTCGAATTTCTTCTATCATGACCGATGCTTTAGGTC 2554

Qy 2493 GCGGGTTTCGCCATTGAGTGGCCGGTTATGTCATTTGTCAGCTCTTTGGAAGAGGAAAACCTCATTT 2552
Db 2555 AGGGATATCCGTATATTAGTGGGGTTATTCCTTAGGAGTAGTCTAAAGATTAATGTGAGTGT 2614

Qy 2553 ATAAGAATTCCTTAGTGCTGTCGTCCATTTTCAGCTCTTTGGAAGAGACTACTTGTTAG 2612
Db 2615 --TCGATGTTGGTTCTAGACATTACCGAAGTATTTGGTAGATCTAAAGATTAATGTAGTGT 2674

Qy 2613 CTAAGAATCAAGGTACAGTCACGGAGGAACTCTCTATTACCAGCAGGAACCTATA 2655
Db 2675 GTCGTTCCAATCATCATGCTTGCATAGGATC-----------------------CGTTTA 2333

Qy   2256  TCTCTCTTCCTTGCAAATACGGCCTTGTTCGTTGTCTTATGTTCCTACAGAGATTCCTG 2315
                 |||||||| ||||| ||                      ||| |||||||||
Db   2334  TCTATCTACCCAACAAGCT--------TTATGTGGATCCTATTTGTTCGGAGATGCGTT 2384

Qy   2316  TTCTCTTTTCAGAAAACCTAGCTACACCCATACGGATAACGATCTCGAAAACCAAGTATA 2375
                 ||||  ||||||||||   |||||||| || |||| || ||||||||||||
Db   2385  TATCCGT--------GCTAGTACGGGTTTGGGAATCAGCATATGAAAAACCTCATATA 2434

Qy   2376  CAACATATCCTACTGTTAAAGGAAGCTCGGGGAATGATAGTTTCGCTTTAGAATTCGGTG 2435
                 ||       |||||| ||||||||| ||||||| |||   |||||  ||| ||
Db   2435  CATTTGCAGGAGGAGGAGCCGATGTTCGTTGGGATAATAACTGTCTCGGCTCGGAGGATTGGAG 2494

Qy   2436  GAAGAGCTCCGATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTACATG---CCCTTCA 2492
                 |||||||| || ||| |||||||||| |||| || ||||||||         |||||
Db   2495  CGGGATTACCGGATTGTGATTACTCCATCTAAGCTCTATTTGAATGAGTTGCGTCCTTTCG 2554

Qy   2493  TGAAATTGCAGTTTGTCTATGCACATCAGGAAGGTTTTAAAGAACAGGAACAGGAGAGCTC 2552
                 ||||||||||  ||| ||| || |||||| |||| |||||||||||||||| ||||
Db   2555  TGAAGCTGAGTTTTCTTATGCCGATCATGAATCTTGCCTTACCTATCGGGATCCGATTTGATC 2614

Qy   2553  GTGAATTGGAAGTAGCCGTCTGTGTGAAATCTTGCCTTACCTATCGGGATCCGATTTGATA 2612
                 | ||| ||||| ||  |||||||||| |||||||||||||||||||||||
Db   2615  GGGCATTCAAGAGCGGACAATCTCCTAAATCTACAATCTAACTCATCATCAGTTCCGTTGT 2674

Qy   2613  AGGAATCAGACTGCCAAGATGCAAGTACAAATCTAAATATAGCTTATATGGCGGCTTATAT 2672
                  |||||  |||| ||||| || || |||||| ||||||||||| |  || ||| | |
Db   2675  GATGTTCTAGTACACATCCTAATAAATATAGCTTATATGGCGGCTTATATCTGTGATGCTT 2734

Qy   2673  TTCGTAGTAACCCGACTGTACGACACACTGCGAATTAGCGGTGATCTTTCTTGGAAAACCT 2732
                  ||| ||||||| |||||||| |||| |  |||||||||| ||||||||| |||||||
Db   2735  ATCGCACCATCTCTGGTACTGAGACAACGCTCCATCCCATCAAGAGACATGGACAACAG 2794

Qy   2733  TCGGTACGAATTTGGCAAGACAAGCTTTAGTCCTTCGTGTGCAGGAAACCATTTTTGCTTTA 2792
                 |||||||||||||||||| |||| || ||| |||| | | |||||||||||||
Db   2795  ATGCCTTTCATTTAGACAAGACAAGATGAGTTGTGTTAGAGGATCTCATGTATGTCTTCTAA 2854

Qy   2793  ACTCAAATTTGAAGCCTTTAGCCAATTTCTTTTGAATTGCGTGGGTCATCCTCGCAATT 2852
                 ||||||| ||||||  ||||| ||||||||    |  ||||| |
Db   2855  CAAGTAATATAGAAGTATATGGCCATGGAAGATATACCGAAGATGAGTATCGGAAGATGCTTCTCGAGGCT 2914

Qy   2853  ACAATGTAGACTTAGGAGGACAAAATACCAATTCTAA 2887
                 |  ||| |:||||| |||| |
Db   2915  ATGGTTTGAGTGCAGGMAGTAAAGTCYGGTTCTAA 2949

RESULT 9
US-09-556-877-169
; Sequence 169, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
;   APPLICANT:   Probst, Peter
;   APPLICANT:   Bhatia, Ajay
;   APPLICANT:   Skeiky, Yasir
;   APPLICANT:   Fling, Steve
;   APPLICANT:   Maisonneuve, Jeff
;   TITLE OF INVENTION:   COMPOSITIONS AND METHODS FOR TREATMENT AND
;   TITLE OF INVENTION:   DIAGNOSIS OF CHLAMYDIAL INFECTION
;   FILE REFERENCE:   210121.469C5
;   CURRENT APPLICATION NUMBER:   US/09/556,877
;   CURRENT FILING DATE:   2000-04-19
;   NUMBER OF SEQ ID NOS:   305
;   SOFTWARE:   FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 169
;   LENGTH:   2643
;   TYPE:   DNA
;   ORGANISM:   Chlamydia
US-09-556-877-169

Query Match             1.7%;   Score 50.6;   DB 4;   Length 2643;
Best Local Similarity   50.6%;   Pred. No. 0.00018;
Matches  122;   Conservative   0;   Mismatches 119;   Indels   0;   Gaps   0;

Qy   1387  AGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAGCCTGTAACTCTTTCAGG 1446
                 |||||||||||||  ||||| |||||| |||||||||||||||||||||||||
Db   1218  AGAAGAAAAAACCTCGATAAACCTCCCAACTACAGCAGCCTATCGAACTGAAATC 1277

Qy   1447  AGTACTCTATCTTTAAAACATGGAGTGACTCGCAGACTACTGCGATTCACTCAACAGGC 1506
                 ||||||||| |||||| ||||||  ||||||  |||||||  |  |||| |||||||
Db   1278  CGGACGCGTTAGTTTTTAAAGATCGCGCTGTGCGCCTTCCGGCCTTCTCTCTCCTCAGGATCC 1337

Qy   1507  AGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAACCTGCTAGATACTAGCACCAT 1566
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1338  TCAAGCTCTCCTCATTATGGAAGCGGGAACTTCTTAAAAACTTCCTCGATTTGAAGTT 1397

Qy   1567  AAACAATTTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGAAGGCAAAAATAGAAAC 1626
                 ||||||||||||||||||||||||  ||||||||| |||||||| | ||||||||||
Db   1398  AGCTACGCTAAGTATTCCCCTTCATTCCTTAGATACTGAAAAAAGCGTAACTATCCACGC 1457

Qy   1627  C 1627
Db   1458  C 1458

RESULT 10
US-09-620-412C-169
; Sequence 169, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
;   APPLICANT:   Steven P. Fling
;   TITLE OF INVENTION:   COMPOSITIONS AND METHODS FOR TREATMENT AND
;   TITLE OF INVENTION:   DIAGNOSIS OF CHLAMYDIAL INFECTION
;   FILE REFERENCE:   210121.469C7
;   CURRENT APPLICATION NUMBER:   US/09/620,412C
;   CURRENT FILING DATE:   2000-07-20
;   NUMBER OF SEQ ID NOS:   363
;   SOFTWARE:   FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 169
;   LENGTH:   2643
;   TYPE:   DNA
;   ORGANISM:   Chlamydia
US-09-620-412C-169

Query Match             1.7%;   Score 50.6;   DB 4;   Length 2643;
Best Local Similarity   50.6%;   Pred. No. 0.00018;
Matches  122;   Conservative   0;   Mismatches 119;   Indels   0;   Gaps   0;

Qy   1387  AGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAGCCTGTAACTCTTTCAGG 1446
                 |||||||||||||  ||||| |||||| |||||||||||||||||||||||||
Db   1218  AGAAGAAAAAACCTCGATAAACCTCCCAACTACAGCAGCCTATCGAACTGAAATC 1277

Qy   1447  AGTACTCTATCTTTAAAACATGGAGTGACTCGCAGACTACTCACTCAACAGGC 1506
                 ||||||||| |||||| ||||||  ||||||  |||||||  |  |||| |||||||
Db   1278  CGGACGCGTTAGTTTTTAAAGATCGCGCTGTGCGCCTTCCGGCCTTCTCTCTCCTCAGGATCC 1337

Qy   1507  AGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAACCTGCTAGATACTAGCACCAT 1566
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1338  TCAAGCTCTCCTCATTATGGAAGCGGGAACTTCTTAAAAACTTCCTCGATTTGAAGTT 1397

Qy   1567  AAACAATTTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGAAGGCAAAAATAGAAAC 1626
                 ||||||||||||||||||||||||  ||||||||| |||||||| | ||||||||||
Db   1398  AGCTACGCTAAGTATTCCCCTTCATTCCTTAGATACTGAAAAAAGCGTAACTATCCACGC 1457

Qy   1627  C 1627
Db   1458  C 1458

RESULT 11
US-09-598-419-169
; Sequence 169, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
;   APPLICANT:   Skeiky, Yasir A.W.
;   APPLICANT:   Scholler, John
;   TITLE OF INVENTION:   COMPOUNDS AND METHODS FOR TREATMENT AND

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; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 169
; LENGTH: 2643
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-598-419-169

Query Match             1.7%;    Score 50.6;  DB 4;  Length 2643;
Best Local Similarity   50.6%;   Pred. No. 0.00018;
Matches  122; Conservative    0; Mismatches  119;  Indels    0;  Gaps     0;

Qy    1387 AGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAGCCTGTAACTCTTTCAGG 1446
           |||||  |||||   || ||||  ||||||  |||||||||||||||||||| |||||||
Db    1218 AGAAGAAAAAACTCCTGATAACCTCACTTCCCAACTACAGCAGCCTATCGAACTGAAATC 1277

Qy    1447 AGGTACTCTATCTTTAAAACATGAGTGACTCTGCGAGACTCAGGCATTCACTCAACAGGC 1506
           |||| ||  | || ||||| ||||||||||||| |||||| |||||||||||| ||||||
Db    1278 CGGACGCTTAGTTTTAAAAGATCGCGCGTGTCCTTTCCGGCCTTCTCTCTCAGGATCC 1337

Qy    1507 AGATTCTCGTCTCGAAATGACGTAGGAACTACTCTAGAACCTGCTGATACTAGCACCAT 1566
           |||||||||||||| ||| |||  |||||||| |||||||  ||||||||||||||||||
Db    1338 TCAAGCTCTCCTCATTATGGAAGCGGGAACTTCTTTAAAAACTTCCTCTGATTTGAAGTT 1397

Qy    1567 AAACAATTGGTCATTAACATCAGTTCTATAGACCGGTGCAAAGAAGGCAAAAATAGAAAC 1626
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    1398 AGCTACGCTAAGTATTCCCCTTCATTCCTTAGATACTGAAAAAGCGTAACTATCCACGC 1457

Qy    1627 C 1627
           |
Db    1458 C 1458
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RESULT 12
US-09-556-877-181
; Sequence 181, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 181
; LENGTH: 2601
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-556-877-181

Query Match             1.7%;    Score 50.2;  DB 4;  Length 2601;
Best Local Similarity   50.2%;   Pred. No. 0.00024;
Matches  121; Conservative    1; Mismatches  119;  Indels    0;  Gaps     0;

Qy    1387 AGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAGCCTGTAACTCTTTCAGG 1446
           |||||  |||||   || ||||  ||||||  |||||||||||||||||||| |||||||
Db    1176 AGAAGAAAAAACTCCTGATAACCTCACTTCCCAACTACAGCAGCCTATCGAACTGAAATC 1235

Qy    1447 AGGTACTCTATCTTTAAAACATGAGTGACTCTGCGAGACTCAGGCATTCACTCAACAGGC 1506
           |||| ||  | || ||||| ||||||||||||| |||||| |||||||||||| ||||||
Db    1236 CGGACGCTTAGTTTTAAAAGATCGCGCGTGTCCTTTCCGGCCTTCTCTCTCAGGATCC 1295

Qy    1507 AGATTCTCGTCTCGAAATGACGTAGGAACTACTCTAGAACCTGCTGATACTAGCACCAT 1566
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Db    1296 TCAAGCTCTCCTCATTATGGAAGCGGGAACTTCTTTAAAAACTTCCTYTGATTTGAAGTT 1355

Qy    1567 AAACAATTGGTCATTAACATCAGTTCTATAGACCGGTGCAAAGAAGGCAAAAATAGAAAC 1626

Db    1356 AGCTACGCTAAGTATTCCCCTTCATTCCTTAGATACTGAAAAAGCGTAACTATCCACGC 1415

Qy    1627 C 1627
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Db    1416 C 1416
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RESULT 13
US-09-620-412C-181
; Sequence 181, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 181
; LENGTH: 2601
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-181

Query Match             1.7%;    Score 50.2;  DB 4;  Length 2601;
Best Local Similarity   50.2%;   Pred. No. 0.00024;
Matches  121; Conservative    1; Mismatches  119;  Indels    0;  Gaps     0;

Qy    1387 AGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAGCCTGTAACTCTTTCAGG 1446
           |||||  |||||   || ||||  ||||||  |||||||||||||||||||| |||||||
Db    1176 AGAAGAAAAAACTCCTGATAACCTCACTTCCCAACTACAGCAGCCTATCGAACTGAAATC 1235

Qy    1447 AGGTACTCTATCTTTAAAACATGAGTGACTCTGCGAGACTCAGGCATTCACTCAACAGGC 1506
           |||| ||  | || ||||| ||||||||||||| |||||| |||||||||||| ||||||
Db    1236 CGGACGCTTAGTTTTAAAAGATCGCGCGTGTCCTTTCCGGCCTTCTCTCTCAGGATCC 1295

Qy    1507 AGATTCTCGTCTCGAAATGACGTAGGAACTACTCTAGAACCTGCTGATACTAGCACCAT 1566
           |||||||||||||| ||| |||  |||||||| |||||||  ||||||||||||||||||
Db    1296 TCAAGCTCTCCTCATTATGGAAGCGGGAACTTCTTTAAAAACTTCCTYTGATTTGAAGTT 1355

Qy    1567 AAACAATTGGTCATTAACATCAGTTCTATAGACCGGTGCAAAGAAGGCAAAAATAGAAAC 1626
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    1356 AGCTACGCTAAGTATTCCCCTTCATTCCTTAGATACTGAAAAAGCGTAACTATCCACGC 1415

Qy    1627 C 1627
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Db    1416 C 1416
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RESULT 14
US-09-598-419-181
; Sequence 181, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 181
; LENGTH: 2601
; TYPE: DNA
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Search completed: December 16, 2003, 15:35:01
Job time : 175 secs

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; ORGANISM: Chlamydia
US-09-598-419-181

Query Match          1.7%;   Score 50.2;  DB 4;  Length 2601;
Best Local Similarity  50.2%;  Pred. No. 0.00024;
Matches 121;  Conservative  1;  Mismatches 119;  Indels  0;  Gaps  0;

Qy  1387 AGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAGCCTGTAACTCTTTCAGG 1446
              ||||   ||||||    ||||| |    |||||   ||    ||||||    |
Db  1176 AGAAGAAAAAACTCCTGATAACCTCACTTCCCAACTACAGCAGCCTATCGAACTGAAATC 1235

Qy  1447 AGTACTCTATCTTAAAACATGGAGTGACTCTGCAGACTCAGGCATTCACTCAACAGGC 1506
              ||   ||||| | || || |    || |   | |    ||| |||  ||||
Db  1236 CGGACGCTTAGTTTTAAAAGATCGCGCTGTCCTTCCGSGCCTTCTCTCTCCAGGATCC 1295

Qy  1507 AGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAACCTGCTGATACTAGCACCAT 1566
              ||||| |||||||  |||||   ||||| || |  |    ||||  |||   |
Db  1296 TCAAGCTCTCCTCATTATGGAAGCGGGAACTTCTTTAAAAACTTCCTYTGATTTGAAGTT 1355

Qy  1567 AAACAATTTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGAAGGCAAAAATAGAAAC 1626
              |||   ||||||  |||  || |||| |||| ||    ||| ||||  ||||
Db  1356 AGSTACGSTAAGTATTCCCCTTCATTCCTTAGATACTGAAAAAAGCGTAACTATCCACGC 1415

Qy  1627 C 1627
         |
Db  1416 C 1416


RESULT 15
US-08-213-419B-3/c
; Sequence 3, Application US/08213419B
; Patent No. 6333406
; GENERAL INFORMATION:
; APPLICANT: Inselburg, J. et al.
; TITLE OF INVENTION: GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: JII-D02CNCP
; CURRENT APPLICATION NUMBER: US/08/213,419B
; CURRENT FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: US 07/870,506
; PRIOR FILING DATE: 1992-04-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 6124
;   TYPE: DNA
;   ORGANISM: Plasmodium falciparum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (2407)..(2439)
;   NAME/KEY: CDS
;   LOCATION: (2598)..(3404)
;   NAME/KEY: CDS
;   LOCATION: (3580)..(3720)
;   NAME/KEY: CDS
;   LOCATION: (3850)..(5835)
US-08-213-419B-3

Query Match          1.4%;   Score 42.4;  DB 4;  Length 6124;
Best Local Similarity  57.6%;  Pred. No. 0.075;
Matches 76;  Conservative  0;  Mismatches 56;  Indels  0;  Gaps  0;

Qy    28 ATTTCTTGACTTGTTTCTCCTATTGGTGTATCTCTTAAAATATTAAATTCAAAATCAAAG 87
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Db  2288 ATTTATTTTTTTTTTATTTTTTTTTTTGGACAATCTAATTTAATTTAAAATTAAAAATTTAT 2229

Qy    88 TATATATTTTACAATGAAGTCTCTTTCCCCAAGTTTGTATTTCTCACATTTGCTATTTT 147
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Db  2228 TATATTATATATATAAATTAATAAATAATATTTAAATTATTTTAAATT 2169

Qy   148 CCCTTTGTCTAT 159
              |||||
Db  2168 TTATTTTTTTAT 2157
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us-09-428-122-1.rnpb

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OM nucleic - nucleic search, using sw model

              GenCore version 5.1.6
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Perfect score: 3000
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Scoring table: IDENTITY_NUC
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Searched:      2201672 seqs, 1661799599 residues

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Minimum DB seq length: 0
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                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3000	100.0	3000	13	US-09-428-122-1	Sequence 1, Appli
2	546.6	18.2	2781	13	US-09-738-269-56	Sequence 56, Appl
3	546.6	18.2	2781	14	US-10-023-437-56	Sequence 56, Appl
4	506.6	16.9	3050	9	US-09-452-380-1	Sequence 1, Appl
5	506.6	16.9	3050	13	US-10-324-129-1	Sequence 1, Appli
6	477	15.9	2808	9	US-09-452-380-2	Sequence 2, Appli
7	477	15.9	2808	13	US-10-324-129-2	Sequence 2, Appl
8	348.4	11.6	2520	13	US-09-738-269-22	Sequence 22, Appl
9	348.4	11.6	2520	14	US-10-023-437-22	Sequence 22, Appl
10	271.8	9.1	2950	9	US-09-886-468-6	Sequence 6, Appli
11	218	7.3	4224	13	US-09-841-132-486	Sequence 486, App
12	148.2	4.9	487	13	US-09-738-269-54	Sequence 54, Appl
13	148.2	4.9	487	14	US-10-023-437-54	Sequence 54, Appl
14	132.2	4.4	3021	9	US-09-841-132-182	Sequence 182, App
15	131.4	4.4	2949	9	US-09-841-132-170	Sequence 170, App

16	84	2.8	1745	9	US-09-886-468-10	Sequence 10, Appl
17	82.2	2.7	2040	13	US-09-738-269-52	Sequence 52, Appl
18	82.2	2.7	2040	14	US-10-023-437-52	Sequence 52, Appl
19	81.4	2.7	2816	9	US-09-886-468-8	Sequence 8, Appli
20	61.2	2.0	3050	10	US-09-779-081-1	Sequence 1, Appl
21	61.2	2.0	4830	13	US-09-841-260-59	Sequence 59, Appl
22	61.2	1.9	4830	14	US-10-007-693-59	Sequence 59, Appl
23	55.8	1.9	379	13	US-09-738-269-20	Sequence 20, Appl
24	55.8	1.9	379	14	US-10-023-437-20	Sequence 20, Appl
25	51.2	1.7	5172	9	US-09-841-132-374	Sequence 374, App
26	51.2	1.7	5172	9	US-09-841-132-375	Sequence 375, App
27	50.6	1.7	2643	9	US-09-841-132-169	Sequence 169, App
28	50.2	1.7	2601	9	US-09-841-132-181	Sequence 181, App
29	45.2	1.5	591	13	US-09-738-269-50	Sequence 50, Appl
30	45.2	1.5	591	14	US-10-023-437-50	Sequence 50, Appl
31	44.2	1.5	3673778	13	US-10-312-841-1	Sequence 1, Appl
32	43.6	1.5	12025	13	US-10-311-455-1271	Sequence 1271, Ap
33	42	1.4	3673778	13	US-10-312-841-2	Sequence 2, Appli
34	41.6	1.4	7049	13	US-10-311-455-129	Sequence 129, App
35	41.6	1.4	7049	13	US-10-240-452-5	Sequence 5, Appl
36	41.2	1.4	18997	13	US-10-311-455-543	Sequence 543, App
37	41.2	1.4	18997	15	US-10-172-086-17	Sequence 17, Appl
38	40.8	1.4	9539	13	US-10-240-453-54	Sequence 54, Appl
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41	40.6	1.4	3048	14	US-10-007-693-80	Sequence 80, Appl
42	40.6	1.4	4190	13	US-10-311-455-415	Sequence 415, App
43	40.2	1.3	18683	13	US-10-311-455-286	Sequence 286, App
44	40.2	1.3	18683	13	US-10-240-452-34	Sequence 34, Appl
45	40.2	1.3	24264	13	US-10-017-161-665	Sequence 665, App

ALIGNMENTS

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RESULT 1
US-09-428-122-1
; Sequence 1, Application US/09428122
; Publication No. US20030170259A1
; GENERAL INFORMATION:
;  APPLICANT: Connaught Laboratories Limited
;  APPLICANT: Murdin et al.
;  TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
;  TITLE OF INVENTION: USES THEREOF
;  FILE REFERENCE: 19721-007-019
;  CURRENT APPLICATION NUMBER: US/09/428,122
;  CURRENT FILING DATE: 1999-10-27
;  EARLIER APPLICATION NUMBER: 60/106,046
;  EARLIER FILING DATE: 1998-10-28
;  EARLIER APPLICATION NUMBER: 60/132,271
;  EARLIER FILING DATE: 1999-05-03
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 1
;  LENGTH: 3000
;  TYPE: DNA
;  ORGANISM: Chlamydia pneumoniae
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (101)..(2884)
US-09-428-122-1

  Query Match         100.0%;  Score 3000;  DB 13;  Length 3000;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 3000;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Db  1441  TTCAGGAGTACTCCATCTATCTTTAAAACATGGAGTGCTCTGCGACTTCTGCAGCATTCACTCA  1500

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Db  1801  GAAATTCCATTACGGCTATCAGGGAACTTGGGGCCCAATTGTTTGGGGACAGGGGCTTC  1860

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Qy  1921  CTCTTTAGTCCCTAATAGCTTATGGAATGCATTTATAGATATATTAGTGCTCTCCATTATCT  1980
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Qy  1981  TATGGAGACTGCAAACGAAGGGTTGCAGGGAGAACACGACCGGGCGGTTCGCGACCGGGGCCGG  2040
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Db    231  TTTTGTTCAGACTGCAGACAACCTAACTTTCAAAGGAACAACCATTATCCATAAC  290

Qy    388  AACGGTGATGCAGGGACTGTAGCAGGGCGTCTGTTAACAGACAGCGTGGTAGTAAATC  447
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Db    465  TATTCTGTTTGATCAGAACTATTCCGGTGAGCTGAGATGGTGGAGCCATCTTCTTGCAAAGCTTT  524

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Db    757  ------GATGGTTGCGGTGACGCTATCCATTGTGAGCAAAACAGGTTCAGCACCGACCCT  809

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Qy   1225  TTTGCGTTCTGCTGGTAGGACGCTCCTATGATCCCATAACTACTTCTATGATCAGGATCATC  1284
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Db   1107  CTTACGTGCAGCGTGCAGATCGATTTCTTTCTTCATGATCCTATCACAGTTG------  1159

Qy   1285  CACAAGTTACAGATGTCTTAAAAGTTAATGACTCCGCAGATTCTCGCACTACAATA  1344
           |  || || || | ||  | ||  | || |    |      |  |  |||  | ||
Db   1160  -----AAGGTAAATGCTGCTGCATCTTCTCACTTTGAATAAAGTGAGGGTGATAAAACGTA  1214

Qy   1345  TACAGGGAACAATCATCTTCACAGAGAAAAAGTTATCAGACGAGAAAAGTTCTAA  1404
           || |  |  |||  | | |  ||   || | || |  ||| |   |||| || | ||
Db   1215  TAATGGAAGAATTATTTTTTCAGGAGAAAAGCTCACTGAAGAACAAGCTGCTTGTTGCGGA  1274
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Db   2281  TTTGTTCCGTGTCTTATGTTCCTACAGAGATTCCGTTCTCTTTTCAGGAAACCTTAGCTA  2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2341  CACCCATACGGATAACGATCTGAAAACCAAGTATACAACACATATCCTTCTGTTAAGGAAG  2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  CACCCATACGGATAACGATCTGAAAACCAAGTATACAACACATATCCTTCTGTTAAGGAAG  2400

Qy   2401  CTGGGGGAATGATAGTTCGCTTTAGAATTCGGTGGAAGAGCTCCGATTTGCTTAGATGA  2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  CTGGGGGAATGATAGTTCGCTTTAGAATTCGGTGGAAGAGCTCCGATTTGCTTAGATGA  2460

Qy   2461  AAGTGCTCTATTTGAGCAGTACATGCCCTTCATGAAATTGTCTATGCACATCA  2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  AAGTGCTCTATTTGAGCAGTACATGCCCTTCATGAAATTGTCTATGCACATCA  2520

Qy   2521  GGAAGGTTTTAAAGAACACAGGAACAGAGAGCTCGTGAAGTTGGAAGTAGCCGTCTTGTGAA  2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  GGAAGGTTTTAAAGAACACAGGAACAGAGAGCTCGTGAAGTTGGAAGTAGCCGTCTTGTGAA  2580

Qy   2581  TCTTGCCTTACCTATCGGATCCGATTTGATAAGGAATCAGACTGCCAAGATGCAACGTA  2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  TCTTGCCTTACCTATCGGATCCGATTTGATAAGGAATCAGACTGCCAAGATGCAACGTA  2640

Qy   2641  CAATCTAACTCTGGTTATACTGTGGATCTGTTCGTAGTAACCCCGACTGTACGACAAAC  2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  CAATCTAACTCTGGTTATACTGTGGATCTGTTCGTAGTAACCCCGACTGTACGACAAAC  2700

Qy   2701  ACTGCGGAATTAGCGGTGATTCTTGGAAAACTTCGGTACGAATTTGGCAAGACAAGTTT  2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  ACTGCGGAATTAGCGGTGATTCTTGGAAAACTTCGGTACGAATTTGGCAAGACAAGTTT  2760

Qy   2761  AGTCCTTCGTGCAGGGAACCATTTTGCTTTAACTCAAATTTTGAAGCCTTAGCCAATT  2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  AGTCCTTCGTGCAGGGAACCATTTTGCTTTAACTCAAATTTTGAAGCCTTAGCCAATT  2820

Qy   2821  TTCTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTAGACTTAGGAGCAAAATACCA  2880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  TTCTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTAGACTTAGGAGCAAAATACCA  2880

Qy   2881  ATTCTAATGCGTTAGCTTGGTAAAGAGCTCGAAGGGAAAGAGCTTTTAAG  2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881  ATTCTAATGCGTTAGCTTGGTAAAGAGCTCGAAGGGAAAGAGCTTTTAAG  2940

Qy   2941  ATTTCTTGAAGGCTCTTTTCGATTTCGATTTTCATTTGTTTTAGTGTTTTGCTAAAACACTTTC  3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941  ATTTCTTGAAGGCTCTTTTCGATTTCGATTTTCATTTGTTTTAGTGTTTTGCTAAAACACTTTC  3000
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RESULT 2
US-09-738-269-56
; Sequence 56, Application US/09738269
; Publication No. US20030185848A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEMKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
; TITLE OF INVENTION: NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
; TITLE OF INVENTION: CHLAMYDIA PSITTACI
; FILE REFERENCE: UTSD:659
; CURRENT APPLICATION NUMBER: US/09/738,269
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 56
; LENGTH: 2781
; TYPE: DNA
; ORGANISM: Chlamydia psittaci
US-09-738-269-56

Query Match 18.2%; Score 546.6; DB 13; Length 2781;
Best Local Similarity 53.7%; Pred. No. 5.2e-142;

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Qy  2461  AAGTGCTCATTTGAGCAGTACATGCCCTTCATGAAATTGCAGTTTGTGTCTATGCACATCA  2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2355  TTCTTCTATCTTTGATAGTTATGTATGCACCGTTTGCAAAATTACAAGTTGTCTATGCGCACCA  2414

Qy  2521  GGAAGGTTTTAAAGAACAGGGAACAGAAGCTCGTGAATTGGAAGTAGCGCTCTTGTGAA  2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2415  AGATGACTTTAAAGACCAACAACAGCAGAGGCCGGGTCTTTGAAAGCAGCGATCTTCTCAA  2474

Qy  2581  TCTTGCCTTACCTATCGGGATCCGATTCGATTTGATAAGGAATCAGACTGCCAAGATGCAACGTA  2640
          |||||||||||||||||||||||||||||||||||||||||
Db  2475  CGTTTCGTACCTATAGGTAGTATAAAATTTGAGAAACTCCTATGGAGAGGAAGTGCTTA  2534

Qy  2641  CAATCTAACTCCTTGGTTATACGTGTGTGATGTCTTGTTCGTGAGTAACCCCGACTGTAGGACAAC  2700
          ||||||||||||||||||||
Db  2535  TGATCTTTACACTGATGTATATACCGTCATGATGTGTACCGTCATAATCCAAGTGTATGACAGG  2594

Qy  2701  ACTGCGAATTAGCGGTGATTCTTGGAAAACCTTCGGTACCGAATTTGGCAAGACAAGCTTT  2760
          |||||||||||||||||||||||
Db  2595  ATTGGCGATCAATGACGTTTCCTGGTTAACCACAGCTACGAATCTTGCTAGAACAAGCTTT  2654

Qy  2761  AGTCCTTCGTGCAGGGAACCATTTTGCTTTAACTCAAATTTTGAAGCCTTTAGCCAATT  2820
          |||||||||||||||||||||||
Db  2655  CATAGTTCGCGCGGCGGGGTAACCATATTGCCCTTAACCTTCTGTGTTTGAGATGTTCAGTCAGTT  2714

Qy  2821  TTCTTTTGAATTGCTGGGTCATCCGCAATTACAATGTAGACTTAGGAGCAAAAATACCA  2880
          ||||||||||||||
Db  2715  TGGTTTGTGAATTACAGAAGCTCTTCAAGAATAATATACGTAGATCTTGGGCGCTAGGTCGC  2774

Qy  2881  ATTCTAA  2887
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Db  2775  GTTCTAA  2781
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RESULT 3
US-10-023-437-56
; Sequence 56, Application US/10023437
; Publication No. US2002018327A1
; GENERAL INFORMATION:
;   APPLICANT: JOHNSTON, STEPHEN A.
;   APPLICANT: STEMKE-HALE, KATHERINE
;   APPLICANT: SYKES, KATHRYN F.
;   APPLICANT: KALTENBOECK, BERNHARD
;   TITLE OF INVENTION: METHODS AND compositions for Vaccination COMPRISING NUCLEIC ACI
;   TITLE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
;   FILE REFERENCE: UTSD:736US
;   CURRENT APPLICATION NUMBER: US/10/023,437
;   CURRENT FILING DATE: 2001-12-17
;   PRIOR APPLICATION NUMBER: 60/225,839
;   PRIOR FILING DATE: 2000-12-15
;   NUMBER OF SEQ ID NOS: 69
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
;   LENGTH: 2781
;   TYPE: DNA
;   ORGANISM: Chlamydia psittaci
US-10-023-437-56

  Query Match             18.2%;  Score 546.6; DB 14;  Length 2781;
  Best Local Similarity   53.7%;  Pred. No. 5.2e-142;
  Matches 1390;  Conservative   0;  Mismatches 1134;  Indels   63;  Gaps   10;
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Qy   328  TTTTAACAACACTAAGGCGCGATTTGACTTTCACAGTAACGGGAACTCTCTATTGTTCCA  387
          |||||||||||||||||||||||||||||
Db   231  TTTTGTTCAGACTGCAGACAACCTAACTTTCAAAGGAACAACCATAGCCATTATCCATAAC  290

Qy   388  AACGGTGGATGCAGGGACTGTAGCAGGGACGCTGCTGTGTTAACAGCAGCGGTGGTAGATAAATC  447
          |||||||||||||||||||||||||
Db   291  GAACGGCAGAATGCCCGGAGCTAATCC---TGCGGGAATTAACGTTAACACTGCCGATAAGAT  347

Qy   448  TACCACGTTTATAGGGTTTTCTTCGCTATCTTTATTGCGTCTCCTGGAAGTTCGGATAAC  507
          |||||||||||||||||||||||
Db   348  TCTTACGCTGCAGATTTTTCTAAGTTGGAGCTTTAAGGAATGCCCATCTTCTCTAGTGAA  407
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Qy  1405  AAATCTTACTTCGAAGCTACTACAGCCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAA  1464
          |||||||||||||||||||||||||||||||||||||
Db  1275  TAACCTAAAGACAACATTTACACAGACCTATCACTTTAGCTGCTGCTGTGAACTTGTGTTACG  1334

Qy  1465  ACATGGAGTGACTCTGCAGACTCAGGCATTCACTCAACAGGCAGATTCTCGTCTCGAAAT  1524
          |||||||||||||||||||||||||||||||||||||||||||||
Db  1335  CAGCCGGTGTGGAAGTAGAAGCAAAACAGTCGTGCAAACAGCAGAGATCTTTGATTCTGAT  1394

Qy  1525  GGACGTAGGAACTACTCTA---GAACCTGTGATACTAGCACATACAACAATTGGTCAT  1581
          |||||||||||||||||||||
Db  1395  GGATGCAGGCACAAAGTTATCCGCAAACAGAGATGCTACACTGACGAATCTGGCTAT  1454

Qy  1582  TAACATCAGTTCTATAGACGGTGCAAAGAGGCAAAATAGAAACCAAAGCTACGTCAAA  1641
          ||||||||||||||||||||||||||||||||||||||
Db  1455  TAAATCCGAATACCTTAGATGGGAAAAAATTCGCCGTAGTCGATGCGGTTGCTGCTGGGAA  1514

Qy  1642  AAATCTGACTTTATCTGGAACCATCACTTTATTGGCGTTTGATCCTACAGGGAAGTTTTATGAAAA  1701
          ||||||||||||||||
Db  1515  GAATGTGACTTTATCAGGTGCTATTGGCGTTATTCAGCTCAAGAGCTCAAGCTCTTCTGGGAAAGGTTCGGT  1574

Qy  1702  TCATAGTTTAAGAAATCCTCAGTCCTACGACATCTTAGAGCTCAAAGCTTCTCTGGAACTGT  1761
          ||||||||||||||||||||
Db  1575  CCATAAGCTAAATGATACGTTAGCTTTAGGAGGAATTCAACTTTCTGGGAAAGGTTCGGT  1634

Qy  1762  AACAAGCACCGCAGTGACTCCAGATCCTATAATGGGTGAGAAATTCCATTACGGCTATCA  1821
          ||||||||||||||
Db  1635  GACAACAACCAAACGTGCCTAGTCATGTTGTGTTGCTGAAACCCACTATGTGTTATCA  1694

Qy  1822  GGGAAC--------TTGGGGCCCAATTGTTGTGGGGACAGGGGCTTCTACGACTGC  1869
          ||||||
Db  1695  AGGAAACGTGTCTGTCAGTTGGGTGGTCAAAGATAATAACTCTGATCCTAAAACACAAACAGC  1754

Qy  1870  AACCTTCAACTGGACTAAAAACTGGCTATATTCCTAATCCCGAGCGTATCGGCTCTTTAGT  1929
          |||||||||||||||||||||||||||||||||
Db  1755  AATCTTTACCTGGAATAAAAAACAGGATATGTTCCAAATCCTGAACGTCGTTGCTGCTCCGCTAGT  1814

Qy  1930  CCCTAATAGCTTATGGAATGCATTTATAGATATTTAGCTCTCTCCATTATCTTATGGAGAC  1989
          |||||||||||||||||||||||||
Db  1815  ACTCAATAGCCCTTTGGGGATCCTTTATAGATTTTACGTTCTATTCAAGATGTCTTGGAACG  1874

Qy  1990  TGCAAACGAAGGGTTGC---AGGAGAACCGTGCTTTTTGGTGTGCTGATTATCTAACTT  2046
          |||||||||||||
Db  1875  TAGTGTTGATAGTATTCTTGAGACACGTCCGGTTGTGTGGGTCTCCTGGAATTGGGAACTT  1934

Qy  2047  CTTCCATAAGGATAGTAGCATCAAAAACAGACGCGGGTTCCGCCATTGAGTGCCGGTTATGT  2106
          ||||||||||||||
Db  1935  CTTCCATAAAAGAATGCTGGAATGCTCGAAATGCAAATTCCCGTACATATCAGTTCGGGATATGT  1994

Qy  2107  CATAGGAGGAGAAAACCTACATACTTGTTCAGATAAGAGATTCTTAGTGTCGCATTTGTCAGCT  2166
          |||||||||||||
Db  1995  GTTAGGAGCGCCACAACAAATACCTCGAGAGGAGATTCTTCCTCTAGTGTGGCCTTCTCTGTCAGTT  2054

Qy  2167  CTTTGGAAGAGATAGAGACTACTTTGTAGCTACGAGAATCAAGGTACAGTCTACGGAGGAAC  2226
          ||||||||||||||||||||||||||
Db  2055  ATTTGCAAAAGATAAAAGATAAAGACTACCTTGTAAGCAAGAACGTCTATGCGGGTTC  2114

Qy  2227  TCTCTATTACCAGCA------CAACGAAACCTATATCTCTTCCTTGCAAACTACGGCC  2280
          ||||||||
Db  2115  TGTATATTATTATCAGCATGTGAGCATGCAAGTTTGATGATCCTCACGCGGTTATTTAATGGGCCTAA  2174

Qy  2281  TTGTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCTTTTTCAGGAAACCTTAGCTA  2340
          ||||||||||||||||||||||||||||
Db  2175  CACGTGTTGTTCAGGGTTTTCAGGGTTTTCTTCTTCTAAAGATGCACAACAAATTACCTA  2234

Qy  2341  CACCCATACGGATAACGATCTGAAAACCAAGTATACAACATATCCTACTGTTAAAGGAAG  2400
          |||||||||||||||||||||||||
Db  2235  TTGCCACACGGCCAACACGACATGACAACGTCCTATACGACTATCCTGAAGTGAAGTGAAAGGTTC  2294

Qy  2401  CTGGGGAATGATGATAGTTTCGCTTTAGAATTCGGTGGAAGAAGCTCCGATTGCTTAGATGA  2460
          |||||||||||||||||||||||
Db  2295  TTGGGGTAATGAATGTACCCGTGGCTTGCTACTAGCCGTACCTATCCCGGTATTTAG  2354
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Qy   508  TACCGGCAAAGGAGCCGTTAGCTGCTCACGGTAGCTTGAGTTTGACAAAAATGTCAG   567
          ||||  |||| |||                                  |||||
Db   408  TACTGGAAAAGGGGGC---TATGAAATCCGGAGGAGCATTAAACTTAGCGAATAATGCCAG   464

Qy   568  TTTGCTCTTCAGCGAAAACTTTTCAACGGATAATGGCGGGTGCTATCACCGCAAAAACTCT   627
          | | || || ||| ||||  || ||| || ||  |   ||| |||| ||  |||||| ||
Db   465  TATTCTGTTTGATCAGAACTATTCCGCTGAGAACTATTGTGGAGCCATCTTGCGAAAGCTTT   524

Qy   628  TTCATTAACAGGACTACAATGTCAGCTCAGTTCTGTTTCTGAAAAATAACCTCCTCAAAGAAAGG   687
          ||   | || || ||| ||||| |||| ||||  | ||| ||||||||| |||| |||||| |||
Db   525  TTCTCTAACCGGCTGAGACAATCAGCTTCACCACTAACTCTACTCTGCGAAAAAAGG   584

Qy   688  CGGAGCCATTCAGATCTTCCGATGCCCGTCCACTAACTACTGGAAACCAAGGGAGTCTCTTT   747
          ||||||||  |||||  |||||  || || ||                 ||||| ||| |||
Db   585  TGGAGCCGATTGCTGCTCACGCGGGAATAGCTCATCTTGCCTAGTCATGTGTTGGTGAAACAACCACCAAGGCACACAATCAGATT   644

Qy   748  TTCTGACAATACTTCTTCGGATTCTCGAGCTGCCAATTTTACAGAAGCCTCGGTGACTAT   807
          |||  || || ||||| | ||| ||| ||||| |  || ||||||||| ||||||| | |
Db   645  TTCTGGGAACACTGCTGTGAATTCTCGGGGAGCAGTATTCTGGGAGGAGCTTCTATGGACGAT   704

Qy   808  TTCTAATAATGCTAAAGTTCCTTTATTGACAATAAGGTCACAGGAGCGAGCTCCTCAAC   867
          |  | |||| ||| ||| ||||    ||||  ||  ||| |  |||| || ||| ||
Db   705  TGCAGGTAACAACCACGTTGCTTTAGCAACAAATGTCTTGTTCCGGTTCATCT--------   756

Qy   868  AACGGGGGATATGTCAGGAGGTGCTATCGTGCTTATAAAACTAGTACAGATACTAAGGT   927
          |  |  |  |  || | || |||||| || ||  ||||| | ||   |||||  |||||
Db   757  ------GATGGTTGCGGGTGAGAGCTATCCATTGTGGGGATCCTTTATTGCTGGCCAATGCAT   809

Qy   928  CACCCTCACTGACAATCAGATGTTATCCGCCGATAGTGGTGACATTGTCTTTCTGTTTTAGGGAA---TACAGTCACTTC   987
          ||| |||| ||  ||   |||  || || |||||||  || |||  ||| | ||    ||| ||      ||||||  ||
Db   810  TACTATAAGGATAACAAGTCTGAATTCTGGGGAGTAAAAGTATACTTCTTCAGGAGGATTAACCTGATGGCCACACA   869

Qy   988  AGCTATCTATGTGAAAAAAGCTGAACTGGCTTCCGGAGGACTTACCCTATTCAGTAGAAA   1047
          |||| || || ||||||||| |||| ||  | || ||||| ||   |  |||||||| ||
Db   870  AGCGGATTTACACCGGATAAACTCATATTGACTTCTCTGGTGGGCCTACGGCATTTATCAATAA   929

Qy  1048  TAGTGTCAATGAGCTCCTAAAGTGAGCCATAGCTATCGAAGATAGTGGGA   1107
          |  | | || |  || || ||  || || ||| ||| ||||| | ||||
Db   930  CAAAGTTACCCATGCTACA---CCTAAGGGTGGAGCCGTATTGGTATTGCTGCCAATGGAG   986

Qy  1108  ATTGAGTTTATCCGCCGATAGTGGTGACATTGTCTTTTTAGGGAA---TACAGTCACTTC   1164
          ||  ||| ||||| || ||  ||  ||   || | |||| |||        || |||||
Db   987  ATGTAGTTAACCGCTGAAACATGGGAACTCTGAAATCTTTTCAGGGGATATATAACCTGATGATAACCGAT   1046

Qy  1165  TACTACTCCTGGGACGAATAGAGAGTAGTAGTATCGATCCTAGGAACGAGTGCAAAGATGACAGC   1224
          || |||  |||| || ||||  |||| || | ||  || || ||| || ||  ||| |||||||
Db  1047  AGACAATGCTACAATAAAAGAAAATGCCATTAACTACTCTTGAAGGCAATGGTAAATTCGTCAA   1106

Qy  1225  TTTGCGTTCTGCTGCGGTCGTGGTAGAGCACCATCTAATGATCCCATACTAACTACAGGGATCATC   1284
          ||  || ||| || |  || |  | ||||| ||| ||| || | ||| |||| |||| |||||
Db  1107  CTTAGCGTGTGTGCAGCCGTGCTGGAAAAGACGATTTCTTTCTTTGGATGCACAAATTACCTA   1159

Qy  1285  CACAACAGTTACAGATGTCTTAAAAGTCAATGAGACTCCGGCAGATTCTGCACTACAAATA   1344
          ||| || | ||  |||  | |||||| ||| ||  || ||| || ||| | ||| |||
Db  1160  -----AAGGTAATGCTGCTGATCTCCACTTGACTTTAAAGAAAGCTGAGGGTGATAAAACGTA   1214

Qy  1345  CACAGGGAACATCATCTCAGAGAAAAGTTATCAGACAGACAGAGAGGCCCGCAGAATTCTAA   1404
          || || |||| |||||| |||| |||  |  | ||||| ||||||| || || |||| |||
Db  1215  TAATGGAAGAATTATTTTCAGGAGAAAAGCTCACTGAGAACAGAAGCTGCTGTACTCTGTTGCGGA   1274

Qy  1405  AAAATCTTACTTCGAAGTACTACAGCCTGTAACTCTTCTATCTTTAAA   1464
          |||  |||  || ||| | || ||  || | | ||||| | || |||
Db  1275  TAACCTAAAGACAACATTTACACAGCGCCTATCACTCTTTGAGTTGTGTTACG   1334

Qy  1465  ACATGGAACTGACTCTGCAGGCATTCACTCAACAGGCAGATTCTCGTCTCGAAAT   1524
          |||  | ||| ||||  |||| | ||||| ||  |||||| |||| || ||||
Db  1335  CAGGCCGGTGTGGAAGTAGAGCAAAAACAGAGCTGCTGCAACAGAGGCGGATTCTTGATTCTGAT   1394

Qy  1525  GGACGTAGGAGGACTACTCTA---GAACCTGCTGAGACTCGTGATACTGAAGATGCAACGTA   1581
          ||||| ||| || | ||||       || || |  |||| || || |  |  | || |||
Db  1395  GGATGCAGGCAACAAAAGTTATCCGCAAAACAGAGAAGCTGCCACTGACTCTTTGATTCTGCTAT   1454

Qy  1582  TAACATCAGTTCTATAGACGGTGCAAAGAGAGGCAAAAATAGAAAACCAAAGTCACGTACGTCAAA   1641
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Qy  1455  TAATCCGAATACCTTAGAT   1514
          |||
Db  1642  AAATCTGACTTTATCTGAACCATCACTTATTGGACTAATGGAAAAAAATTCGCCGTAGTCGATGTCCGTTGCTGGAA   1701

Qy  1515  GAATGTGACTTTTATCAGGTGCTATTGATCCTAACACAAAACAGCTC   1574
          ||  |||||
Db  1702  AAATGTGACTTTATTCAGCGTGCTATTTGATGGGTTATTGATCTCTAGAGGGAGTTTTTATGAAAA   1761

Qy  1575  CCATAAGCTAAATGTAACGTTAGCTTTAGGAGGAATTCAACTTCTCTGGGAAAAGGTTCGGT   1634
          ||
Db  1762  TCATAGTTTAAGAAATCCTCAGTCCTACGACATCTTAGAGCTCTAGAGCTTCAAAGCTTCTGGAACTGT   1821

Qy  1635  GACAACAACCACGTGCCTAGTCATGTGTTGGTGCTGAAACCCACTATGTTATCA   1694
          ||
Db  1822  AACAAGCACCGAGTGACTCCAGAATCCTATAATGGGTGAGAATTCCATTACGGCTTATCA   1869

Qy  1695  AGGAAACTGGTCTGTCAGTTGGGTAGAAGTTTCTCATGACGAT   1754
          ||
Db  1870  TTGGGGCCCAATTGTTGGGGGACAGGGGCTTCTACGACTGC   1929

Qy  1755  AATCTTTACCTGGAATAAACAGGATAATGTTCCAAATCCTGAAATCCTGACGTCTCCGCTAGT   1814
          ||
Db  1930  AACCTTCAACTGGACTAAAACTGCTATAATTCCTAATCCCGAGCGTATCGGCGCTTCTTTAGT   1989

Qy  1815  ACTCAATGACCCTTTGGGGATCCTTTATTGGGATCCCATATTGGTATTGCTGCCAATGCAT   1874
          ||
Db  1990  TGCAAACGAAGGGTTGC---AGGGAGACCCGGTGCTTTTTGGTGGTGCTAAGAATCAAGATGCTCTAACGACTTGGTGTGCTGATTATCTAACTT   2046

Qy  1875  TAGTGTTGATAGTATTCTTGAGACAAATAAAGAAGATCAAAGCGCCGAAACGTCTATGGGAACTT   1934
          ||
Db  2047  CTTCCATAAGGATAGTAGTACAAAAAACACGACGCGGGTTTCGCCCATTGAGTGGCGGTTATGT   2106

Qy  1935  CTTCCCATAAAGATCGGAATAGCTGAAAATCCGTGAAAATCGAAGATATGT   1994
          ||
Db  2107  CATGAGGAGGAAACCTACACATACTTGTTCAGATAAGATTCTTAGTGCTGCAGCT   2166

Qy  1995  GTTAGGAGCCCAACACAAATAACCTCGAGAGAGAATTGCTGCCAATGATGT   2054
          ||
Db  2167  CTTTGGAAGAGATAGAGCACTACTTTGAGTAGCTGAGAATCAAGAAGTACAGTCTACACGGAGGAAC   2226

Qy  2055  AATTGCAAAGATAAAGACTAACTACCTTTGTAAGCAAGAACGTCATGCGGGTTC   2114
          ||
Db  2227  CAACGAAACCTATATCTCCTTGCGCAAACTACACGGCC   2280

Qy  2115  TGTATATTATCAGCATGTGAGCAAGTTTGATGAGATTTGATGGATGCAAAAT   2174
          ||
Db  2281  TTGTTCGTTGCTTTATGTCCTAAAGATAGTGGGACTATTTTCAGGAAACCTTAGCTA   2340

Qy  2175  CACGTGTTGTTCAGGGTTTCTAAAGAGATTTTCTATATACTGATGCACAAATTACCTA   2234
          ||
Db  2341  CACCCATAACGATAGTAAACGATCTGAAAAACTCAGAAGTGACTGTGAAGAAG   2400

Qy  2235  TTGCCACGGCCAACAACATGACAACGTCCATACAGACTCATCCTGAAGTGAAAGGTTC   2294
          ||
Db  2401  CTGGGGGAATGATAGTTTCGCTTTAGAGGGAGAGAGCTTCGGATTTGCTTAGATGA   2460

Qy  2295  TTGGGGTAATGATACCCGGGCTTAACTTGTTCTACTAGCTGTTATCCCGGTATTTAG   2354
          ||
Db  2461  AAGTGCTCTATTTGACGAGTATCATGGAACTTGTCAGTTGTCTATGCGCACATCA   2520

Qy  2355  TTCTTCTATCTTTGATAGTTATGATAATTACAAGTTGTCATATGCGCACACCA   2414
          ||
Db  2521  GGAAGGTTTTAAAGAACAGGGAACAGGAACTTCGTGAATTTGGAAGTAGCCGTTCTTGTGAA   2580

Qy  2415  AGATGACTTTAAAGAACCAACAACAGAGGCCGGGGTCTTTGCAAAAGCCGAATCTTCTCAA   2474
          ||
Db  2581  TCTTGCCTTACCTATCGGATCGTTTGATTTGATAAGGAATCGAACAAACGTCCTTGTGAA   2640

Qy  2475  CGTTTCTGCTACCTATAGGTTATGGAAGTTGAGAAAATTTGAGAAACTCTCCTATGGAAGAAGTGCTTA   2534

Db  2641  CAATCTAACTCTGGTTGTTGGATCTTGTTCCTGATCGTGTGTCTTATGTGAGTAACCCCGACTGTACGACAAC   2700
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Db   2535 TGATCTTACACTGATGTATATACCTGATGTGTACCGTCATAATCCAAGCTGTATGACAGG 2594

Qy   2701 ACTGCGAATTAGCGGTGATTCTTGGAAAACCTTCGGTACGAATTTGGCAAGACAAGCTTT 2760
              | || || | | | ||| ||| |||| | |||||||| | || |||||||||||
Db   2595 ATTGGCGATCAATGACGTTTCCTGGTTAACCACAGCTACGAATCTTGCTAGACAAGCTTT 2654

Qy   2761 AGTCCTTCGTGCAGGGAACCATTTTTGCTTTAACTCAAATTTTGAAGCCTTTAGCCAATT 2820
                | |||| || || |||||| || ||| | ||| | |||| || || || ||
Db   2655 CATAGTTCGCGCGGGTAACCATATTGCCTTAACCTCTGGTGTTGAGATGTTCAGTCAGTT 2714

Qy   2821 TTCTTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTAGACTTAGGAGCAAAATACCA 2880
              | ||| ||||| || | || || | ||||| || ||||| | || || || |
Db   2715 TGGTTTCGAATTACGAAGCTCTTCAAGAAATTATAACGTAGATCTTGGCGCTAAGGTCGC 2774

Qy   2881 ATTCTAA 2887
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Db   2775 GTTCTAA 2781

RESULT 4
US-09-452-380-1
; Sequence 1, Application US/09452380
; Patent No. US20020094340A1
; GENERAL INFORMATION:
; APPLICANT: MURDIN, Andrew D.
; APPLICANT: OOMEN, Raymond P.
; APPLICANT: WANG, Joe
; APPLICANT: DUNN, Pamela
; TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 032931/0216
; CURRENT APPLICATION NUMBER: US/09/452,380
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/132,272
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/113,439
; PRIOR FILING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 3050
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (101)..(2908)
US-09-452-380-1

  Query Match   16.9%; Score 506.6; DB 9; Length 3050;
  Best Local Similarity   51.3%; Pred. No. 9.5e-131;
  Matches 1473; Conservative   0; Mismatches 1324; Indels   72; Gaps   10;

Qy   66 AATATTAAATTCAAAATCAAAGTATATATTTTACAATGAAGTCTTCTTTCCCCAAGTTTG 125
              ||| | | | | | || | | || |||||||||| || | | | |||
Db   66 AATTTAATTTCCTTGTTTCAAAAAAGTGCTTACAAATGAAGTCCTCTGTCTCTTGGTTGT 125

Qy   126 TATTTTCTACATTTGCTATTTTCCCTT---TGTCTATGATTGCTACCGAGACAGTTTTGG 182
              | |||||| || | | | || | | | ||||| | || | ||| || |
Db   126 TCTTTTCTTCAATCCCGCTCTTTTCATCGCTCTCTATAGTCGCGGCAGAGGTGACCTTAG 185

Qy   183 ATTCAAG---TGCGAGTTTCGATGGGAATAAAAATGGTAATTTTTCAGTTCGTGAGAGTC 239
              || || | || | ||||| ||| || || | || | | |
Db   186 ATAGCAGCAATAATAGCTATGATGGATCTAACGGAACTACCTTCACGGTCTTTTCCACTA 245

Qy   240 AGGAAGATGCT---GGAACTACCTACCTATTTAAGGGAAATGTCACTCTAGAAAATATTC 296
               ||| | |||| ||||||||||| || | || | | |||||
Db   246 CGGACGCTGCTGCAGGAACTACCTATTCCTTACTTTCCGACGTATCCTTTCAAAATGCAG 305

Qy   297 CTGGAACAGGCACAGCAATCACAAAAAGCTGTTTTAACAACACTAAGGGCGATTTGACTT 356
                | ||| | | | | | | || || | | |||||| | ||||
Db   306 GGGCTTTAGGAATTCCCTTAGCCTCAGGATGCTTCCTAGAAGCGGGCGGCGATCTTACTT 365

Qy   357 TCACAGGTAACGGGAACTCTCTATTGTTCCAAACGGTGGATGCAGGGACTGTAGCAGGGG 416
              || ||| || | | || ||| | | |||| || || || ||
Db   366 TCCAAGGAAATCAACATGCACTGAAGTTTGCATTTATCAATGCGGGCTCTAGCGCTGGAA 425

Qy   417 CTGCTGTTAACAGCAGCGTGGTAGATAAATCTACCACGTTTATAGGGTTTTCTTCGCTAT 476
              ||| | | | | | | |||||| | |||| | |||||| || |
Db   426 CTGTAGCCAGTACCTCAGCAGCAGATAAGAATCTTCTCTTTAATGATTTTTCTAGACTCT 485

Qy   477 CTTTTATTGCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGCCGTTAGCTGCTCTA 536
              || |||| | | ||| ||| || || | | | | | |||
Db   486 CTATTATCTCTTGTCCCTCTCTTCTTCTCTCTCCTACTGGACAATGTGCTTTAAAATCTG 545

Qy   537 CGGGTAGCTTGAGTTTGACAAAAAATGTCAGTTTGCTCTTCAGCAAAAACTTTTCAACGG 596
               ||| | | | | || ||| | | | || | | ||||| || | |
Db   546 TGGGGAATCTATCTCTAACTGGCAATTCCCAAATTATATTTACTCAGAACTTCTCGTCAG 605

Qy   597 ATAATGGCGGTGCTATCACCGCAAAAACTCTTTCATTAACAGGGACTACAATGTCAGCTC 656
              |||| ||||||| ||||| | |||| | | |||| ||||||| | || ||
Db   606 ATAACGGCGGTGTTATCAATACGAAAAACTTCTTATTATCAGGGACATCTCAGTTTGCGA 665

Qy   657 TGTTTTCTGAAAATACCTCCT------CAAAGAAAGGCGGAGCCATTCAGACTTCCGATG 710
                ||||| ||| ||| ||| ||||||| | || | || | |
Db   666 GCTTTTCGAGAAACCAAGCCTTCACAGGGAAGCAAGGCGGTGTAGTTTACGCTACAGGAA 725

Qy   711 CCCTTACCATTACTGGAAACCAAGGGGAAGTCTCTTTTTCTGACAATACTTCTTCGGATT 770
              | | || || | || ||| ||| || || ||| | || | | |
Db   726 CTATAACTATCGAGAACAGCCCTGGGATAGTTTCCTTCTCTCAAAACCTAGCGAAAGGAT 785

Qy   771 CTGGAGCTGCAATTTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTTCCT 830
              |||| | ||| | | | | | | ||| | |||| | |||| ||
Db   786 CTGGCGGTGCTCTGTACAGCACTGACAACTGTTCGATTACAGATAACTTTCAAGTGATCT 845

Qy   831 TTATTGACAATAAGGTCACAGGAGCGAGCTCCTCAACAACGGGGGATATGTCAGGAGGTG 890
              || | ||||| | | ||| | |||| |||
Db   846 TTGACGGCAATAGTGCTTGGGAAGCCGCTCAAGCTCAGGGCGGGGCTAT----------- 894

Qy   891 CTATCTGTGCTTATAAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGT 950
                        || | |||| ||||||| | || || || ||||| || | |
Db   895 ----------TTGTTGCACTACGACAGATAAAACAGTGACTCTTACTGGGAACAAAAACC 944

Qy   951 TACTCTTCAGCAACAATACATCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTCG 1010
              | |||| || |||||| | ||| || ||||| |||| || ||| ||
Db   945 TCTCTTTCACAAATAATACAGCATTGACATATGGCGGAGCCATCTCTGGACTCAAGGTCA 1004

Qy   1011 AACTGGCTTCCGGAGGACTTACCCTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTC 1070
                 | | | ||||| ||||| ||||| | ||| | | | | ||
Db   1005 GTATTTCCGCTGGAGGTCCTACTCTATTTCAAAGTAATATCTCAGGAAGTAGCGCCGGTC 1064

Qy   1071 ---CTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATA 1127
                     ||| ||||| || ||| | | | ||||||| | | | || || |
Db   1065 AGGGAGGAGGAGGAGCGATCAATATAGCATCTGCTGGGGAACTCGCTCTCTCTGCTACTT 1124

Qy   1128 GTGGTGACATTGTCTTTTTAGGGAATACAGTCACTTCTACTACTCCTGGGACGAATAGAA 1187
               ||| || ||| ||| || |||||| | | | || | |
Db   1125 CTGGAGATATTACCTTCAATAACAACCAAGTCACCAACGGAAGCACAAGTACAAGAAACG 1184

Qy   1188 GTAGTATCGACTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTGCTGGTAGAG 1247
                | || | | | || || || | ||| | | || |||||| || |
Db   1185 CAATAAATATCATTGATAC---CGCTAAAGTCACATCGATACGAGCTGCTACGGGGCAAT 1241

Qy   1248 CCATCTACTTCTATGATCCCATAACTACAGGATCATCCACAACAGTTACAGATGTCTTAA 1307
              | ||||| |||||||||||||| || | | | || || | ||| || || |
Db   1242 CTATCTATTTCTATGATCCCATCACAAATCCAGGAACCGCAGCTTCTACCGACACATTGA 1301

Qy   1308 AAGTTAATGAGACTCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAG 1367
              | | | | | || | || | | ||| || || |||| | |
Db   1302 ACTTAAACTTAGCAGATGCGAACAGTGAGATCGAGTATGGGGGTGCGATTGTCTTTTCTG 1361

Qy   1368 GAGAAAAGTTATCAGAGACAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTAC 1427
              |||||||| | || ||||| ||| || ||| | || || | | | ||
Db   1362 GAGAAAAGCTTTCCCCTACAGAAAAAGCAATCGCTGCAAACGTCACCTCTACTATCCGAC 1421

Qy   1428 AGCCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAACATGGAGTGACTCTGCAGACTC 1487
              | |||| | | | | || ||| | ||||||| || |
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Db 1422 AACCTGCAGTATTAGCGCGGGAGATCTTGTACTTCGTGATGGAGTCACCGTAACTTTCA 1481

Qy 1488 AGGCATTCACTCAACAGGCAGAATTCTTCGTCTCGAAATGGACGTAGGAACTACTCTAGAAC 1547
            ||||| ||| ||||||| |||||| |||| ||||| |||||||||| || |||
Db 1482 AGGATCTGACTCAAAGTCCAGGATCCCGCATCTTAATGGATGGGGGACTACACTTAGTG 1541

Qy 1548 CT--GCTGATACTAGCACCATAAACAATTGGTCATTAACATCAGTTCTATAGACGGTG 1604
            || ||| ||| |||| || || || ||||| ||| |||| ||||
Db 1542 CTAAAGAGGCAAATCTTCGTAATGGCTTAGCAGTAGAATCCTCTCCTCTTTAGATGGAA 1601

Qy 1605 CAAAGAAGGCAAAAAATAGAACCAAAGCTACGTCAAAAATCTGACTTTATCTGAACCA 1664
            |||| ||||| ||||||| ||| ||| || |||| ||||| ||||
Db 1602 CCAACAAGGGCAGCTTAAAAACAGAGCTGCAGATAAAAATATCAGCCTATCGGGGAACGA 1661

Qy 1665 TCACTTTATTGGACCCGACGGGCACGTTATGTAGAAATTTAAGAAATCCTCAGT 1724
            || ||| || ||||| ||||||||| || || || |||||| || |||
Db 1662 TTGCGCTTATTGACACGGAAGGGGTCATTCTATGAATCATGAGAATCATAAACTTAAAGTGCTAGTA 1721

Qy 1725 CCTACGACATCTTAGAGCTCA-------AAGCTTCTGAACTGTAACAGCACCGCAG 1775
            ||| |||| ||| ||| |||||| ||| ||| ||||| ||||
Db 1722 CCTATCCTGTCTTCTTGAACTTACCACCGCAGGAGCCAACGGAACGGATTACTCTCGGGAGCTC 1781

Qy 1776 TGACTTCCAGATCCTCATAATGGGTGAGAAATTCCATTACGCTATCACGGAACTTGGGGCC 1835
            | ||||| ||| || ||||| |||| |||||||||| ||||| || |||
Db 1782 TTTCTACCCTGACTCTTCAAGAACCTGAACCCACTACGCGTATCCAAGGAACCTGCAGT 1841

Qy 1836 CAATTGTTGGGGGACAGCAGGGGCTTCTCACGACTTCTCACTCGACTAAAACTGGCT 1895

Db 1842 TGTCTTGGGCAAATGCAACACTATCCTCAAAAATAGGAAGCATCAACTGGACCCGTACCAGGAT 1901

Qy 1896 ATATTCCTAATCCCGAGCCGTATCGGCTTCTTAGTCCCTAATAGCTTATGGAATGCATTTA 1955
            ||||| || ||||| |||| ||||||| |||| ||||| ||||| ||||||
Db 1902 ACATTCCTAGTCCTGAGAGAAAAAGTAATCTCCCTCTAAATAGCTTATGGGAAACTTTA 1961

Qy 1956 TAGATATTAGCTCTCTCCATTATCTTATGAGACTGCAAACGAAGGGTTGCAGGGAGACC 2015
            |||||| |||||| ||| || |||| |||||||||| || ||||||| |||||||
Db 1962 TAGATATACGCTCGGATCAATCAGCTTATAGAAACCAAGTCCAGTGGGAGCCTTTTGAGC 2021

Qy 2016 GTGCTTTTGGTGTGCTGGATTAATCGAACTTCTTCCATAGGATAGTAGTACAAAACACGAC 2075
            |||| | ||| ||| || | |||| |||| ||| ||| ||||| ||| | ||| ||
Db 2022 GTGAGCTATGGCTTTCAGGAATTGCGAATTTCTTCTATAGAGATTCTATGCCCACCCGCC 2081

Qy 2076 GCGGGGTTTGCGCCATTTGAGTGCGGTTATGTCATAGGAGGAAACCTACATACTTGTTCAG 2135
            |||| ||| |||||| ||| || | |||| ||| |||||| ||| ||| |||||
Db 2082 ATGGTTTTCCCGCCATATCAGCTGCCGGGGTTATGCCATAGGGGATCACAGCAGACTCCTGCCG 2141

Qy 2136 ATAAGATTCTTAGTGCTGCAGTTTGTCAGCTCTTTGGAAGAGAGATAGAGACTACTTTGTAG 2195
            |||| || |||| ||| ||||| ||||| |||| ||||| |||| |||| ||||
Db 2142 AGGATCGACTTACTTTGCCCTCTGCCAGCTCTTTGCCAGCTGCAATCATATATTACAG 2201

Qy 2196 CTAAGAAATCAAGGTACAGTCTACGGAGGAGAACTCCTCTATTACCAGC---------- 2240
            | ||| ||||||| ||| ||| |||| ||| || ||||| ||||||
Db 2202 GTAAGAACACGGAGATACTTACGTGCCCTCTTCTTTGTATTTCCACCATACAGAAGGGCTCT 2261

Qy 2241 --ACAACGAAACCTATATCTCTTCCTTGGGGAAAAGCAACCCGAGTCCCTGGGTGCTTCTGA 2297
              || |||||| ||| || |||||| ||||||| ||| ||| ||| || |||| ||||
Db 2262 TCGACATCGCCAATTCCTGGGAAAGCAACGAACCCGAGTCCCTGGGTGCTCCTTGGGTTGT 2321

Qy 2298 TTCCTACAGATTCCTGTTCTCTTTCAGGAAAACCTTAGCTACACCCATACGGATAACG 2357
            || ||||| ||| || || ||| ||| ||||| |||| ||| |||| |||| ||||
Db 2322 TCTCCCGATCAATTCCTTTATGTCGATGCTAAATTCAGTTAATCTCCATACAGACAACC 2381

Qy 2358 ATCTGAAAAACCAAGTATACAACATATATCCACTGTTAAGGAAGCTGGGGAATGATAGTT 2417
            |||| ||| |||| || || |||| || |||| ||||| || |||||| |||
Db 2382 ACATGAAGACATATTATACCGATAACTCTATCATCCAAGGGTTCTTGGAGAAAACGATGCCT 2441

Qy 2418 TCGCTTTAGAATTCGGTGAAGAGAGCTCCGATTTGCTTAGATGAAAGTGCTCTATTTGAGC 2477
            ||| | |||| ||||| |||| | | ||| || ||| | || || || ||||||||
Db 2442 TCTGTGCAGATCTTGGAGCTGCCTGCCTTCGTTCCGTTGTATTTCGTCGACATCCATAGCGTGAAAG 2501

Qy 2478 AGTACATGCCCTCATGAAAGTTGTCAAAGTACAGTATATATCGCATGCACACTCAGAAGAAC 2537
            | || |||| | |||||| | ||| ||| |||| |||||||||| || ||||
Db 2502 AAGTCGAACCTTTTGTCAAATGACAGTTCATCAGCAGGGCCATCAGCAGACTTCACGCGAGC 2561
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Db  2538  AGGGAACAGAGAGCTCGTGAAATTTGGAGTAGCCGTCTTGTGAATCTTGCCTTACCTATCG  2597

Qy  2562  GTCATGTGTGAAGGACGCGGCTTTCAATAAAGCGAGCTTATCAACGTAGAGAATTCCTATAG  2621

Db  2598  GGATCCGATTTGATAGGAATCAGACTTGCCAAGATGCAAGATGAACGTACAATCTAACTCTTGGTT  2657

Qy  2622  GCGTCACCTTCGAAAGAGACTCAAAATCAGAAAAGGGAACTTACGATCTTACTCTTATGT  2681

Db  2658  ATACTGTGGATCTTGTTCGTAGTAACCCGACTGTACGACAACACTGCGAATTAGCGGTG  2717

Qy  2682  ATATACTTCGATGCTTACCGACGGCAATCCTAAATGTCAAACTTCCCTAATAGCTAGGCGATG  2741

Db  2718  ATTCTTGGAAAACCTTCGGTACGAATTTGGCAAGACAAGCTTAGTCCTTCGTCGCAGGGA  2777

Qy  2742  CTAACTGGATGGCCTATGGCCTATGGTACCAACCTCGCACGACAAGGTTTTCTGTTCGTCGTGCTCGA  2801

Db  2778  ACCATTTTGCTTAACTCAAATTTGAAGCCTTAGCCAATTTCTTTTGAATTGCGTG  2837

Qy  2802  ACCATTTCCAAGTGAACCCCCACATGGAAATCTTCGGTCAAGTTTGGAAGTACGAA  2861

Db  2838  GGTCATCTCGCAATTACAATGTGAGACTTAGGAGCACAAATACCAATTCTA  2886

Qy  2862  GTTCTTCACGAAATTATAATACAAACCTAGGCTCTAAGTTTTGTTTCTA  2910
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RESULT 5
US-10-324-129-1
; Sequence 1, Application US/10324129
; Publication No. US20030157124A1
; GENERAL INFORMATION:
;  APPLICANT: Murdin et al.
;  TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses the
;  FILE REFERENCE: 77813-4
;  CURRENT APPLICATION NUMBER: US/10/324,129
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: US 60/113,439
;  PRIOR FILING DATE: 1998-12-01
;  PRIOR APPLICATION NUMBER: US 60/132,272
;  PRIOR FILING DATE: 1999-05-03
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
;  LENGTH: 3050
;  TYPE: DNA
;  ORGANISM: Chlamydia pneumoniae
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (101)..(2908)
US-10-324-129-1

  Query Match       16.9%;  Score 506.6;  DB 13;  Length 3050;
  Best Local Similarity  51.3%;   Pred. No. 9.5e-131;
  Matches 1473;  Conservative  0;  Mismatches 1324;  Indels  72;  Gaps  10;

Qy   66  AATATTAAATTCAAAATCAAAATCAAAGTATATATTTACAATGAAGTCTTCTTCCCAAGTTTG  125
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Db   66  AATTTAATTTCCTTGTTCAAAAAAGTGCTTACAAATGAAGTGTCCTCCTGTCTCTTGGGTTGT  125

Qy  126  TATTTTCTACATTTGCTATTTTCCCTT---TGTCTATGATTGCTACCGAGACAGTTTGG  182
           | |||||| || || ||||||| ||||    ||| |||| || |||| ||||||||||
Db  126  TCTTTTCTTCTCAATCCGTCTCTTTTCATCGTGCTTCTATAGTCGCGGGCAGAGGTGACCTTAG  185

Qy  183  ATTCAAG---TGCGAGTTTCGATGGGAATAAAAATGGTATTTTTCAGTTCGTGAGAGTC  239
           |||| |||   || ||  || || ||  |||| || ||||| ||| || ||  || |||
Db  186  ATAGCAGCAATAAATAGCTATGATGGATCTAACGAACTACCTTCACGGTCTTTTCCACTA  245

Qy  240  AGGAAGATGCT---GGAACTACCTATTTAAGGGAAATAGTCACTCTAGAAAAATATTC  296
           |  ||| | |||    || ||||| ||  ||  ||||| ||| || ||||| |||||||
Db  246  CGGACCGCTGCGACGAGGCAGGAACTAACGGAACTACCTTCCTTACTTTTCCGACTATCCTTTCAAAATGCAG  305

Qy  297  CTGGAACAGGCACAGCAGCAATCACAAAAAGCGTGTTTTAACACACTAACGGCGATTTGCACTT  356
           |||||  |||  |||||| ||||| || ||||||| |||| |||| |||||| ||||| |||||
Db   (continues)
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Qy    1428 AGCCTGTAACTCTTTCAGGAGTACTCTATCTTTAAAACATGAGTGACTCTGCAGACTC 1487
                 |||||         |||||||||||||  |    | | |||||||| ||||||
Db    1422 AACCTGCGTATTAGCGGCGGGGGGATCTTGTACTTCGTGATGAGTCACCGTAACTTTCA 1481

Qy    1488 AGGCATTCACTCAACAGCGCAGATTCTCGTCTCGAAATGGACGTAGGGACTACTCTAGAAC 1547
                 ||||   ||    | |    ||||| |  ||||||  ||    ||||||
Db    1482 AGGATCTGACTCAAAGTCCAGAATCCCGCATCTTAATGGATGGGGGACTACACTTAGTG 1541

Qy    1548 CT---GCTATACTAGCACCATAAACAATTGGTCATTAACATCAGTTCTATAGACGGTG 1604
              |    ||     |  | | |||  |||| ||||  |||| |  ||||
Db    1542 CTAAAGAGCAAATCTTTCGCTTAATGGCTTAGCAGTAGAATCTTCCCTCTTTAGATGGAA 1601

Qy    1605 CAAAGAAGGCAAAAATAGAAACCAAAGCTACGTCAAAAAATCTGACTTTATCTGGACCA 1664
              ||   ||||       || |  ||  |||  ||  ||||  | || |||||||||
Db    1602 CCAACAAGCAGCTTAAAAACAAGAAGCTGCAGATAAAATATCAGCCTATCGGGACGACGA 1661

Qy    1665 TCACTTTATTGGACCCGACGGGCACGTTTATGGTGAGAAATCATCAGTTAAGAAATCCTCAGT 1724
              ||||  | || |||||||   | | ||||||  ||||  ||||||||  ||||||||
Db    1662 TTGCGCTTATTGACACGGAAGGGTCATTCTATGGAGAATCATAACTTAAAAAGTGCTAGTA 1721

Qy    1725 CCTACGACATCTTAGAGCTCA------------AAGTTCTGGAACTGTAACAAGCACCGCAG 1775
              ||||  |  | |||||||                 |||||  |||||||||
Db    1722 CCTATCCTCTTGAACTTGCCACCGGCAGGAGCCCAACCGGAACGATTACTCTGGGGAGTC 1781

Qy    1776 TGACTCCAGATCCTATAATGGGTGAGAACTTTGAGGAATTCATGGCCTATCGGGAATTGGGGCC 1835
              ||||    |||  |   || || |  | || |||||||  ||||||
Db    1782 TTTCTACCCTGACTCTTCAGAGACCTGCGAATTTCTCTATAGAGAAACTGGCAGT 1841

Qy    1836 CAATTGTTTGGGGACCAGGGGCTTCTCAACGGGCTTTCAACTTCACTGCTAAAACTGGCT 1895
              |||||  | |||        |||  | |  |     |||| ||||  ||||||
Db    1842 TGTCTTGGGCAAATGCAACATCCTCAAAAATAGGAAGCATCAACTGACCCGTACAGAT 1901

Qy    1896 ATATTCCTAATCCCGAGCCTATGGCTCTTTAGTCTTATGGAATGCATTTA 1955
              | | | |  |  | ||||||  | |   || ||  ||||||  | |||||
Db    1902 ACATTCCTAGTCCTCTGAGACGAAAAGTAATAATCTTATGGGAAAACTTTA 1961

Qy    1956 TAGATATTTAGCTCTCTCCATTATCTTATGGAGACTGCAAAGGAAGGGTTGCAGGGGAGACC 2015
              ||||||   |||| | || |||||||  |||||  |  | ||||||||||
Db    1962 TAGATATACGCTCTGATCAATCAGCTTATGAAACCAAGTCCAGTGGGGAGCCCTTTTGAGC 2021

Qy    2016 GTGCTTTTTGGTGTGCTGATTAATCTAACTCTTCCATAAGAGTAGTAGTACAAAAACACGAC 2075
              ||   || |||| | | ||  |||   || |||||   |||| || ||| |||| |||
Db    2022 GTGAGCGTATGGCTTTCAGGAATTGCGAATTTCTTCTATAGAGATTTCTATGCCCACCCGCC 2081

Qy    2076 GCGGGTTTCGCCATTGAGTGCCGTTATGTCAATGGAGAAAACCTACATACTTGTTCAG 2135
              |   ||||||  ||   | ||  |||| ||| || |||| |  ||||  |||||
Db    2082 ATGGTTTCCGCCATATCAGCGGGTTATGCGGAGGTTCATCACAGCAGCATCAACTCCTGCCG 2141

Qy    2136 ATAAGATTCTTAGTGCTGCAATTTGTGCAGCTCTTGGAGAGATAGAGACTACTTTGTAG 2195
              | ||||| |  ||||    |||| ||| |||  |||||||| |||| |  |||||
Db    2142 AGGATCAGCTTACTTTGCCTTTGCCTTGCTAGCCAGTCTTTGCTAGAGATCGAATCATATTACAG 2201

Qy    2196 CTAAGAATCAAGGTACAGTCTACGGAGAACTCTCTATTACCAGC----------- 2240
              ||||||||   | ||||  ||  ||||||| ||  | ||  |
Db    2202 GTAAGAACCACGAGATACTTACGGTGCCTCTTTGTATTTCCACCATACAGAAGGGCTCT 2261

Qy    2241 ---ACAACGAAACCTATATCTCCTTCCTGCAAACTACGGCCTTCCTGGTGTCGTTCTTATG 2297
                    ||   ||  | ||| |  ||  ||||   ||||    |  |||||  | |||||
Db    2262 TCGACATGCCAATTTCCTCTGGGGAAAAGCAACCCGAGCTCCTCCGGGTGCTCTCTGAGA 2321

Qy    2298 TTCCTACAGAGATTCCCTGTTCTCTTTTCAGGAAACCTTAGCTACACCCATACACGGATAACG 2357
              |||| |  | |  | || |  ||   | |||||  ||  |||   || ||||   ||
Db    2322 TCTCCCAGATCATTCCTTTTCGATGCTAAATTCAGTTATCCTATCACACAGCAAACC 2381

Qy    2358 ATCTGAAAACCAAGTATACAACACCAGTCATCAACACATATCTTACTGTTTAAAGGAAGCTGGGG 2417
              | ||| | |  || || ||  ||  ||  ||||| |||     ||||||||||
Db    2382 ACATGAAGACATATTATACCGATAACTCTCATCATCAAGGGTTCTTGGAGAAAACGATGCCT 2441

Qy    2418 TCGCTTTAGAATTCGGTGGAAGAGCTCCGATTTGCTTGAGTGAAAGTGCTCTATTTGAGC 2477
              |||  | | |||||| |||| || ||| ||| |  | |||  |||||||||
Db    2442 TCTGTGCAGATCTGGAGCTAGCCTGTCGTCAAAATGCCCCTTTGTATTTCGTGCCGTATCTTCCCGAC 2501
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RESULT 6
US-09-452-380-2
; Sequence 2, Application US/09452380
; Patent No. US20020094340A1
; GENERAL INFORMATION:
;   APPLICANT: MURDIN, Andrew D.
;   APPLICANT: OOMEN, Raymond P.
;   APPLICANT: WANG, Joe
;   APPLICANT: DUNN, Pamela
;   TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
;   TITLE OF INVENTION: USES THEREOF
;   FILE REFERENCE: 032931/0216
;   CURRENT APPLICATION NUMBER: US/09/452,380
;   CURRENT FILING DATE: 1999-12-01
;   PRIOR APPLICATION NUMBER: US 60/132,272
;   PRIOR FILING DATE: 1999-05-03
;   PRIOR APPLICATION NUMBER: US 60/113,439
;   PRIOR FILING DATE: 1998-12-01
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 2808
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-09-452-380-2

Query Match   15.9%;   Score 477;   DB 9;   Length 2808;
Best Local Similarity   51.4%;
Matches 1451;   Conservative   0;   Mismatches 1300;   Indels   74;   Gaps   12;
Pred. No. 1.8e-122;

Qy   101   ATGAAGAGTCTTCTTCTTCCCCAAGTTTGTATTTTCTACATTTGCTATTTCCCTT---TGTCT   157
Db   1   ATGAAGTCGGATGCTCTCTGTTGTTCTTTTTCTCATCCGCTCTTTTCATCCGTCTCT   60

Qy   158   ATGATTGCTACCGAGACAGTTTGGATTCAAG---TGCGAGTTTGCGATGGGAATAAAAAT   214
Db   61   ATAGTGCCGGCGGAGTGACCTTAGAATAGCAGCAATATAGTATGATGGAATGAATGAGGA   120

Qy   215   GGTAATTTTCAGTTGCTACCGAGAGTCAGGAAGAGATGCT---GGAACTACCTACCTATTTAAG   271
Db   121   ACTACCCTTCACGGTCTTTTCCACTACGGACGCGTCGCGCAGAGAACTACCTATTCCTTACTT   180

Qy   272   GGAAATGCACTCTACAGAAAATATTCCTGAACAGCACAGCCAATCACAAAAAGCTGTTTTT   331
Db   237   GTATGTGGGGTGGCGATTGTCTTTTTCTGGAGAAATGTTCCCTAGAAAAGCAATCGC   1296

Qy   1103   GGGGAATTGAGTTATCCGCCGAATAGAAGTAGTATCGACTTAGGAACGAGTGCAAAGATGACA   1162
Db   1000   GGGGAACTCCGGTCTCTCTGCTACTTCTGGAGATATTACCTTCAATAACAACCAAGTCACC   1059

Qy   1163   TCTACTACTCCTGGGACGACGAATAGAAGTAGTATCGACTTAGGAACGAGTGCAAAGATGACA   1222
Db   1060   AACGGAAGCACAAGTACAAGAAACGCAATAAATATCATTGATAC---CGCTAAAGTCACA   1116

Qy   1223   GCTTTGCGTTCGCGCTGGTAGAGCCATCTACTTCTATGATCCA-TAACTACAGGATC   1281
Db   1117   TCGATACGAGCTGCTACGGGCCAATCTATCTATTCTATGATCCATTCTATGAT   1176

Qy   1282   ATCCACCAACAGTTACAGATGTTCTTAAAGTTAATGAACTTAAACTTGACATTGAACTTAAACTTGAGGA   1341
Db   1177   AACCGCAGCTTCTTCACCGACACATTAAACTTGACATTGAACTTAGCAGATGAGAATCGA   1236

Qy   1342   ATATACAGGAACATCATCTTCACAGGAGAAAAGTTATCAGAGAAAAGCAATCGC   1401
Db   1237   GTATGTGGGGTGGCGATTGTCTTTTTCTGGAGAAATGTTCCCTAGAAAAGCAATCGC   1296

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Qy   181   TCCGACGTATCCTTCAAAATGCAGGGGCTTTAGGAATTCCCTAGCCTCAGGAGATGCTTC   240
Db   332   AACAAACACTAAGGCGGGGCGATCTTACTTCCAAGGAAATCAACATGCACGGCTGGTGTAGATAAATCTACC   391

Qy   241   CTAGAAGCGGGGCGGGGCGATCTTACTTCCAAGGAAATCAACATGCACGGCTGGTGTAGAGATTTGCATTT   300
Db   392   GTGGATGCAGGAGACTGTAGCAGGGCTGGAACTGTAGCGCAGTGACCTCAGCGATAAGAAATCTT   451

Qy   301   ATCAATGCGGGGCTGGACTGTCTTTATTGGTCTCCTGGAAGTCGATAACTACC   360
Db   452   ACGTTTATAGGGTTTCTTCGTCATCTTTAGTGCTGTGGCCCTCCTCTTCGTCCCT   511

Qy   361   CTCTTTAATGATTTTCTAGACTCTGCTTATTATCTCTTGCAAATTAACCGGATG   420
Db   512   GGCAAAGGAGCCGTAGCTGCTCTACCGGTAGCTTGACAAAAAATGTCAGTTG   571

Qy   421   ACTGGACAAATGTCTTTAAAATCTGTGGGAATCATCTCTAACTGGCAATTCCCAAATT   480
Db   572   CTCTTCAGCAAAAACTTTCAACGGGATAATGGCGGTGCTATCCAGCAAAAACTCTTCA   631

Qy   481   ATATTTACTCAGAACTTCTCGTCAGATAACGGCGGTGTTATCAATACGAAAAACTTCTTA   540
Db   632   TTAACAGGGACTACAATGTCAGCTCTGTTTTCTGAAAATACCTCTCA------AAGAAA   685

Qy   541   TTATCAGGGACATCTCAGTTTGCGAGCTTTCGAGAAACCAGCCCTTCACAGGGGAAGCAA   600
Db   686   GGCGGAGCCATTCAGACTTCCGATGCCCTACAGAACTATTACTCGAGAACAGCCCTGGGATAGTTTCC   745

Qy   601   GGCGGTGTAGTTTACGTCACGAATCATCAGGAACTATAACTATCGGAAAACAGCCCTGGGATAGTTTCC   660
Db   746   TTTTCTGCACAATACTTCTTCGAGTTGCAATTTTACAGAAGCCTCCGGTGACT   805

Qy   661   TTCTCTCAAAACCTAGCAGAAGGATCTGGCGTCTGTACAGCACTGACAACTGTTCG   720
Db   806   ATTTCTAATAATGCTAAAGTTCCTTTATTGACAATAAGGTCACAGGAGCGGAGCTCCTCA   865

Qy   721   ATTACAGATAAACTTTCAGTGATCTTTGACGCGCAATAGTGCTTGGAAGCCCGCTCAAGCT   780
Db   866   ACAACCGGGGAATGTCAGGAGGTGCTGCTATCGTGTGCTTATAAAAACTAGTACAGATACTAAG   925

Qy   781   CAGGGCGGGGGCTAT------TTGTTGCTACTACGACACGATAAAACA   819
Db   926   GTCACCCTCACTGGAAATCAGATGTTACTCTTCAGCAACAATCATCGACAACAGCGGGA   985

Qy   820   GTGACTCCTTACTGGGAACAACAAAAACCTCTCTTTCACAACATAATATACAGCATAGCGGC   879
Db   986   GGAGCTATCATGTGAAAAAGCTGAAACTGGCTTCCGGAGGACTTACCCTATTCAGTAGA   1045

Qy   880   GGAGCCATCTCTGGACTCAAGGTCAGTATTTTCCGCTGGAGGTCCTACTCTATTTCAAAGT   939
Db   1046   AATAGTGTCAATGAGGTACAGCTC---CTAAAGGTGGAGCCATAGTATCGAAGATAGT   1102

Qy   940   AATATCTCAGGAAGTAGCGCCGGTCAGGAGGAGGAGCCGATCAATATAGCATCTGCT   999

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Qy   2478   AGTACACTGCCCTTCATGGAAGTTGCAGTTGTCTATGACATCAGGAAGGTTTTAAAGAAC   2537
Db   2502   AAGTCGAACCTTTTGTCAAAGGAGCTGCAAGTACAGTATATCTATCGCAGCAAGACTTCTACGAGC   2561

Qy   2538   AGGGAACAGAGACGGCGGCTTTCGTGAATTTGGAAGTCAGGAAGTAGGCGGTG   2597
Db   2562   GTCATGCTGAGGGACGCGGCTTTCAATAAAAGGAGCTTATCACGTAGAGATTCCTATAG   2621

Qy   2598   GGATCCGATTTGATAAGGAATCAGAATCAGACTCAAAATCAAGAAAAGGAACTTACGGATCTTACTCTTGGTT   2657
Db   2622   GCGTCACCTCGAAAGATCGTTGTTCGTAGTAACCCGACTGTACGACAACACTGCGAATTAGCGGTG   2681

Qy   2658   ATACTGTGGATCTTGTTCGTACCGACGCGGCAATCCTAAATGTCAAAACTTCCCTAATAGTCTAGCGATG   2717
Db   2682   ATATACTGATGCCTATGGCCATATGGTTAACCTCGACGCACGAAGAGGTTTTCGTTGTGTGCGGA   2741

Qy   2718   ATTCTTGGAAAACCTTCGGTACGAATTTGGCAAGACAAGCTTAGTCCTTGTTCGTGCGAGGGA   2777
Db   2742   CTAACTGGATGGCCTATGGTTAACCTCGCACGAAGAGGTTTTCGTTGTGTGCGCGA   2801

Qy   2778   ACCATTTTGCTTTAACTCAAATTTGAAGCCTTTAGCCAATTTCTTTTGAATTGCGTG   2837
Db   2802   ACCATTTTCCAAGTGAACCCCCACATGGAAATCTTCGGTCAATTCGGTCAATTCGCTTTGAAGTAGCAA   2861

Qy   2838   GGTCATCTCGCGAATTACAATGTAGACTTAGGAGCAAAATACCAATTCTA   2886
Db   2862   GTTCTTCACGAAATTATAATACAAACCTAGCCTCTAAGTTTGTTTGTTTCTA   2910

Qy 2452 CTTAGATGAAAGTGCTCTCATTTGAGCAGTACATGCCCTTCATGAAATTGCAGTTGTCTA 2511
         |||||| | |||| ||| ||||||||||||||||| | ||||||||||| |||||||||||
Db 2376 TATTTCCGTTCCGTAACTTCTGAAAGAAGTCGAACCTTTTGTCAAAGTACAGTATATCTA 2435

Qy 2512 TGCACATCAGGAGGTTTTAAAGAACAGGAGAACAGAGAGCTCGTGAATTGGAAGTAGCCG 2571
         |||| ||| | || |||| ||||| ||||||||||||||| ||||||||||||||||||||
Db 2436 TGCGCATCAGCAGACTTCTACGAGCGTCATGCTGAAGGACGGCGTCTTCAATAAAAGCGA 2495

Qy 2572 TCTTGTGAATCTTGCCTTACCTATCGGGATCCGATTGATAAGGAATCAGACTGCCAAGA 2631
         ||||||| | ||| || | | ||||||||||||||||||||| |||| |||| || |||||
Db 2496 GCTTATCAACGTAGAGATTCCTATAGGCGTCACCTTCGAAAGAGACTCAAATCAGAAA 2555

Qy 2632 TGCAACGTACAATCTAACTCTTGTTATACTGGTATACGTGAGATCGTTGTTCGTAGTAACCCGACTG 2691
         ||| |||||||| ||| ||| |||||||| || ||||||| |||| ||||| |||||||||| |||
Db 2556 GGGAACTTACGATCTTACTCTTATGTGTATATACTCGATGCTTACCGACGCAATCCTAAATG 2615

Qy 2692 TACGACAACACTGCGAATTAGGGGTGATTCTTGGTGAAAAACCTTCGGTACGAATTGGCAAG 2751
         || |||| |||| ||||||| | ||||||||||||||||||||||||||||||||
Db 2616 TCAAACTTCCCTAATAGCTAGCCATGTCTAACTGGATGGCCTATGGTACCAACCTCGCACG 2675

Qy 2752 ACAAGCTTTAGTCCTTCGTGCGCAGGAGGATCCATCTTTGCTTAACTCAAATTTGAAGCTT 2811
         ||||||| |||||| ||||| ||||||||||| |||||||||||
Db 2676 ACAAGGTTTTTCGTTCGTCGTGCGAACCATTCCAAGTGAACCCCACATGGAAATCTT 2735

Qy 2812 TAGCCAATTTCTTTGAATTGCGTGGGTCATCTGCAATTACAATAGAAGTTCTTCACGAAATTATAATAACAAACCTAGGCTC 2871
         |||||||||| | ||||||||||| || || ||| ||||| |||||
Db 2736 CGGTCAATTGCGTTTTGAAGTACGAAGTTCTTCACGAAATTATAATAATAACAAACCTAGGTC 2795

Qy 2872 AAAAT 2876
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Db 2796 TAAGT 2800

RESULT 7
US-10-324-129-2
; Sequence 2, Application US/10324129
; Publication No. US20030157124A1
; GENERAL INFORMATION:
; APPLICANT: Murdin et al.
; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses the
; FILE REFERENCE: 77813-4
; CURRENT APPLICATION NUMBER: US/10/324,129
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/113,439
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/132,272
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 2808
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2808)
US-10-324-129-2

Query Match   15.9%; Score 477; DB 13; Length 2808;
Best Local Similarity   51.4%;   Pred. No. 1.8e-122;
Matches 1451; Conservative   0; Mismatches 1300; Indels   74; Gaps   12;

Qy   101 ATGAAGTCTTCTTTCCCCAAGTTGTATTTCTACATTTGCTATTTCCCTT---TGTCT 157
         ||||| || |||| ||| | |||||| ||||| ||||| | ||||||
Db   1 ATGAAGTCCTCTGCTCTGGTGTTGTTCTTTCAATCCGCTCTTTCTCATCCGCTCTCT 60

Qy   158 ATGATTGTACCGAGACAGTTTTGATTCAAG--- TGCGAGTTTCGATGGGAATAAAAAT 214
         |||||| | | || | || || ||| |||| |||| | || | || ||| |||
Db   61 ATAGTCGCGCGACGCAGAGGTGACCTTAGATACAGCAGCAATAATAGCGATCTAACGGA 120

Qy   215 GGTAATTTTCAGTTCGTGAGAGTCAGGAAGAGATGCT---GGAACTACCTACCCATTTAAG 271
         || ||| | |||| | |||| | |||| ||| | ||| |||| ||| || | |||
Db   121 ACTACCTTCACGCGGTCTTTTCCACTACGACGCTCGCGAGGAACTACCTTCATTCCTTACTT 180

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Qy  1342  ATATACAGGGAAACATCATCTTCACGAGGAGAAAGTTATCAGAGACAGAGGGCCGCAGATTC  1401
               |||||  | |||||| ||||||||||||||||||||||||||||||
Db  1237  GTATGGGGTGCGATTGTCTTTTCTGGAGAATCTTCCCCACCAGAAAAAGCAATCGC        1296

Qy  1402  TAAAAATCTTACTTCGAAGCTACACAGCCTGTAACTCTTCTCAGAGGTACTCTATCTTT    1461
               |||||||||||| ||||||||| |||| |||||||||||||||
Db  1297  TGCAAAGTCACCTCACTACTATCCGACAACCTGCAGTATTAGCCGCGGGGAGATCCTTGTACT  1356

Qy  1462  AAAACATGGACTCTGCAGACTCAGCATTCACTCAACAGCAGACGCAGATTCTCGTCTCGA   1521
               ||||||||||||||| ||||  |||||||  |||||| ||||||||||
Db  1357  TCGTGATGGAGTCACCGTAACTTTCAAGGATCGACTCAAAGTCCAGGATCCCGCCATCTT    1416

Qy  1522  AATGGACTAGGAACTACTCTAGAACCT---GCTGATACTAGCACCATAAACAATTGGT    1578
               ||||| |||| |||||||||||||||     ||||| ||||||||||||
Db  1417  AATGGATGGGAGGGATACACTTAGTGCTAAAGAGAGGCAAATCTTCGCTTAATGGCTTAGC   1476

Qy  1579  CATTAACATCAGTTCTATAGACGGTGCAAAGAGAGGCAAAAATAGAAACCAAAGTACGTC   1638
               |||||||||||||||||||| ||| |||||||||  ||||||| || |||||||
Db  1477  AGTAAAATCTCTCCTCTTTAGATGCAAACCAACAAGGCAGCTTTAAAAACAGAAGCTGCAGA  1536

Qy  1639  AAAAAATCTGACTTTATCTGGACCATCACTTTATTGGACCCGACGCGGCACGTTTTATGA   1698
               ||||||| ||||| |||||||||||||| || ||||||| ||| |||| ||||
Db  1537  TAAAAATATCAGCCTATCGGGAACGATTGCGCTTATTGGACCACGGAGGGTCATTCTATGA   1596

Qy  1699  AAATCATAGTTTAAGAAAATCCTCAGTCCTACGACATCTTAGAGCTCA------AAGC   1749
               |||  | |||||||||||  |||||| |||||||| || ||||||
Db  1597  GAATCATAACTTAAAAAGTGCTAGTAACCTTACCTATCCTCTTCTGAACTTACCACCCGCAGGAGC  1656

Qy  1750  TTCTGGAACTGTAACAAGCACCCCAGTGACTCCAGATCCTCCATAATGGGTGAGAAATTCCA   1809
               |||||||||| |||| |||||||||||||| |||||||||| |||||||||| ||||||
Db  1657  CAACGGAACGATTACTCTGGGGAGCTCTTTCTCACCCTGACTCTTCAAGAGAACCTGAAACCCA   1716

Qy  1810  TTACGGCTATCAGGGAACTTGGGGCCCAATTGTTTGGGGACAGGGCTTCACGACTGC   1869
               || || || ||||| |||||||||| |||||||| || |||| |||||||||||||
Db  1717  CTACGGGTACAAGGAAACTGGCAGTTGTCTTGGGCAAATG-CAACATCCTCAAAAATAGG    1775

Qy  1870  AACCCTCAACTGGACTAAAACTGGAATGCATTTATAGATATTAGCTCTCTCCATTATCTTATGGAGAC  1929
               || |||||||| |||| |||||| || |||||| ||||| ||||||||  |||| || |||||
Db  1776  AAGCATCAACTGGACCCGTACAGGGATAACAATTCCTAGTCCTGAGAGAAAAGTAATCTCCC    1835

Qy  1930  CCCTAAGTACTTATGGAGTCATTTATAGATCATTTATGATATTAGCTCTCTCCATTATCTTATGGAGAC  1989
               |||| ||| ||| ||| ||| |||| |||||||| || ||| ||||||||||| |||||
Db  1836  TCTAAATAGCTTATGGGGAAACTTTTATAGATATATACGCTCCAGTCCTTATAGAAC    1895

Qy  1990  TGCAAACGAAGGGTTGCAGGGAGACCCGTGCTTTTGTGTGCGGGATAATCTAACTTCTT    2049
               |||| |||||| |||||| ||||||||||||||| |||||| ||||||||||| ||||
Db  1896  CAAGTCCAGTGGGGGAGCCTTTGAGCGTGAGCCTTTCAGGAAGTTGCGAATTTCTT       1955

Qy  2050  CCATAAGGATAGTACAAAAACACGACGCGGGGTTCGCCATTGAGTGGCGGTTATGTCAT    2109
               ||||| ||||| |||||| ||||||||||||||||||| ||| || ||||||| |||||
Db  1956  CTATAGAGATTCTATGCCCAACGCCACCCGCCATGGGTTTCCGGCCATATCAGCGGGGTTATGCACT  2015

Qy  2110  AGGAGGAAACTACATACTTGTTCAGATAAGATTCTTAGTGCTGCATTTTGTCAGCTCTT    2169
               ||| ||||| | ||||| |||||| ||||| || ||||||||| |||| ||||||||||
Db  2016  AGGGATCCACACGCACACTCCTCCGCCGACAACTTCCGCGAAGAGTCGGAAGCGATCCAGCTCTT  2075

Qy  2170  TGGAAGAGATAGAGACTACTTTGTAGCTAAGAATCAAGGTACAGCTCTAAGGAACTCT    2229
               |||| ||||||| || ||| ||| ||||| ||||| |||||||||| || ||||||||
Db  2076  TGCTAGAGATCGCAATCAATCATATTACAGGGATAAGCTAAGGACAGGTAAGACTGCCCTCTT  2135

Qy  2230  CTATTACCAGC--------------------------ACAACGAAACCTATATCCTCTTCTTCCTTGCAA  2271
               ||||| ||||                           |||||  | |||
Db  2136  GTATTTCCACCATACAGAAGAGGGCTCTTCGACATCGCGCCAATTTCCTCTGGTTCTCTTTATGTCAACAAC  2195

Qy  2272  ACTACGGCCCTTGTTCGTTGTCTTATGTTCCTACAGAGATCTCTTCCTTGCAA          2331
               |||| |||||||||||| |||| |  || ||||||| ||||| |
Db  2196  CCGAGCTCCCCTGGGTGCTCTCTGAGATCTCCCAGATCCCCAGATTCCTTCCGATGCTAA           2255

Qy  2332  CCTTAGCTACACCCATACGGATGAAAACGATCTGAAAAACTGAGAAAAAGCAACAAGTATACAACACATCCTACTGT  2391
               |||| |||| || ||| ||  || ||  ||  |||||||||||| |||||  ||||||||
Db  2256  ATTCAGTTATCTCCATACAGCAACCACCACATGAAAGACATATTATACCGGATAACTCTTATCAT    2315

Qy  2392  TAAAGGAAGCTGGGGGAATGAATAGTTTCGCTTTAGAATTCGGTGGAAGAGCTCCGATTTG  2451
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Qy  272   GGAAATGTCACTCTTGAGAAATATTCCTGGAAACAGGCACAGCAATCACAAAAAGCTGTTT  331
               ||||  || | |||| ||||||||| ||||| || || ||| |||| ||||||
Db  181   TCCGACGTATCCTTTCAAAATGCAGGGCGATTTGACTTTCACAGGGCAACTTCTCTATTGTTCCAAACG  240

Qy  332   AACAACACTAAGGGCGCGGCGGCGATTTGACTTCACAGGTAACGGGGAACTCTCTATTGTTCCAAACG  391
               |||| |||||| ||  || || ||||||||||| || ||||||| |||||  ||||||
Db  241   CTAGAAGCGGGGCGGCGGCGATTTGACTCTTACTTTCCAAGGAAATCAACATGCACTGAAGTTTGCATTT  300

Qy  392   GTGGATGAGGGACTGTAGCAGGGGCTCTGTTAACAGCCTGGTAGATAAATCTACC  451
               | || |||||||| || ||| || ||||||||| ||| |||| ||||| |||
Db  301   ATCAATGCGGGGCTCTAGCGCTGGAACCTGTAGTACCAGCAGATAAGAATCTT    360

Qy  452   ACGTTTATAGGGTTTTCTTCGCTATCTTTATTGCGTCTCCTGGAAGTTCGATAACTACC  511
               || ||||| ||| |||| |||| |||||||| || ||||||||| |||  |||||||||
Db  361   CTCTTTAATGATTTTTCAACACTCTTCTATTATCTTCTGTCCCCTCTCTTCTCTCTCCT  420

Qy  512   GGCAAAGGAGCCGTTAGCTGCTTCTACGGTAGCTTGACTTGACAAAAAATGTCAGTTTG  571
               ||| |||| ||| || || |  ||| || | ||||| |||| ||||||  ||||| |||
Db  421   ACTGGACAATGTGCTTTAAAATCTGTGGGAATCTATCTCAACTGGCAATTCCCAAATT  480

Qy  572   CTCTTCAGCAAAAACTTTCAACGGATAATGCGGGTGCTATCACCGCAAAAACTCTTTCA  631
               ||||| |||||||||||| |||| | |||||| ||| |||||  | ||| |||| || ||
Db  481   ATATTTACTCAGAACTTCTCGTCAGATAAACTACCGGTTATCAATACGCAGAAAAACTTCTTA  540

Qy  632   TTAACAGGGACTACAACATGTCAGCTCTGTTTTCTGAAAATACCTCCTCA------AAGAAA  685
               || |||||||||| | ||||||||| ||||| || ||||||||  |||
Db  541   TTTATCAGGGACACATTCAGTTTGCGAGCTTTTGCGAGCCTTTCGAGAAACCAAGCCCTTCCGCAGGGAAGCAA  600

Qy  686   GGCGGAGCCAATTCAGACTTCAGACTTCCGATGCCCTTACCATTACTGGAAAATAATCGTCT  745
               ||| ||||| || ||| |||| ||| ||||| |||| |||| || || ||| |||| |||
Db  601   GGCGGTGTAGTTTACGCTACAGGAACTATAACTATCGAGAAACTATAACACAGCCCTGGGATAGTTTCC  660

Qy  746   TTTTCTGACAATACTTCTTCGGATTCTGGAGCTGCAATTTTTACAGAAGCCTCGGTGACT  805
               ||| ||||||| || || |||| | || ||||| |||||||| ||||  |||| | |||
Db  661   TTCTTCAAAACCTAGGCGAAAGGATCTGGGGTGCTCTGTACAGCACTGACACAACTGTTCG  720

Qy  806   ATTTCTAATAATGCTAAAGTTTCCTTTATTGACAATAAGGTCACAGGAGCGAGCTCCTCA   865
               || || ||||  | ||  | ||||||| ||||| ||||| |||||| ||||| |||
Db  721   ATTAACAGATAACTTTCAAGTGATCTTTTGACGGCAATAGTGCTTGCTGGGAAGAAAAGTAATCTCCC  780

Qy  866   ACAACGGGGATATGTCAGGAGGTCTATCTGTGCTATAAAACTAGTAGATACTAAG  925
               |||| || |||||||  ||| || ||||| || | |||||  |||||| |||
Db  781   CAGGGCGGGGCTAT--------------------TTGTTGCACTACGACAGATAAAACA  819

Qy  926   GTCACCCTACTGGAAATCAGATGTTACTCTTCAGCACAACATCGACACAGCGGGGA    985
               ||||| ||  | |||| |||||||||| || ||||||||||||| |||| || |||
Db  820   GTGACTCTTACTGGGAACACAAAAAAACCTCTCTTTCACAACATATACGCATTCTATATGGC  879

Qy  986   GGAGCTATCATGTGAAAAAGCTCGAACTGCTTCCGGAGACTTACCCTATTCAGTAGA  1045
               |||||| | | ||||| ||| |||| |||  |||||| || |||| || ||||| |
Db  880   GGAGCCATCTCTGGGACTCAGTGGTTCCGCCCATGGTTTCCGGCCATATCAGCGGGGTTATGCACT  939

Qy  1046  AATAGTGTCAATGGAGGTACAGCTC----CTAAAGGTGGAGCCCATAGCTATCGGAAGATAGT  1102
               |||| | || |||| ||||| |||||    |||| || || ||| ||||| || || |
Db  940   AGGGATCCACACGCACACTCCTCCGCCGGTCAAT---CGCTCAAAAGTCACA  999

Qy  1103  GGGGAATTGAGTTTATCCGCCGATAGTTGGTGACATTGTCTTTTAGGGAATAACAGTTCACT  1162
               ||||||||| || || || || || || ||| |||| | || |||||||||| ||| |||
Db  1000  GGGGAACTCGCTGCTCTCTGCTGCTGTCTCGGGCCAATCTCCAGATAACAACCAAGTCACC  1059

Qy  1163  TCTACTACTCCTGGGACGAATATGAAGAGTAGTATCGACTTAGGAACGAGTGCAAAGATGACA  1222
               ||||| || |||| ||| || | |||||||||| ||||  ||||| |||| ||| |||||
Db  1060  AACGGAAGCACAAGTACAAGGAAACGCAATAATCATTGATAC---CGCTAAAGTCACA  1116

Qy  1223  GCTTTGCGTTCGTCGCTGCTGCTGTAGCCGATAGTTGGTGTGCTGTAGCCGATCTCACTACTACTTCTATTATTCTCTT-TAACTACAGGATC  1281
               ||||| | ||| || || || || || ||| || || ||||| |||| || || ||||
Db  1117  TCGGATACGGACTGCTTACGCGGGGCCAATCTATCATTCTATGATCCCATTCACAAATCCAGG  1176

Qy  1282  ATCCACAAACAGTTACAGATGTCTTAAAGTTAATGAGACTCCGGCAGATTCTGCACTACA  1341
               || || ||||| | ||||||| | ||| |||||| |||| ||||| |||||||||| ||
Db  1177  AACCCAGCAGCTTCTTACCGACACATTGACACAGTGAAGATGCGGAAGATGAGATCGA  1236
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Db    486 AGCAGAAGGTGGGCTATCCAGTGTAAAGGAAGCAGTGATGCTGAATTAAAAATAGAAAA 545
             |||||     |||  |||||||        ||  |||||     |||||  ||
Qy    940 AAATCAGATGTACTCTTCAGCAACAATACATCGACACAGCGGAGGAGCTATCTATGT 999

Db    546 TAATCAGAATCTGGTTTCTCAGAAAACTCCTCCACTTCAAAAGGCGGGGCTATTTATGC 605
             |||||    |||||||  |||||   ||||  |||||  |  ||||||
Qy    606 TATTTCCGTTCCGTAACTTCTGAAAAGAGTCGAACCTTTTGTCAAAGTACAGTATATCTA 665

Qy   1000 GAAAAAGCTCGAACGGCTTCCGGAGGACTTACCCTATTCAGTAGAAAGTGTCAATGG 1059
             |||||    ||||    ||||  ||||||||||  |  ||||||
Db    606 TGATAAACTCACCATTGTCTCAGGTGGGCCTACATTATTTCTAACAACTCGTATCCAA 665

Qy   1060 AGGTACAGCTCCTAAAGGTGGAGCCATAGCTATCGAAGAT---AGTGGGGAATTGAGTTT 1116
             |||| |||    |||||     |||  |||  ||||   ||||||     |||
Db    666 CGGTTCATCCCCTAAAGGCGGGCTATTAGCATAAAGATTCAAGTGGTGGTGAATGTAGCCT 725

Qy   1117 ATCCGCGATAGTGTGACATTGTCTTTTAGGAATACAGTCACTTCTACTACTCCTGG 1176
             |||| ||     ||||| ||| ||| ||||       |||||
Db    726 AACCCGTGATCTCGGAGATATTACCTTCGATGGGGAACAAAATCATCAAAACTAGTGGTGG 785

Qy   1177 GACGAATAGAGTAGTAGTGATGTGACTTAGGAACG------AGTGCAAAGATGACAGCTTGCG 1230
             ||||           |||  ||||        |       || | |||   || || ||||
Db    786 AAGTTCTACAGTAACAAGAAATTCCATAGATCTCGGCACAGGGAAATTTACAAAGCTACG 845

Qy   1231 TTCTGCTGCTGGTAGAGCCATCTCATTGTATCCTCATGATGCCTATTACAGGATCATCCACAAC 1290
             |||  |||  |  |||||  ||||||   |||||   |||   ||||  ||||
Db    846 TGCTAAAGACGGCTTCGGAATTTTCTTCTTCATGAGCCTATTACTGGGGAGGATCTGATGA 905

Qy   1291 AGTTACAGATGTCTTAAAGTTAATGAGACTCCGGCAGATTCTCGACTACAATATACAGG 1350
             ||||       | |||   ||||        |||||           ||||||  |||
Db    906 ACTAAACATTAATAACAAAAGAAACTG--------------TTGATTATACAGG 944

Qy   1351 GAACATCATCTTCACAGAGAGAAAAGTTATCAGACAGAGAGCGCCGCAGAATCCTAAAAATCT 1410
             |||||||    |||  |||| ||||    |||||||||||||||  ||||  |||
Db    945 AAAGATCGTCTTCTCAGGTGAAAAATATCCGATGAAGAAAAGCACGACGCGAAAACCT 1004

Qy   1411 TACTTCGAAGCTACTACAGCCTGTAACTCTTTCAGGAGTACTCATCTTTAAAACATGG 1470
             |||||| ||||||||||||||    ||||  |||||||||||
Db   1005 AGCTTCTACTTTCAACCAACCATCACATTATCAGGATCTTCTTGTACTTAAAGATGG 1064

Qy   1471 AGTGACTCTCGAGATCTCAGGCATCAGGCTCAACGAGCAGTTCTCGTTCGAAATGGACGT 1530
             |||| ||||||||||     ||||||||| ||||  ||||||  ||||||  ||| |||
Db   1065 TGTATCTGTAACCGCAAAACAAGTAACGCAGGAAGCGGGATCTACCGTTGTCATGGATCT 1124

Qy   1531 AGGAACTACTCTAGAACCTGCT----------GATACTAGCACCATAAACAATTTGGT 1578
             |||| ||||||   |||| |||          |||  || ||||  |||| ||||
Db   1125 AGGGACCACATTACGACGCCTTCTTCAGGTGGAGAAAACCATCACCCTAACTAATCTAGA 1184

Qy   1579 CATTAACATCAGTTCTATAGACGTGCAAAGAAGGCAAAAATAGAAA------CCAAAGC 1632
             |||||||||||||  |||  |||        |||| |||  ||||      ||||||
Db   1185 TATTAACATCGCCTCGTTGGGGGGGGGGGGGGGTACCTCCTCTAAACTCGCAACAA 1244

Qy   1633 TACGTTCAAAAAATCTGACTTTATCTGGAACCATCACTACTTATTGGACACCGGACGGGCACGTT 1692
             |||| |||||  |||| ||||   || ||||   ||||| ||| ||| |||
Db   1245 TACAGCAAGTCAAGCTATAACTATTAAGCTGTCAATCTGGTAATCAGTTCAAT 1304

Qy   1693 TTATGAAAATCATAGTTTAAGAAAATCCTCAGCTTAAGGCTGA 1752
             ||||   |||  ||||  ||||| ||||||  ||||||||||
Db   1305 TTATGAAGATCCTATTCTTGCTACGTCTAAACCTTTCACAGCAATAGTAGCTACAAACTAA 1364

Qy   1753 TGGAACTGTAACAAGCACCGCAGTGACTCCAGATCCTCAGAATGGGTGAGAAATTCCATTA 1812
             ||||  ||||    |||||||||    |||| |  ||||| ||| |||||||||
Db   1365 CGCTAGTACAGTCACACAGCCTACAGATAATCTAACAAATTATGTCCCTCCTACTCCATTA 1424

Qy   1813 CGGCTATCAGGAACTTGGGGCCCAATTGTTTGGGGGGACAGGGGGCTTCTACGACTGCAAC 1872
             ||||           |||||||   ||||||||||||||||  |||| ||||
Db   1425 CGGTTACCAAGGAAATTGGACAGTAACCTTGGGACACCGAAAACAGTACAAAAACAGCCAC 1484

Qy   1873 CTTCAACTGACTACTTTATTGACAATAAGGTCACAGGAGGCGAGCTCCTCAACAACGGGGGGATAT 1932
             ||||     |||   | | |||||     ||||| ||||||  ||||  ||||||
Db   1485 TCTAACTTGGGAACAAAACTGGCTACTCCCCTAACCAGAACGTCAAGGACGTTTAGTCCC 1544

Qy   1933 TAATAGCTTATGGAATGCATTTATAGAAGTCTTCTCCATTATCTTATGGAGACTGC 1992
             |||| | |||||  || ||| | | || ||||||||
Db   1545 GAATACTCTTGGGGTGCATTCTCTGACCTCAGAGTACACAGATACTAATGGATAATTAG 1604
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Db   2316 CAAGGGTTCTTGGAGAAACGATGCCTTCTGTCGCAGATCTTGGAGCTAGCCTGCCTTTGT 2375
             |||||      |||  |||    ||||||||  |||||||
Qy   2452 CTTAGATGAAAGTGCTCTATTTGAGCAGTACATGCCCTTCATGAAATTGCAGTTTGTCTA 2511

Db   2376 TATTTCCGTTCCGTAACTTCTGAAAAGAGTCGAACCTTTTGTCAAAGTACAGTATATCTA 2435

Qy   2512 TGCACATCAGGAAGTTTTAAAGAAACAGGGAACAGGGAAGCTCGTGAAGTCGGAAGTAGCCG 2571
             |||   ||||   |||||        |||    |||    ||||||
Db   2436 TGCGGCATCAGCAAGACTTCACGAGCGGCGTCATGCTGAAGGACGCGCGTTCAATAAAGCGA 2495

Qy   2572 TCTTGTGAATCTTGCCTTACCTATCGGGATCCGATTTGATAAGGAATCAGACTGCCAAGA 2631
             ||       ||||||      || ||| |||  ||||||  |||||  ||||||
Db   2496 GCTTATCAACGTAGAGATTCCTATAGGCGTCACCTGGAGAGACTCAAAATCAGAAAA 2555

Qy   2632 TGCAACGTACAAATCTAACTCTTGGTTATACTGTGGAAAAACCTTCGGTACGAATTTGGCAAG 2691
             ||||   ||||   ||| ||||||  ||||         |||||||
Db   2556 GGGAACTTACGATCTTACTCTTATGTATATACTACTGGATGGCCTATGCGGCAATCCTAAATG 2615

Qy   2692 TACGACAACACTGCGAATTAGCGGTGAATTCTTGGAAAAACCTTCGGTACGAATTGGCAAG 2751
             ||  ||      |||||||||||   |||||  |||   ||||||||
Db   2616 TCAAACTTCCCTAATAGCTAGCTGGATGCTAATACTGTTATATACTACTGGATGCCTATGCC 2675

Qy   2752 ACAAGCTTTAGTCCTTCGTGTGCAGGGAACCATTTTGCTTTAACTCAAATTTTGAAGCCTT 2811
             ||||    |||  |  |||||  |||||  |||||  |||||  |||||||
Db   2676 ACAAGGTTTTCTGTTCGTGCTGCGCGAACCATTTCCAAGTGAACCCCCACATGGAAATCTT 2735

Qy   2812 TAGCCAATTTCTTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTAGACTTAGGAGC 2871
             |||    ||| ||||||  |  |||||  | ||||||||
Db   2736 CGGTCAATTCGCTTTGAGTCACGAAGTTCTTCACGAAGAAGTTATAATACAAACCTAGGCTC 2795

Qy   2872 AAAAT 2876
             |||||
Db   2796 TAAGT 2800
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RESULT 8
US-09-738-269-22
; Sequence 22, Application US/09738269
; Publication No. US20030185848A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEMKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
; TITLE OF INVENTION: NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
; TITLE OF INVENTION: CHLAMYDIA PSITTACI
; FILE REFERENCE: UTSD:659
; CURRENT APPLICATION NUMBER: US/09/738,269
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 2520
;   TYPE: DNA
;   ORGANISM: Chlamydia psittaci
US-09-738-269-22

  Query Match   11.6%;   Score 348.4;   DB 13;   Length 2520;
  Best Local Similarity 50.6%;   Pred. No. 2.1e-86;
  Matches 1101;   Conservative   0;   Mismatches 1006;   Indels 69;   Gaps   8;

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Qy    760 TTCTTCGGATTCTGAGCTGCCAATTTTACAGAAGCTTCGGTGACTATTTCTAATAAATGC 819
             ||||    |||||||  |||       | |||||||||||
Db    366 TTCTTTTATTTTCATGCTCATTGTCCTCCAGGCACAACTGGTTACGGAGCTATACAGAC 425

Qy    820 TAAAGTTTCCTTTATTGACAATAAGGTCACAGGAGGCGAGCTCCTCAACAACGGGGGATAT 879
             ||||||   |||  |||||| |||||||  ||||||   ||||  ||||| |
Db    426 TAAAGGCAACAACTTAAAAGATAACTCTAGTCTTGCTTGTCTTTCCATAAAAACTGCTCAAC 485

Qy    880 GTCAGGAGGTGCTATCTGTGCTTATAAAAACTAGTACAGATACTAAGGTCACCCTCACTGG 939
             ||  |||||
Db    880 GAATACTCTTGTGGGTGCATTCTCTGACCTCAGAGTACACAGATACTAATGGATAATTAG 939
```

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;     APPLICANT:  SYKES, KATHRYN F.
;     APPLICANT:  KALTENBOECK, BERNHARD
;     TITLE OF INVENTION:  METHODS AND compositions for Vaccination COMPRISING NUCLEIC ACI
;     TITLE OF INVENTION:  AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
;     FILE REFERENCE: UTSD:736US
;     CURRENT APPLICATION NUMBER: US/10/023,437
;     CURRENT FILING DATE: 2001-12-17
;     PRIOR APPLICATION NUMBER: 60/225,839
;     PRIOR FILING DATE: 2000-12-15
;     NUMBER OF SEQ ID NOS: 69
;     SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
;     LENGTH: 2520
;     TYPE: DNA
;     ORGANISM: Chlamydia psittaci
US-10-023-437-22

Query Match             11.6%;     Score 348.4;  DB 14;     Length 2520;
Best Local Similarity   50.6%;     Pred. No. 2.1e-86;
Matches 1101; Conservative    0; Mismatches 1006;  Indels     69;  Gaps      8;
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Qy   760 TTCTTCGGATTCTGGAGCTGCAATTTTACAGAAGCCTCGGTGACTATTTCTAATAATGC 819
           |||||| |||| || ||| ||||||||
Db   366 TTCTTTATTTCATGTGCTTATTGTCCTCCAGGCACAACTGGTTACGGAGCTATACAGAC 425

Qy   820 TAAAGTTTCCTTTATTGACAATAGGTCACAGGAGCGAGCTCCTCAACAACGGGGGATAT 879
                    | | | || |||| |||||
Db   426 TAAAGGCAACACAACTTAAAGATAACTCTAGTCTTGTTCTTCCATAAAACTGCTCAAC   485

Qy   880 GTCAGGAGGTGTCATCTGTGCTTATAAAACTAGTACAGATACTAAGGTCACCCTCACTGG 939
                       |||||||| | ||| |||
Db   486 AGCAGAAGGTGGGGCTATCCAGTGTAAAGGAAGCAGTGATGCTGAATTAAAAATAGAAAA 545

Qy   940 AAATCAGATGTTACTCTTCAGCACAATAACATCGACAGCGGGAGGAGCTATCTATGT 999
                     | || | |||||| |
Db   546 TAATCAGAATCTGGTTTTCTCAGAAAACTCCTCCACTTCAAAAGGCGGGGCATTTATGC 605

Qy   1000 GAAAAAGCTCGAACTGGCTTCCCGGAGACTTACCCTATTCAGTAGAAATAGTGTCAATGG 1059
           ||| || || | ||||| ||||| | | ||
Db   606 TGATAAACTCACCATTGTCCAGGTGGGCCCTACATTATTTCTAACAACTCTGTATCCAA 665

Qy   1060 AGTACAGCTCCTAAAGGTGGAGCCATAGCTATCGAAGAT--AGTGGGGAATTGAGTTT 1116
               | |||||||| | |||| ||| |||| ||| ||| |||||
Db   666 CCGGTTCATCCCCTAAAGGCGGAGCTATTAGCATATAAAGAATTCAAGTGGTGAATGTAGGCTT 725

Qy   1117 ATCCGCCGATAGTGGTGACATTGTCTTTTAGGGAATACAGTCACTTCTACTACTCCTGG 1176
           | | | | | ||||||| || ||
Db   726 AACCGCTGATCTCGGAGATATTACCTTCGATGGGAACAAAATCATCAAAACTAGTGGTGG 785

Qy   1177 GACGAATAGAAGTAGTATCGACTTAGGAACG------AGTGCAAAGATGACAGCTTTGCG 1230
           || ||| | || || || || || || |||| |
Db   786 AAGTTCTACAGTAACAGAGAAAATTCCATAGATCTCGGCACAGAGAAATTTACAAAGCTACG 845

Qy   1231 TTCTGCTGCTGGTGTAGAGCCATCTTTAACTCAAATTTGAAGCCTT 1290
           || | ||| || || |||| | | | | || |||| ||
Db   846 TGCTAAAGACGGCTTCGGAATTTTCTCTTTAAGTCACACAATAGAAATCTT 905

Qy   1291 AGTTACAGATGTCTTAAAGTTAATGAACTTCGACTTAGGAGC--------TTGATTATACAGG 1350
           || | || | |||| | | ||| || || ||| ||| ||| ||||
Db   906 ACTAAACATTAATAAAAAAGAAACTG----------TTGATTATACAGG 944

Qy   1351 GAACATCATCTTCAGCAGAGAAAAGTTATCAGACAGAGAGGCCGCAGATTCTAAAAATCT 1410
           || | |||| | ||| || | ||| | ||||||||||| |||||||| ||||| |
Db   945 AAAGATCGTCTTCTCAGGTGGAAAAATTATCCGATGAAGAAAAAGCACGAGCGGAAAACCT 1004

Qy   1411 TACTTCGAAGCTACTACAGCCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAACATGG 1470
           ||||||||||| | ||||| || | | ||| |||||| || | |||||||| ||||
Db   1005 AGCTTCACTTTCAACCACCATCACATTATCAGCAGGATCTTGTACTTAAAGATGG 1064

Qy   1471 AGTAGCCTGCAGATCTCAGGCATTCACTCAACAGGCGGTACCGGAAGCGGGATCTGTCTGGAACGT 1530
           || || ||| || ||| ||||||||| ||||| |||||| || | || || || ||
Db   1065 TGTATCTGTAACCGCAAAACAAGTAACGCAGGAAGCGGGATCTACCGTTGTCATGGATCT 1124

Qy   1993 AAACGAAGGGTGCAGGGAGACCGTGCTTTTTGGTGTGCTGGATTATCTAACTTCTTCCA 2052
           ||| | || |||
Db   1605 CGTCAATGGCGCTGACTACCATAGAGGTTTTTGGGTTTTGGTCGTAACTCTTACA 1664

Qy   2053 TAAGGATAGTAGTACAAAAAAACAGACGCGGGTTCGCCATTTGAGTGGCCGTTATGTCATAGG 2112
                                      || ||||||| ||
Db   1665 CAAAAGTGGCTCGATACTAAACGCAAGTTCCGTCACAATAGCGCCGGATACGGCTTTAGG 1724

Qy   2113 AGGAAACCTACATACTTGTTCAGATAGATTCTTAGTGCTGCAGTCTTCTTGG 2172
           ||||| | | || | | |||
Db   1725 CGTCTACAGGCAAAAAACCTCCTCTGATGATATTTTCAGTGCGGCTTTCTGCCAACTCTTCGG 1784

Qy   2173 AAGAGATAGAGACTACTTTGTAGCTAAGAATCAAGGTACAGTCTACGGAGGAACTCTCTA 2232
           ||| | | | | ||| ||
Db   1785 AAAGGACAAAGACTATTTAGTCGCAAAAACACGCCAACATTTACGCAGGTTCTCTCTA 1844

Qy   2233 TTACCAGCACACAGCGAAACCTATATCTCCTTCCTTGCAAACTACGGCCTTGTTCGTTGTC 2292
           |||||||
Db   1845 TTATCAGCATATCTCCTATTGGAGCGCTTGGCAGAGTCTGCAGAATCTGCTACAAAACACTTCGGTGC 1904

Qy   2293 TTATGTTCCTACAGAGATTCCTGTTCTCTTTTCAGGAAAACCTTAGCTACACCCATACGGA 2352
                     | | || || | || | |
Db   1905 AGAAGCTTCCGTTAGTCCTTAAGCGCACAGTTAACTTATTGTCAATGCTTCAAAGACATGAA 1964

Qy   2353 TAACGATCTGAAAACCAAGTAT----------ACAACATATCCTACTGTTAAAGGAAG 2400
                       | || || ||||| |||
Db   1965 AACCAACATGACGACTACTTACGCTCCTCGTGTAAAATCAGAAATCAAGGGTGA 2024

Qy   2401 CTGGGGAATGATAGTTCGCTTTAGAATTCGGTGGAAGAGCTCCGATTTGCTTAGATGA 2460
           | | | |||||
Db   2025 TTGGGGTAACGATTGTTTCGGAGCTTGGTGCAACTGTGCAACTGTGCATACGGACCACCA 2084

Qy   2461 AAGTGCTCTATTTGAGCAGTACATGCCCTTCATGAAATTGTCTATGCACATCA 2520
                     | ||| | |
Db   2085 TTCTCCTATTCGATATGTACTTTCAACTTCCTGAAGTTTCAACTGTGCATACGACGCACCA 2144

Qy   2521 GGAAGGTTTAAAGAACAGCAGGAACAGAA--GCTCGTGAATTGGAAGTACTTCGAAGACAGCAATCTCAC 2577
                         ||| || | || | | | | || |||
Db   2145 AGATGACTTTAAGGAAAAACAATAGCGATCAGGGAAGAGAAACTTCTGAAAGACAGCAATCTCAC 2204

Qy   2578 GAATCTTGCCTTACCTACTCGGAATCCGATTTGATAAAGGAATCAGACTGCCAAGATGCAAC 2637
           ||| || || | | | || ||||| | | | |||
Db   2205 CAACCTTTCTCTGCCTATCGGCATCGGCATCCATGAGCATCAAGTTTGCTAACAACGATACAGCTTC 2264

Qy   2638 GTACAATCTAACTCTTGGTTATACTGTGGATCTGTTCGTAGTAACCCCGACGTGTACGAC 2697
                     ||| ||| || | ||| | ||
Db   2265 TTATCATGTCACTGCTGCTTATTCTCCTGATATCGTAAGGAGTAACCCCTGACTGTACTAC 2324

Qy   2698 AACACTGCGAATTAGCGGGTGATTCT------TGGAAAACCTTCGGTACGAATTTGGCCAAG 2751
           ||| || || ||| |||| |||| || | |||||||
Db   2325 TTCTCTGTTAGTGATGTAAGCCCGACTCGTCGTGTCGGGTAACGGAAGCCAACAACCTTGCGCG 2384

Qy   2752 ACAAGCTTAGTGCTTCGTCGTGCGAGGGAACCCATTTTGCTTTAACTCAAATTTTGAAGCCTT 2811
           | |||| || || | || || ||
Db   2385 AAGCGGCCTTCATGCTACAAAGCGAGACTACTTGTCTTTAAGTGTCTTTAAGTCACACAATAGAATCTT 2444

Qy   2812 TAGCCAATTTTCTTTTGAATTGCGTGGGTCATCTCGCAATTACAACTTACTAGGAGC 2871
           |||||||| | ||||| | |||||
Db   2445 CAGCCAGTTCGGTTCGAGTTCGGAGCTCAGGGGGATCTTCCACGAACCTTATAACTTACTATAGGATC 2504

Qy   2872 AAAATACCAATTCTAA 2887
           |||| | || || |
Db   2505 GAAGATCAGTTCTAA 2520

RESULT 9
US-10-023-437-22
;   Sequence 22, Application US/10023437
;   Publication No. US20020183272A1
;   GENERAL INFORMATION:
;   APPLICANT: JOHNSTON, STEPHEN A.
;   APPLICANT: STEMKE-HALE, KATHERINE

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Qy  2205 CAACCTTCTCTGCCTATCGCCATCAAGTTGAGAGATTTGCTAACAACGATACAGCTTC 2264
              |||||  |||| ||||| |||||||  |||||  || || |||| |||||||  |||
Db  2638 GTACAATCTAACTCTTGGTTATACTGCTGGATCTTGTCTGAGTAGTAACCCGACTGTACGAC 2697

Qy  2265 TTATCATGTCACTGCTGCTTATTCTCCTGATATCGTAAGAAGTAACCCTGACTGTACTAC 2324
              ||| |||    |||  ||||          ||||||||||||
Db  2698 AACACTGCGAATTAGCGGTGATTCT------TGGAAAAACCTTCGGTACGAATTGGCAAG 2751

Qy  2325 TTCTCTGTTAGTAGTAAGCCCGACCTCGCTGCTGTCTGGGTAACGAAAGCCAACAACCTGCGGCG 2384
              || |||||||  ||||||| ||||||  ||   ||||||||||
Db  2752 ACAAGCTTTAGTCCTTCGTGCAGGGAACCATTTTGCTTTAACTCAAATTTGAAGCCTT 2811

Qy  2385 AAGGCCTTCATGCTACAAGCAGGAGAAACTACTTGTCTTTAAGTCACACATAGAAATCTT 2444
              || |||||||||||||| ||||||||||| ||||| |||||||||||||
Db  2812 TAGCCAATTTCTTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTAGACTTAGGAGC 2871

Qy  2445 CAGCCAGTTCGGTTTCGAGCTCAGGGGATCTTCACGAACCTATAACGTAGAATCTCGGATC 2504
              |||||||| |||||  ||||||||||||||||
Db  2872 AAAATACCAATTCTAA 2887

Qy  2505 GAAGATCCAGTTCTAA 2520
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Db  2520
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RESULT 10
US-09-886-468-6
; Sequence 6, Application US/09886468
; Patent No. US2002003 7293A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pasteur Limited
; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses the
; FILE REFERENCE: 77813-5
; CURRENT APPLICATION NUMBER: US/09/886,468
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,280
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,281
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,282
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,283
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,284
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,285
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,385
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114,050
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,056
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,057
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,058
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,059
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,061
; PRIOR FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 6
; LENGTH: 2950
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(2866)
US-09-886-468-6

Query Match   9.1%;   Score 271.8; DB 9; Length 2950;
Best Local Similarity   48.0%;   Pred. No. 7.5e-65;

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Qy  1531 AGGAACTACTCTGAACCTGCT-----------GATACTAGCACCATAAACAATTGGT 1578
              ||  || ||||||||||||                |||  ||||||| ||||||||
Db  1125 AGGGACCACCATTACAGACGCGCCTTCTTCTTCAGGTGGAGAAACCATCACCCTAACTAATCTAGA 1184

Qy  1579 CATTAACATCAGTTCTATAGACGGTGCAAAGAAGGCAAAAATAGAAA------CCAAAGC 1632
              ||    ||||||||||||                    ||| ||   ||||||
Db  1185 TATTAACATCGCCTCCGTCGTTGGGGGGGGGGGGTACCTCCTCCTGCTAAACTCGCAACAA 1244

Qy  1633 TACGTCAAAAAATCGACTTTATCTGGAACCATCACTTATTGGACCCGACGCGGGCACGTT 1692
              ||||||| ||||   ||| ||||||| |||||||||||||
Db  1245 TACAGCAAGTCAAGCTATAACTATTAACCGTCAATCTAGTCGATGCTCGATGGCAATGC 1304

Qy  1693 TTATGAAAATCATAGTTAAGAAATCCTCAGTCGTCGACATCTTAGAGCTCAAAGCTTC 1752
              |||| || ||||| |||||||||||||| |||||| |||||||||||||||||||||
Db  1305 TTATGAAGATACTTCTTGCTACGTCTAAACCTTTCACAGCAATAGTAGCTACAACTAA 1364

Qy  1753 TGGAACTGTAACAGCACCGCAGTCCAGATCCTATAATGGGTGAGAAATTCCATTA 1812
              |||| |||| |||| ||||| |||||||||||||  |||||||||||||||||||
Db  1365 CGCTAGTAGCAGTCACACAGCCTACAGATATAATCTTAACACAAATTATGTCCCCTCTACTCATTA 1424

Qy  1813 CGGCTATCAGGGAACTGGGGCCCAATTGTTGGGGGACCAGGGGCTTCTACGACTGCAAC 1872
              ||||||||| ||||||| |||   |||||||||||| ||||| |||||||||||| |||
Db  1425 CGGTTACCAAGGAAATTGGACAGTAACTTGGGACACCGAAACAGCTACAAAAACAGCCAC 1484

Qy  1873 CTTCAACTGGACTAAAACTGGCTATATTCCTAATCCCGAGCGTATGGCTCTTTAGTCCC 1932
              |||||||| |||| || |||| |||||| |||||   ||| ||| ||||||||||||||
Db  1485 TCTAACTTGGGAACAAACTGGCTACTCCCCTAACCCAGAAACGTCAAGGACCTTTAGTCCC 1544

Qy  1933 TAATAGCTTATGGAATGCATTATAGATATTAGCTCTCCATTATCTTATGGAGACTGC 1992
              |||| ||  |||||  |||| |||  ||||| ||| |||||||||   ||||| |||
Db  1545 GAATACTCTTTGGGGTGCATTCTCTGACCTCGAGCTATACAAAACTTAATGGATATTAG 1604

Qy  1993 AAACGAAAGGGTTGCAGGGAGACCGTGCTTTTGGTGTCTGATTATTCTAACTTCTTCCA 2052
              |||||| ||||| || ||  ||||||| ||  ||||| ||| |||| ||||||||||
Db  1605 CGTCAATGGCGCTGACTACCATAGAGGTTTTTGGGTATCCGGTCTAGCTAACTTCTTACA 1664

Qy  2053 TAAGGATAGTACAAAAACGACGGGGTTCGCCATTGAGTGCGGTTATGTCATAGG 2112
              |||| ||| |||| || ||| |||||||| ||||||| ||||| |||| ||||
Db  1665 CAAAAGTGCTCTGATACTAAACGCAAGTTCCGTCACAATAGCGCCGGATACGTTTAGG 1724

Qy  2113 AGGAAAACTACATACTTGTTCAGATAAGATTCTTAGTGCTGCATTTTGTCAGCTCTTTGG 2172
              |||||| |||| ||||||| |||| |||| || ||||||||| |||| |||| |||  |
Db  1725 CGTCTCACGCAAAAAACTCCTTCTGATGAGATATTTCCAGTGCGGCGTTTTCTGCCAACTTCTCGG 1784

Qy  2173 AAGAGATAGAGACTACTTTGTAGTCTAAGAATCAAGTACAGTCTACGGAGGAACTCTCTA 2232
              ||||||| |||||||| |||| |||| ||| ||||  ||| ||||||||| |||| ||
Db  1785 AAAGGACAAAGACTATTTAGTGTCGAAAAACACGCCAACATTTACGCAGGTTCTCTCTA 1844

Qy  2233 TTACCAGCACAACGAAACCTATATCTCCTTGCAAACTACGGCCTTGTCTGTTGTGTTGTC 2292
              ||||| ||  ||||||| ||||||||||| ||| ||| |||||  |||||| ||||||
Db  1845 TTATCAGCATATCTCCTATTGGAGCGCTTGGCAGAATCTGCTACAAAAACACTATGCGGTGC 1904

Qy  2293 TTATGTTCCTACAGAGATTCCTGTTCTCTTTTCAGGAAAACCTTAGTCTACACCCATACCGA 2352
              |||| || ||||||||| |||| |||| |||||| ||||  ||||||   ||||| ||||
Db  1905 AGAAGCTTCGGTAGTCCTTAGTTAACGCACCAGTTAACTTATTGTCATGCTTCAAACGACATGAA 1964

Qy  2353 TAACGATCTGAAAACCAAGTAT-----------ACAACATATCTCACTCTGTTAAAGGAAG 2400
              |||| |||| ||||||||  ||             ||||||| || |||| |||||||||
Db  1965 AACCAACATGACGACTACTTACGCTCCTGTGTAAAACAACCTATGCAGAAATCAAGGGTGA 2024

Qy  2401 CTGGGGGAATGATAGTTTTCGCTTTAGAATTCGGTGGAGAGCTTCCGATTTGCTTAGATGA 2460
              || |||||| ||||||| ||| |||||||||||||| ||| |||| |||||||||| |
Db  2025 TTGGGGTAACAGTTGTTTTCGGAGTCGAAGCTTGGTGCAACTGGCCTATCCAAACAGAATC 2084

Qy  2461 AAGTGCTCTATTTGAGCAGTACATGCCCTTCATGGAAATTGCAGTTGTCTATGCACATCA 2520
              ||||| ||| ||| ||| ||| |||  || ||||||   | ||||  ||||  |||||||
Db  2085 TTCTCCTATTCGATATGTACTACCCTTCCTGCACTTCAACTTGTGCATACGCACCA 2144

Qy  2521 GGAAGGTTTTAAAGAACAGGGAACAGAA--GCTCGTGAATTGGAAGTAGCCGTCTTGT 2577
              || |||||||||||||  ||||| || |  |||||| ||||||||||||| ||||| |
Db  2145 AGATGACTTTAAGGAAAAACATAGCCATCAGGGAAGCATCAGGAACATACTTCGAAAGCAGCAATCCAC 2204

Qy  2578 GAATCTTGCCTACCTATCGGATCCGATTTGATAAGGAATCAGAATCAGACTGCCAAGATGCAAC 2637
              |||||| ||||||| || ||||| |||| ||| ||||||| ||| |||||||||||||||||||
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Matches 1351; Conservative 0; Mismatches 1362; Indels 102; Gaps 16;

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Qy   122  TTTGTATTTTCTACATTGCTATTTCCCTTTGTCTATGATGATTGCTACCGAGACAGTTTTG  181
               |||   || |||| |  ||  ||||| |      |  ||| |||||  ||  |||
Db   134  TTTTCTTTTATAATTGCTCTCAGTCTTCGACACTTCTTTGAGTGCTACTACGATTTCTTTA  193

Qy   182  GATTCAAGTGCGAGTTTCGATGGGAATAAAAATGGTAATTTTCAGTTCGTGAGAGTCAG   241
          |  ||| |||    || |||   ||  |||| ||  |||     |  ||||  ||  |
Db   194  ACCCCAGAAGATAGTTTTTCATGG-----AGATAGTCAGAATGCAGAACGTTCTTATAAT  247

Qy   242  GAAGATGCTGGAACTACCTATTAAGGGAAATGTCACTCTAGAAAATATTCCTGA       301
          |  ||||  ||      || ||  ||  |  | ||  ||||||||       |
Db   248  GTTCAAGCTGGGGATGTCTATAGCCTTACTGGTGATGTCTCAATAATCTAACGTCGAT--- 304

Qy   302  ACAGGCACAGCAATCACAAAAAGCTGTTTTAACAACTAAGGGCGATTTGACTTTCACA    361
          |||||   | ||    |  |||  || ||   | ||    |  ||  | ||| ||
Db   305  ---AACTCTGCATTAAAATAAAGCCTGCTTCAAAGTGGATGCAGCGAGCTGTGACTTTCCCA 361

Qy   362  GGTAACGGGAACTCTGTATTGTTCCAAACGGTGGATGCGAGGGACTGTA---GCAGGGGCT  418
          |||  || || || |||| || |||| | |  |     ||  || |||    |||| |||
Db   362  GGAAATCATCATGGGTTATATTTAATAATATTTCCTCAGGAACTACAAAGGAAGGAGGGGCT 421

Qy   419  GCTGTTAACAGCAGCGTGGTAGATAAAATCTTACCACGGTTTATAGGGTTTTCTTCGCTATCT  478
          | |||  | ||   |     |   ||  || |  | | |||| | || |||    | ||
Db   422  GTACTTTGTTGCCAAGATCCTCAAGCAACGGCCCACGCGCACGTTTTCTGGGTTCTCCGTCTCT 481

Qy   479  TTTATTGCGTCTTCCTGGAAGTTCGATAACTACCGGCCAAAGGAGCCGTTAGCTGCTCTACG  538
          |||||   | || |  ||||    |  | |  |  | |||||| |  |||   || | |  |
Db   482  TTTATTCAGAGCCCCGGAGATATTAAA------GAACAGGGATGTCTCTATTCAAAA       532

Qy   539  GGTAGCTTGAGTTTGACAAAAAAGTGTCAGTTGCTCTTGCACAAAACTTTTCAACGGAT    598
          || ||| ||||| ||  || |  ||     || || ||  ||||| |||| ||| |||
Db   533  AATGCACTTATGCTCTTAAACAATTATGTAGTGCGTTTGACAAAATACCAAAGTAAGACT  592

Qy   599  AATGGCCGTGCTATCACCCGCAAAAACTCTTTCATTAACAGGGAACTACAAGTCAGCTG   658
          || ||| | ||||     ||  |   | || |  || | ||| |  ||| | |||  ||
Db   593  AAAGGCCGAGCTATTGGGGCGAATGTTACTACTGGTGGGCAATTGTTACTACTAGGCCAACTACG 652

Qy   659  TTTTTCTGAAAATACCTCCTCAAAGAAAGGCCGGAGCCATTCAGACTTCCGATGCCCTTACC  718
          ||||        |  ||| ||||| || |||  ||| ||   || ||||  | | |  |||
Db   653  TTCTATCAGAATGCAGCC-----ACTTTTGGAGGTGCTATCACAATACTTCTTCG---GATTCTGGA 709

Qy   719  ATTACTCGGAAAACCAAGGGGAAGCTGTCTTTTTCTGACAATACTTCTTCG---GATTCTGGA 775
          ||| |   | |  |||| ||  ||    | || |   | |  ||    |      ||||||||
Db   710  ATTGCAGTAAATCAGGCAGGATAATCAGGGTTACACTTGTCACAAATAACTGGTTCTTCGGA  769

Qy   776  GCTGCAATTTTTACAGAAGCCTCGGTGCTATTTCATTAACAGGGACTACAAAGTTCCTTTATT  835
          || |||| |||||| |   ||| ||||| |  |  ||   || |  ||||  || ||| ||
Db   770  GGGGCTTTGCTTTTGTACTCCGATGGTGGTGATATTGATATTGATATTGATATTGATGTTCGA  829

Qy   836  GACAATAAGGTCACAGAGCCGAGCCGAGCTCTCAACAACGGGGGATATGTCAGGAGGTGCTATC  895
          ||| | || ||||| || |  | || |  |  | ||  | ||||  |||  ||| || | |||
Db   830  GAAAATGAGG---CATTGACTACTGCTGTAGGAAGGGCTGTCTGTGTGTCTCCC         886

Qy   896  TGTGCTTATAAAACTAGTACAGATACTCAAGGTCACCCCACTGGAAATCAGATGTTACTC   955
          | |   || |    || | | |  || | | | ||| | |  ||||  | || ||
Db   887  ACTTCAGGAAGTAGTACTCCAGTTCCTATTGTGACTTTCTCTGACAATAAACAGTTAGTC  946

Qy   956  TTCAGCAACAATACATCGACACAGAGTCCCGGTGAAAGCTCTATGTGAAAGTTCCTTTATT  1015
          || ||| || | ||| |||  | | ||  || | ||| || || ||||  | || || ||
Db   947  TTTGAAAGAAACCATTCCATAATGGGTCGCGGCCAGCCGAGCCAGCCATTTATGTTCTTAGGAGATC 1006

Qy  1016  GCTTCCCGGAGGACTTCACAGAGGCAGCTCCTCAACAACGGGGGATATGTCAGGAGGTGCTATC  1075
          || || ||||  || || | | |    ||| ||||| | || |   || | ||| |  |
Db  1007  TCTTCAGGAGGTTCACTCTACTTATCATATTTCATCATTATCAATATATGCAAAAATTTA  1066

Qy  1076  GGTGGAGCCATAGCTATCGAAGATAGTGGTAGTGGGAATTGGGGAATTGAGTGTTATCCGCCGGATAGT  1135
          || |||||| | | ||  | || | |  |   |  | | |||  | || | || | | | |||
Db  1067  GGTGGGAGCTATTGCCAATTGCCATTGTACTCTCCTGGGACATCTCCGGGAGCAGAAAGGAACA  1126

Qy  1136  ATTGTCTTTTTAGGGAATACAGTCACTTCTACTATCTCTGGGACGACTCCTCGTCTACTATCACTTACTCTCTTACGTATC 1195
          |||   |  ||  | ||| || |||  |       | |  ||   ||| |  |
Db  1127  ATTACAATTTCCAAGGAAA------------CCGGACGCGAGCTTACCGTTTCCGTTTTGAATGGCATC 1174
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Qy  1196  GACTTAGGAACGAGTGCAAAGATGACAGTTTGGCGTTCGTCGTGGTAGAGCCATCTAC   1255
           ||    |  || |  ||| |  ||| | | ||    ||   | || ||  ||| |
Db  1175  CATCTTTTACAAAGCTAAATTCCTGAAATTCACAGGCCGAAAATGGATACTCTTAAAGTTAAT 1234

Qy  1256  TTCTATGATCCCATAACTACAGGATCATCCACAACAGTTACAGATGTCTTAAAGTTAAT   1315
           || ||||| ||  |  || | |  ||  ||  |  |||||| | |  |  |||| ||
Db  1235  TTTTATGATCCTATTACTTCTGAGCAATGCAGAACGTTCTTATAAT               1294

Qy  1316  GAGACTCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAGGAGAAAAG  1375
          |  ||| | |  ||    ||    ||||  ||  |||  |  || ||| ||| |  |||
Db  1295  CCTAAAAATAAGAG--------TACACAGGGACCATATAAGAG                 1342

Qy  1376  TTATCAGACACAGAGCCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAGCCTGTA  1435
          |  ||||  || |  |   |  |||  |   |  ||| | ||||   | |  | |  | |
Db  1343  AGTCAGCAAACGATCCTAGGGGATTTTAAA------TCTACAAATCCCTCAGAGACTC    1393

Qy  1436  ACTCTTTCAGGAGTACTCTATCTTTAAAAAACATGGAGTGACTGCTCGCAGACTCAGGCAATC 1495
           |||| | || || |  ||| | |   ||||| | | |  ||  | |  | ||| ||||  ||
Db  1394  AACCTGTCTGCAGGATATTAGTAGTTTAAAAGAGGGGGGCCGAAGCGTCACTACTTCAAAATTC 1453

Qy  1496  ACTCAACAGGCAGATTCTCGTCCTGAAATGTCTCGAAATGGTCATTAACAATTGGTCATTAACAATTGGT 1552
          ||  ||||  ||| || |  | |||||||||   | || ||  ||    ||  || ||||| |
Db  1454  ACGCAGTCTCCAGATCGCATTTGGTTTAGATTTTAGGAATTAGGAACCAAACTGATAGCCTCTAAG 1513

Qy  1553  ---GATACTCAGCACCATAAACAATTGGTCATTAACATCATGTCATTAACATCTTATAGACGGTGCAAAG 1609
               |||| || |   |||| ||| |    ||  |  |  ||| | ||| || ||||  ||| |
Db  1514  GAAGACATTGCCATCACCAGGCCTCGCGATAGTAGAGTATATAGTAGTTAAGGTCATCCTCAACA 1573

Qy  1610  AAGGCAAAATAGAAACCAAAGGTACGTCAAAAAATCTTTATCTGGAACCATCACT  1669
          |||| ||||| | ||  |||| |  | |||||| | |  | |  ||||| | ||
Db  1574  GCACGTGTTATTAAGCAACAAACCGCAAATAAACAGATATCCGTGACGGACTCTATAGAA 1633

Qy  1670  TTATTGGACCCGACGGGCACGTTTTATGCAAATCCTTTAAGAAATCCTCAGTTCCTAC--- 1729
          |||| ||||  |  |||||||  | |   |||  || | ||||| |   ||| |   |
Db  1634  CTTATCTGCCTACTGGCCAATGCCATTTCGTCGGGATTAGATGAGATCTCAGAAGACGTTC 1693

Qy  1730  GACATCTTAGAGCTCAAAGTTCTGGAACTGTAACAAGCACCGGACTCCAGATCCT       1789
          ||||| ||| |    |||| | |   |||| || | ||||   || ||||| |
Db  1694  CCTCTGCTCTTT---AGAGCCTGGAGCGCCGGGGGTGAGCTAGGTAACTGTCTGGAGAT  1750

Qy  1790  ATAATGGGTGAGAAATTCCATTACGGCCATCAGGGAACTGGGGGCCCAATTGTTTGGGGG  1849
          || | |||||| |||| | |  |  | |   |    |||    || |||  |  ||| ||
Db  1751  TTCCTACCGTAGTCCCCATTATGTTTTCAGGCAATTGG---AAATTAGCTTGGACA    1807

Qy  1850  ACAGGGGCTTCAACTGGACTGCAACCTCAACTGGACTAAAACTGGACTATATTCCTAATCCC 1909
          || | |||| | | ||| | | || ||||| |||   ||| |   | ||| |  ||
Db  1808  GGAACTGAAACAAAGTTGGAGAATTCTTCTCGGGATAAAATAAATTATAAGCCTAGACCT  1867

Qy  1910  GAGGGTATCGGCTCTTTAGTCCCCTAATGAGGAGAATGCATTTATATAGATAAGATTTCT  1969
          || ||| | || | |||| |  || | || | || | |  ||||  | |  | || ||
Db  1868  GAAAAAGAAGGAGAAATTTAGTCCTTAATATGTGGGGGAATGCGTAGATGCTGTAGAGTCC 1927

Qy  1970  CTCCATTATCTTATGGAGACTGCAAACGACTGCAAAGCAGGGAGACCGGTGCTTTTTGGTGT  2029
          || ||| | |  | | ||| | || | | |  |  |   |  ||  |  | ||||  | |
Db  1928  TTAATGCAGGTTCAAGAGACTGCAAAGATCATGGGCATCGAGCTGTGTGGATC          1987

Qy  2030  GCTGGATTATCTAACTCTTACAACTTCTTCATAGAGAGATAGTAGTACAAAACGACGCGGCCAT 2089
          |||||| | || || | |  | ||| ||| || | |||| || |  |  ||||   |||| |
Db  1988  GATGGAATTGGGAATTTCTTCCATGGAATTTCCATGTCGCCTGTAATAAACAATAAAGGTACCGTCAT 2047

Qy  2090  TTGAGTGGCGGTTATGTCAGTCCTTAGTCTCCCTAATGAGGAGGAAATGCATTTATATAGTCTTAGT 2149
          ||||| | || | ||| | | ||||||||  | |  |||   || || |  ||| ||||
Db  2048  AACAGCCGGTGGATATGTTCTCTATCGTCTAAATGAATGATCACACAACCACTACTTCG  2107

Qy  2150  GCTGCATTTTGTGCAGCTCCTTTGTGAGGAGCTATCTCTCTGGAGTGGGTTGACTTGTGGTGGTGGGATC 2209
          || |||||   | || |  |||| | ||||  || |   ||  |  |||| | || || |   | | |
Db  2108  ATGGCATTTTCCCAACTCTTTAGTAGAGGACAACGGGTTTCCAACAACGAATAC    2167

Qy  2210  ACAGTCTACGAGGAACTCTCTATTACCGACCCAACGAAACC------             2251
           ||  | ||  | | |  | |||| |  | | ||  ||  |  ||||
Db  2168  AGAATGTATTTAGGATCGTCTATCGTCTCTATCAATATACAACCTCCCTAGGGAATATTTTCCGT 2227
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Qy   1369 AGAAAAGTTATCAGACAGAGGCCGCAGATTCTTAAAAATCTTACTTCGAAGCTACTACA 1428
          |||  ||||||||||||||| ||||| |||||||||| |||| ||||||| ||||||||
Db   2679 TGGAAAACTCCCCAGTCAGATGCCTCGGATTCCTGCAAATACTACCACCATACTGAACCA 2738

Qy   1429 GCCTGTAACTCTTCAGGAGGTACTCATCTTATCTTAAAACATGGAGTGACTCTGCAGACTCA 1488
          ||  |||||||| ||||||||         |||  ||||||| |||||| ||||
Db   2739 GAAGATCAACTTAGCAGGAGGAAATGTCGTTTTAAAGAAGAGGCCACCTACAAGTATA 2798

Qy   1489 GGCATTCACTCAACGACCAGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAACC 1548
          ||||| |||| |||| |||||||||||| | |||||||| |||| ||| ||| |||||||
Db   2799 TTCCTTCACACAGCAGCCTGATTCTCACAGTATCATGGATGCAGGAACGACCTTAGAGAC 2858

Qy   1549 TGTCGATACTAGCACCA------------TAAACAATTGGTCATTAACATCAG 1590
          |     ||||| |     |||||||||||||
Db   2859 CACGACAACTAACAATACAGATGGCAGCATCGAAATAGAAACCAAAGCTACGTCAAAAAATCTGA 2918

Qy   1591 TTCTATAGACGGTGCAAAGCAAATCAGAGAAGGTTTAAAGAACAGGGAAC 1650
          | |||| | |||| |||||  |   |   |||| |||||| || || |||
Db   2919 TGCTTTAGATGGCAAGCGTATGATAACGATTGCCGTAAACAGCACAAGTGGGGATTAAA 2978

Qy   1651 TTTATCTGGAACCATCACTTATTGGACCCGACGGCACGTTTATGAAAATCATAGTTT 1710
          ||||||||||| | | ||||| ||| |  ||||||| ||  ||| || ||  ||||
Db   2979 AATCTCAGGGGATCTGAAATTCCATAACAATGAAGGAGAGTTTCATGACAATCCTGGGTT 3038

Qy   1711 AAGAAATCCTCAGTCCTACGACATCTTAGAGCT---CAAAGCTTCTGAAACTGTAACAG 1767
          | |||||||| || ||| | || |||| ||      ||| ||   || | |||| ||
Db   3039 GAAGCAAACTAAAATCTTCCTTTCTTACTTCAGGAACTGTAAATTT 3098

Qy   1768 CACCGCAGTGACTCCAGATCCTATAAATGGGTGAGAAATTCCATTACGGCTATCAGGGAAC 1827
          |  |||||||||| |||||  |||| ||||| || |||| |||  ||||| ||||| ||||
Db   3099 AGACGACTTCAATCCGATTCCTTCTAGCATGGCGTGCTCCGGATTATGGTATCAAGGGAG 3158

Qy   1828 TTGGGGCCCAATTGTT---TGGGGACAGGGGCTTCTACGACTGCAACCTCAACTGGAC 1884
          ||||| ||||| |      ||| | ||||| |   |   | ||||||| ||||| |
Db   3159 TTTGGACTCTGGTTCCTAAAGTAGGAGCTGGAGGAAGGTGACTTTGGTCGCGGAATGGCA 3218

Qy   1885 TAAAACTGGCTATATTCCTAAATCCTAAACCAGAGCTTCGTGCGCACTTTAGTTCCTAATAGCCTTATG 1944
          ||||||||| || ||| | ||| |  ||||| |||||| | ||| ||||| |||||||||||||||||
Db   3219 AGCGGTTAGGATACACTCCTAAACCAGAGCTTCGTGCGCACTTTAGTTCCTAATAGCCTTTG 3278

Qy   1945 GAATGCATTTATAGATATTGGTCTGCTGGATTATCTAAACTCTTCCATAAGGATAGTAC 2004
          |||||| ||||| | | ||||| ||||| || |  | |||  | ||||| |||||  ||
Db   3279 GAATGCTTATGTAAAACATCCATTCTATACAGCAGGAGATCGCCACTGCCGATGTCGGACGC 3338

Qy   2005 GCAGGGAGCACCGTGCTTTTTGGTGTGCTGGATTATCTAACTTCTTCCATAAGGATAGTAC 2064
          ||| | ||||||   ||| | |   |  | |||| ||| | | ||||||| ||| | |
Db   3339 TCCCTCACATCCAGGGATTTGGATTGGAGGTATTGGCAAGCCTTCCATCCAAGACAAGCA 3398

Qy   2065 AAAAACACGACGCGCGGTTCGCCATTGAGTGGCGGTTATGTCATAGGAGGAAACCTACA 2124
          ||| |||| |||  || |  ||| || ||||||| |||| |||  |||||||||||||
Db   3399 AAAGGAAAATGCAGGATTCCGTTGATTTCTGATTTCCAGAGGTTATATTGTGGTGCAGCATGAC 3458

Qy   2125 TACTTGTTCAGATAAGAGATCTGACTCTTAGTTGTCAGCTCTTTTGTCAGCAGAGATAGAGA 2184
          |||| ||| ||| || || ||| | | || ||||||| ||| | | |  |||| | || |
Db   3459 CACCCCTCAAGAATATACCTTTGCTGGTTGCATTCAGCCAACTCTTTGGCAAATCTAAGGA 3518

Qy   2185 CTACTTTGTTAGCTAAGAAAATCAAGGTACAGTCTACGGAGGAACTCTCTATTACCAGCACAA 2244
          |||  || ||||| | ||| ||||||  ||| | | || |||| | |||   |||||||||
Db   3519 TTTACGTAGTCTCGGATTAAATCTGGATATTAAAATCCAAGTCTATGCAGGAATCTCTGCTCAGAGCTC 3578

Qy   2245 CGAAACCT--------ATATCTCTTCCTTGCAAACTACGGCCTTGTTCGTTGTCTTA 2295
          | ||||            || |||| |   | |   || | | |||  || | |||
Db   3579 TTATGTCATTCCCTGCATAGCTCATTACGTCGCCACGTCCTCTCTTAAGGTCCTTCCAGA 3638

Qy   2296 TGTTCCTACAGAATTCCGTCTGTCTTTCAGGAACCTTAGCTACACCACGGATAA 2355
          ||  || ||||||||||  |  ||| |||||  | |  | | ||||| ||| |
Db   3639 GCTCCCAGGAGAAACTCCCCTTGTTCTCCATGGTCAAGTTCTTATGTGGAAAACCACCA 3698

Qy   2356 CGATCTGAAAACCAAGTATACAACATATCCTACTGTTAAAGGAACATCTTCACAGG 2415
          | ||||| ||| ||||  || |||| || || || |||||| | | ||||||||||
Db   3699 TAATATGACGACAAAGCTTCGGAACAACACACAAGGGAAATCAGACTGCGGGGACTGGCAGCCATAG 3758
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Qy   2252 --TATATCTCTCTTCCTTGCAAACTACGGCCTTGTTCGTTGTCTTATGTGTCTTCCTACAGAGA 2309
            |  |||| |  ||| | | || ||| | |  |||  ||  || |  |||  ||| | |||
Db   2228 TATGCTTCGCGTAACCTAATGTAAACGTCGGGATTCTCTGCAAGACAAGGTTTCTTCAAAAT 2287

Qy   2310 TTCCGTTCTCTTTTCAGGAAGCCTTAGC-TACACCCATACGGATAACGATCTGAAAACC 2368
          | || ||||| | ||||  |||  |    | | |||| |  || |  | |  ||| |
Db   2288 CCTCTTATGATTTTTCATTTTTGTGCTTATCATTGCTTATGGTCATGATGTATGAAAAACA 2347

Qy   2369 AAGTATACAACATATCCTACTGTTAAAGGAAGCTGGGGAATGATAGTTTCGCTTTAGAA 2428
          ||||||| || |||  || |||| || | ||||| | || | | |||| | |||||||
Db   2348 GACTACGCAAATTCCCTATGGTGAAAAAACAGCTGGAGAAACAATTGTTGGGCTATAGAG 2407

Qy   2429 TTCGGTGAAGAGCTCCGATTGCTTGAGTAAGAAGTGCT--CTATTTGAGCAGTACATG 2485
          | ||| ||||| ||| | ||| |||||||| ||| |     |||||||| || |||
Db   2408 TGCGGAGGGAGCATGCCTCTATTGGTATTTGAGAACGGAAGACTTTTCCAAGGTGCCATC 2467

Qy   2486 CCCTTCATGAAATTGCAGTTGTCTATGCACATCAGGAGAAGGTTTAAAGAACAGGGAAC 2545
          || |||ATGAAA || | || ||| ||| || || ||||| ||| |||||| |
Db   2468 CCATTTATGAAACTACTACTAGTTTATGCTTATGCTTATCATGAGGATTTCAAAGAGACGACTCCGCA 2527

Qy   2546 GAAGCTCGTGAATTGGAAGTAGCCGTCTTCGTGTGTGAATCTTGCCTTACCTATCGGGATCCGA 2605
          ||| || | ||  |   ||| || ||   | | |  |||||   ||||| || | ||| |||
Db   2528 GATGGCGTAGATTTAGTAATGGGAGTTTAACATCGATTTCTGTACCTCTCTAGGCATACGC 2587

Qy   2606 TTTGATAAGGAATCAGACTGCCAAGATGCAAGTACAATCTAACTCTTGGTTGTTATACTGTG 2665
          ||||| |||  | |||| ||| | || | | | ||  || || | |||| | ||| |
Db   2588 TTTGAGAAGCTGGCACTTTCTCAGGATGTACTCTATGACTTTAGTTTCTCCTATATTCCT 2647

Qy   2666 GATCTTGTTCGTAGTAACCCGACTGTACGACAACACTGCGAATTAGCGGTGATTCTTGG 2725
          ||| |||||||   || |  | | | |||| ||| | |  ||| |||| |  | ||||
Db   2648 GATATTTTCCGTAAGGATCCTCATGTGAAGCGTCGTGTGATTAGCCGAGACTCCTGG 2707

Qy   2726 AAAACCTTCGGTACGAATTGGCAGAACAAGCTTAGTCCTTGTGTGCAGGGAACCATTTT 2785
          || ||| | | || ||   | | ||| ||     |||  |||||| |||| | ||| |
Db   2708 CTTGTTCCGGCAGCACGTACTCAAGACACATGCTTTTGTAGGGAGTGGAACGGGTCGGTAT 2767

Qy   2786 TGCTTAACCTCAAATTTTGAAGCCTTAGCCCAATTTTCTTTGAATTGCGTGGGTCATCT 2845
          | ||| | |  | |  | ||||| |||| |  |||| | |||| || |  | |  ||||
Db   2768 CACTTTAAGCACTATACTGAGCTCTTATGTCGAGGAAGTATAGATATGCCGCCCCATGCT 2827

Qy   2846 CGCAATTACAATGTAGGAGACGCAAAATACCAATTCTAATGCGTTAGCTTTG 2900
          ||||||| | ||||||  | |||AAATACCAATT |||  |  | |||  ||
Db   2828 AGGAATTATAATAAAACTGTGGAAGCAATTTCGTTTTTAGGAAGGTTTCCCATTG 2882
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RESULT 11
US-09-841-132-486
; Sequence 486, Application US/09841132
; Patent No. US2002006184 8A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
US-09-841-132-486
; SEQ ID NO 486
; LENGTH: 4224
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-841-132-486

Query Match   7.3%; Score 218; DB 9; Length 4224;
Best Local Similarity 48.9%; Pred. No. 1.2e-49;
Matches 788; Conservative 0; Mismatches 785; Indels 39; Gaps 6;

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Qy   1309 AGTTAATGAGACTCCCGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAGG 1368
          ||||  || || || ||  | || ||||| | |||||||| || ||| |  |||  ||
Db   2619 AGTGCCTGTAGTCCCTGTAGCACGTACCTGCAAACCCCAAACCCGGCAAACACAGGGAACTATAGCGAACTATATTTTCTTC 2678
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Qy          2416 TTTCGCTTTAGAATTCGGTGGAAGAGCTCCGATTTGCTTAGATGAAAGTGCTCTATTTGA 2475
                  |||||| | ||| |||||||      |||  |     || |  | ||    |   ||
Db          3759 CTTCGCTGTTGAAGTCGGTGGTTCTCTTCCTGTAGATCTAAACTACAGATACC---TTAC 3815

Qy          2476 GCAGTACATGCCCTTCATGAAATTGCAGTTTGTCTATGCACATCAGGAAGGTTTTAAAGA 2535
                     |||   ||||   ||||| | ||  ||||   || | ||||  |||| ||  ||||
Db          3816 CAGCTACTCTCCCTATGTGAAACTCCAAGTTGTGAGTGTAAATCAAAAAGGATTCCAAGA 3875

Qy          2536 ACAGGGAACAGAAGCTCGTGAATTTGGAAGTAGCCGTCTTGTGAATCTTGCCTTACCTAT 2595
                     |   | ||  | |||   ||||    ||||| ||| || ||  |  |  | |||||
Db          3876 GGTTGCTGCTGATCCACGTATCTTTGACGCTAGCCATCTGGTCAACGTGTCTATCCCTAT 3935

Qy          2596 CGGGATCCGATTTGATAAGGAATCAGACTGCCAAGATGCAACGTACAATCTAACTCTTGG 2655
                  ||  ||   ||  |  | |||||||     |         | |    ||| ||| | ||
Db          3936 GGGACTCACCTTCAAACACGAATCAGCAAAGCCCCCCAGTGCTTTGCTTCTTACTTTAGG 3995

Qy          2656 TTATACTGTGGATCTTGTTCGTAGTAACCCCGACTGTACGACAACACTGCGAATTAGCGG 2715
                 |||  |||| |||  |   ||   | ||||  ||||   |||  |  |   ||  |  ||
Db          3996 TTACGCTGTAGATGCTTACCGGGATCACCCTCACTGCCTGACCTCCTT---AACAAATGG 4052

Qy          2716 TGATTCTTGGAAAACCTTCGGTACGAATTTGGCAAGACAAGCTTTAGTCCTTCGTGCAGG 2775
                     || |||   || || | ||| || ||  || ||||||||||  |   |   ||
Db          4053 CACCTCGTGGTCTACGTTTGCTACAAACTTATCACGACAAGCTTTCTTTGCTGAGGCTTC 4112

Qy          2776 GAACCATTTTTGCTTTAACTCAAATTTTGAAGCCTTTAGCCAATTTTCTTTTGAATTGCG 2835
                     ||| |    ||         | ||||   |||            || |||| ||||
Db          4113 TGGACATCTGAAGTTACTTCATGGTCTTGACTGCTTCGCTTCTGGAAGTTGTGAACTGCG 4172

Qy          2836 TGGGTCATCTCGCAATTACAATGTAGACTTAGGAGCAAAATACCAATTCTAA 2887
                   | || ||  | |  || |||| | |||  ||| |    ||    ||||||
Db          4173 CAGCTCCTCAAGAAGCTATAATGCAAACTGTGGAACTCGTTATTCTTTCTAA 4224

RESULT 12
US-09-738-269-54
; Sequence 54, Application US/09738269
; Publication No. US20030185848A1
; GENERAL INFORMATION:
;  APPLICANT:  JOHNSTON, STEPHEN A.
;  APPLICANT:  STEMKE-HALE, KATHERINE
;  APPLICANT:  SYKES, KATHRYN F.
;  APPLICANT:  KALTENBOECK, BERNHARD
;  TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
;  TITLE OF INVENTION:  NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
;  TITLE OF INVENTION:  CHLAMYDIA PSITTACI
;  FILE REFERENCE:  UTSD:659
;  CURRENT APPLICATION NUMBER: US/09/738,269
;  CURRENT FILING DATE:  2000-12-18
;  NUMBER OF SEQ ID NOS:  61
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 54
;   LENGTH: 487
;   TYPE: DNA
;   ORGANISM: Chlamydia psittaci
US-09-738-269-54

  Query Match             4.9%;  Score 148.2;  DB 13;  Length 487;
  Best Local Similarity   58.5%;  Pred. No. 1.1e-30;
  Matches  280;  Conservative    0;  Mismatches  193;  Indels    6;  Gaps    1;

Qy          2134 AGATAAGATTCTTAGTGCTGCATTTTGTCAGCTCTTTGGAAGAGATAGAGACTACTTTGT 2193
                 |||  |   ||||||||  || || |||||| | |||| || ||||| ||||||| ||||
Db             9 AGAGGATTCTCTTAGTGTGGCTTTCTGTCAGTTATTTGCAAAAGATAAAGACTACCTTGT 68

Qy          2194 AGCTAAGAATCAAGGTACAGTCTACGGAGGAACTCTCTATTACCAGCA------CAACGA 2247
                 |   |||||    |  |  ||||| |  ||  || | ||||| |||||      |||
Db            69 AAGCAAGAACGCCGCAAACGTCTATGCGGGTTCTGTATATTATCAGCATGTGAGCAAGTT 128

Qy          2248 AACCTATATCTCTCTTCCTTGCAAACTACGGCCTTGTTCGTTGTCTTATGTTCCTACAGA 2307
                      || || | |     |  ||    |        |  |  ||     || ||| |||
Db           129 TGATGATCTCACGCGGTTATTTAATGGGCCTAACACGTGTTGTTCAGGGTTTTCTAAAGA 188

Qy          2308 GATTCCTGTTCTCTTTTCAGGAAACCTTAGCTACACCCATACGGATAACGATCTGAAAAC 2367
```

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                 ||||||| || ||||    | | |  ||| |||   ||| ||||  ||| |  ||| |||
Db           189 GATTCCTATTTTCTTGGATGCACAAATTACCTATTGCCACACGGCCAACAACATGACAAC 248

Qy          2368 CAAGTATACAACATATCCTACTGTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTAGA 2427
                     ||||||   ||||||   || |||||    ||||| |||||||   | |  |||
Db           249 GTCCTATACAGACTATCCTGAAGTGAAAGGTTCTTGGGGTAATGATACCCTGGGCTTAAC 308

Qy          2428 ATTCGGTGGAAGAGCTCCGATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTACATGCC 2487
                  ||   |   || |  || ||     ||  |     | || | |||||    ||    ||
Db           309 TTTGTCTACTAGCGTACCTATCCCGGTATTTAGTTCTTCTATCTTTGATAGTTATGCACC 368

Qy          2488 CTTCATGAAATTGCAGTTTGTCTATGCACATCAGGAAGGTTTTAAAGAACAGGGAACAGA 2547
                  ||    ||||| ||  |||||||||| || || || |  ||||||||||    ||||||
Db           369 GTTTGCAAAATTACAAGTTGTCTATGCGCACCAAGATGACTTTAAAGAACCAACAACAGA 428

Qy          2548 AGCTCGTGAATTTGGAAGTAGCCGTCTTGTGAATCTTGCCTTACCTATCGGGATCCGAT 2606
                 ||  || |  |||| ||| |||  |||| | ||  || |  ||||||| || ||   ||
Db           429 AGGCCGGGTCTTTGAAAGCAGCGATCTTCTCAACGTTTCTGTACCTATAGGTATAAAAT 487

RESULT 13
US-10-023-437-54
; Sequence 54, Application US/10023437
; Publication No. US20020183272A1
; GENERAL INFORMATION:
;  APPLICANT: JOHNSTON, STEPHEN A.
;  APPLICANT:  STEMKE-HALE, KATHERINE
;  APPLICANT:  SYKES, KATHRYN F.
;  APPLICANT:  KALTENBOECK, BERNHARD
;  TITLE OF INVENTION: METHODS AND compositions for Vaccination COMPRISING NUCLEIC ACI
;  TITLE OF INVENTION:  AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
;  FILE REFERENCE: UTSD:736US
;  CURRENT APPLICATION NUMBER: US/10/023,437
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: 60/225,839
;  PRIOR FILING DATE: 2000-12-15
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
;   LENGTH: 487
;   TYPE: DNA
;   ORGANISM: Chlamydia psittaci
US-10-023-437-54

  Query Match             4.9%;  Score 148.2;  DB 14;  Length 487;
  Best Local Similarity   58.5%;  Pred. No. 1.1e-30;
  Matches  280;  Conservative    0;  Mismatches  193;  Indels    6;  Gaps    1;

Qy          2134 AGATAAGATTCTTAGTGCTGCATTTTGTCAGCTCTTTGGAAGAGATAGAGACTACTTTGT 2193
                 |||  |   ||||||||  || || |||||| | |||| || ||||| ||||||| ||||
Db             9 AGAGGATTCTCTTAGTGTGGCTTTCTGTCAGTTATTTGCAAAAGATAAAGACTACCTTGT 68

Qy          2194 AGCTAAGAATCAAGGTACAGTCTACGGAGGAACTCTCTATTACCAGCA------CAACGA 2247
                 |   |||||    |  |  ||||| |  ||  || | ||||| |||||      |||
Db            69 AAGCAAGAACGCCGCAAACGTCTATGCGGGTTCTGTATATTATCAGCATGTGAGCAAGTT 128

Qy          2248 AACCTATATCTCTCTTCCTTGCAAACTACGGCCTTGTTCGTTGTCTTATGTTCCTACAGA 2307
                      || || | |     |  ||    |        |  |  ||     || ||| |||
Db           129 TGATGATCTCACGCGGTTATTTAATGGGCCTAACACGTGTTGTTCAGGGTTTTCTAAAGA 188

Qy          2308 GATTCCTGTTCTCTTTTCAGGAAACCTTAGCTACACCCATACGGATAACGATCTGAAAAC 2367
                 ||||||| || ||||    | | |  ||| |||   ||| ||||  ||| |  ||| |||
Db           189 GATTCCTATTTTCTTGGATGCACAAATTACCTATTGCCACACGGCCAACAACATGACAAC 248

Qy          2368 CAAGTATACAACATATCCTACTGTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTAGA 2427
                     ||||||   ||||||   || |||||    ||||| |||||||   | |  |||
Db           249 GTCCTATACAGACTATCCTGAAGTGAAAGGTTCTTGGGGTAATGATACCCTGGGCTTAAC 308

Qy          2428 ATTCGGTGGAAGAGCTCCGATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTACATGCC 2487
                  ||   |   || |  || ||     ||  |     | || | |||||    ||    ||
Db           309 TTTGTCTACTAGCGTACCTATCCCGGTATTTAGTTCTTCTATCTTTGATAGTTATGCACC 368

Qy          2488 CTTCATGAAATTGCAGTTTGTCTATGCACATCAGGAAGGTTTTAAAGAACAGGGAACAGA 2547
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Db        |||   ||||||||  |  ||||||||   |||
      369 GTTTTGCAAAATTACAAGTTGTCTATGCGCACCAAGATGACTTTAAAGAACCAACAACAGA 428

Qy 2548 AGCTCGTGAAGTTGGAAGTAGCCGTCTGTCTATGTGCTATGTGCTCATGCGGATCTTCTTGAAGCTATCGGATCCGAT 2606
Db  429 AGGCCGGGTCTTTGAAGCAGCGATCTTCTCAACGTTTCGTACCTTTCTGTACCTACCTATAGGTATAAAAT 487
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RESULT 14
US-09-841-132-182
; Sequence 182, Application US/09841132
; Patent No. US2002006184A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 182
; LENGTH: 3021
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-841-132-182

Query Match   4.4%; Score 132.2; DB 9; Length 3021;
Best Local Similarity 48.8%; Pred. No. 1.2e-25;
Matches 544; Conservative   0; Mismatches 523; Indels 48; Gaps 5;

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Qy 1776 TGACTCCAGATCCTATAATGGGTGAGAAATTCCATTACGCGTATCAGGGAACTGGGCC 1835
Db 1952 TGACTCTAGGGAATGAGATGCCTAAGTATGCTATCAAGGAAGCTGGAAGCTTGCGTGGG 2011

Qy 1836 CAATTGTTGGGGGACAGGGGCTTCACGACTGCAACCTTCACTGACTAAAACTGGCT 1895
Db 2012 ATCCTAATCACAGCAAATAATGTCTCCTATATAGTGTCCTAATAGCTTATGAATGCATTTA 2071

Qy 1896 ATATTCCTAATCCCGAGGCGTATCAGGCTGTAAAGTTTATGGAATGCATTTA 1955
Db 2072 ATAATCCTGGGCCTGCGAGCGAGTAGCTTTCTTTGGTTCTTCAAATAGTTTTATGGGGATCCATTT 2131

Qy 1956 TAGATATTAGCTCTCTCCATTATCTTATGGAGAGTGCAAACGAAGGGTTGCAGGGAGACC 2015
Db 2132 TAGATATACCGATCTGCGCATTCAGCAATTCAGCAAGCAAGTGTGGATGGCGCTCTATTGTC 2191

Qy 2016 GTGCTTTTTGGTGTGCTGGGATTATCTAACTTCTTCCATAAGGATAGTACAAAAAACACGAC 2075
Db 2192 GAGGATTATGGGTTTCTGGGAGTTTCGAATTTCTTCTATCATCATGACCGCGATGCTTTAGGTC 2251

Qy 2076 GCGGGTTCCGCCATTTGAGTGGCGGGTATGCGTATGTCATAGGAAGATAGAGACTACTTTGTTCAG 2135
Db 2252 AGGGATATCGGTATATTAGTGGGGGTTATTCCTTAGGAGCAAACTCCTACTTTGGATCA- 2310

Qy 2136 ATAAGAATTCTTAGTGCTGCCATTTTGTCTGCAGCTCTTGGAAGAAGATAGAGACTACTTTGTAG 2195
Db 2311 --TCGATGTTTGGTCTTAGCATTTACCGAAGTATTTGGTAGATCTAAAGATTATGTAGTGT 2368

Qy 2196 CTAAGAATCAAGGTACAGTCTACGGAGGAACCTCTCATTACCAGCACAACGAAACCTATA 2255
Db 2369 GTCGTTCCAATCATCATCATGCTTGCATAGGATC---------CGTTTA 2405

Qy 2256 TCTCTCTCCTTGCAAACTACGGCCCTTGTTGTTCTTATGTTCCTACAGAGATTCCTG 2315
Db 2406 TCTATCTACCCCAACAAGCT------TTATGTGGATCCTATTTGTGTTCGGAGATGCGTT 2456

Qy 2316 TTCTCTTTTTCAGGAAGAAACCTTAGCTACACCCATACGGATAACGATCTGAAACCAAGTATA 2375
Db 2457 TATCCGT---------GCTAGCTACGGGGTTTGGGATCACGCATATGAAACCTCTATATA 2506
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Qy 2376 CAACATATCCTACTGTTAAAGGAAGCAGGGAATGATAGTTCGCTTTAGAATTCGGTG 2435
Db 2507 CATTTGCGAGAGAGAGCGATGTTCGTTGGGATAATAATAACTGTCTGGCTGGAGAGATTGGAG 2566

Qy 2436 GAAGAGCTTCCGATTTGCTTAGATGAAAGTGCTCATTGAGCAGTACATG---CCCTTCA 2492
Db 2567 CGGGATTACCGATTGTGATTACTCCATCTAAGCTCTATTGAATGAGTTGCGTCCTTTCG 2626

Qy 2493 TGAAATTGCAGTTTGTTGTCTATGCAGACATCAGGAAGGTTTAAAGAACACAGGGAACGAAGAGCTC 2552
Db 2627 TGCAAGCTGAGTTTTCTTATGCCGATCATGAATCTTTTACAGAGAGGAAGGGGATCAAGCTC 2686

Qy 2553 GTGAATTTGGAAGTAGCCGTCTTGTGAATCTTGCCTTACCTATCGGATACCGATTTGATA 2612
Db 2687 GGGCATTCAAGAGCGGACATCTCCTAAATCTATCAGTTCCTGTTGGAGTGAAGTTTGATC 2746

Qy 2613 AGGAAATCAGACTGCCAAGATGCAACGTACAATCTAACTCTTGGTTATACTGTGGATCTTG 2672
Db 2747 GATGTTCTTAGTACACATCCTAATAAAATAGCTTATGCGGCGTTATATCGTGATGCTT 2806

Qy 2673 TTCGTAGTAACCCCGACTGTACGACAACACTGGCGAATTAGCGTGATGTCTTGAAAACCT 2732
Db 2807 ATCGCACCATCTCTGTACTGAGACAACGCTCCTATCCCATCAAGAGACATGACAACAG 2866

Qy 2733 TCGGTACGAATTGGCAAGACAAGCTTTAGTCCTTCGTGCAGGGAACCCATTTTTGCTTTA 2792
Db 2867 ATGCCTTTCATTTAGCAAGACAACATGGAGTTGTGGTTAGAGGAATCTATGTATGCTTCTCTAA 2926

Qy 2793 ACTCAAATTTTGAAGCCTTTAGCCAATTTTCTTTTGAATTGCGTGGGTCATCTCGCAATT 2852
Db 2927 CAAGTAATATAGAGAAGTATATGGGCATGGAAGATATGAGTATCGAGATGCTTCTCGAGGCT 2986

Qy 2853 ACAATGTAGACTTAGGAGCAAAATACCAATTCTAA 2887
Db 2987 ATGGTTTGAGTGCAGGAGTAAAGTCCGGTTCTAA 3021
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RESULT 15
US-09-841-132-170
; Sequence 170, Application US/09841132
; Patent No. US2002006184A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 170
; LENGTH: 2949
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-841-132-170

Query Match   4.4%; Score 131.4; DB 9; Length 2949;
Best Local Similarity 48.6%; Pred. No. 1.9e-25;
Matches 542; Conservative   2; Mismatches 523; Indels 48; Gaps 5;

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Qy 1776 TGACTCCAGATCCTATAATGGGTGAGAAATTCCATTACGCGTATCAGGGAACTGGGCC 1835
Db 1880 TGACTCTAGGGAATGAGATGCCTAAGTATGCTATCAAGGAAGCTGGAAGCTTGCGTGGG 1939

Qy 1836 CAATTGTTGGGGGACAGGGGCTTCACGACTGCAACCTTCACTGACTAAAACTGGCT 1895
Db 1940 ATCCTAATACACAGCAAATAATGTCTCCTTATACCTGAAAGCTACTACAAAACTGGGT 1999

Qy 1896 ATATTCCTAATCCCGAGGCGTATCAGGCTGTAAAGTTTATGGAATGCATTTA 1955
Db 2000 ATAATCCTGGGCCTGCGAGCGAGTAGCTTTCTTTGGTTCTTCAAATAGTTTTATGGGGATCCATTT 2059
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Qy   1956  TAGATTATTAGCTCTCTCCATTATCTTATGAGACTGCAAACGAAGGGTTGCAGGGAGACC  2015
                 |||||   ||| |||||      |||||||||||  |||||||  |||||  ||| |||
Db   2060  TAGATATACGACTCGCGCATTCAGCATTCAACCAAGCAAGTGTGATGGGCGCTCTTATTGTC  2119

Qy   2016  GTGCTTTTTGGTGTGTGGATTATCTAACTTCTTCCATAAGGATAGTACAAAAACACGAC  2075
                 |||||  |||| |||  |||||||  |||||||  ||||||  |||||| |||
Db   2120  GAGGATTATGGGTTTCGGAGTTTCGAATTTCTTCATCATGACCGCATGCTTTAGGTC  2179

Qy   2076  GCGGGGTTCGCCATTGAGTGGCGGTTATGTCATAGGAGGAAACCTACATACTTGTTCAG  2135
                 |||  |||||| |||||||||  ||||| |||||||  ||||||  |||||||  ||
Db   2180  AGGGATATCGGTATATTAGTGGGGGTTATTCCTTAGGAGCAAACTCCTACTTTGGATCA-  2238

Qy   2136  ATAAGATTCTTAGTGCTGCATTTGTCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAG  2195
                 |||||  ||   ||||  |||||   |||||  |||||||||  ||  ||||||||
Db   2239  --TCGATGTTTGGTCTAGCATTTACCGAAGTAGTTTGGTAGATCTAAAGATTATGTAGTGT  2296

Qy   2196  CTAAGAATCAAGGTACAGTCTACGGAGGAGAACTCTCTATTACCAGCACAACGAAACCTATA  2255
                                                          ------------   |||||
Db   2297  GTCGTTCCAATCATCATGCTTGCATAGGATC-----------------------CGTTTA  2333

Qy   2256  TCTCTCTTCCTTGCAAACTACGGCCTTGTCGTTGTCTTATGTTCCTACAGAGATTCCTG  2315
                 ||| ||   ||||||||       ----------|||| ||||||| |||||  |||
Db   2334  TCTATCTACCCAACAAGCT----------TTATGTGGATCCTATTTGTTCGGAGATGCGTT  2384

Qy   2316  TTCTCTTTTCAGGAAAACCTTAGCTACACACCCATACGGATAAACGATCTGAAAACCAAGTATA  2375
                 ||||          |||||| |||||||  ||||||||||||||| |||||||||||||||||
Db   2385  TATCCGT--------GCTAGCTACGGGGTTTGGGAATCAGCATATCAGAAAAACCTCATATA  2434

Qy   2376  CAACATATCCTACTGTTAAAGGAAGCTGGGGGAATGATAGTTCGCTTTAGAATTCGGTG  2435
                 ||| |||||  ||||     ||| |||||   ||||||||||| ||| ||    ||||||
Db   2435  CATTTGCAGAGGAGAGCGATGTTCGTTGGGATAATAAACTGTCTGGCTGGAGATTGGAG  2494

Qy   2436  GAAGAGCTCCGATTTGCTTGGTGATGAAAGTGCTCTATTTGAGACAGTACATG---CCCTTCA  2492
                 ||||||||      ||||||||  ||||   |||||  ||||||     |||      ||| ||
Db   2495  CGGGATTACCGATTTGTGATTACTCCATCCTATTGAATGAGTTGCCGTCCCTTTCG  2554

Qy   2493  TGAAAATTGCAGTTTGTCTATGCACATCACCAGGAAGGTTTTAAAGAACAGGGAACAGAAGCTC  2552
                 ||||||||  |||| ||| ||||||||| |||||| |||||| ||   |||||| |||||||||
Db   2555  TGCAAGCTGAGTTTTCTTATGCGGATCATGAATCTTCACGAGGAGGCGATCAAGCTC  2614

Qy   2553  GTGAAATTGGAAGTAGCCGTCTTGTGAATCTTGCCTTACCTATCGGGATCCGATTTGATA  2612
                 |||||||| |||||||||| |   |||||||       ||||| |||||||   |||| ||
Db   2615  GGGCATTCAAGAGCGGACATCTCCTAAAATCTATAAAATCTATCAGTTCCTGTTGGAGTGAAGTTTGATC  2674

Qy   2613  AGGAATCAGACTGCCAAGATGCAAGTGCAACGTACAAATCTAACTCTTCGTTATACTGTTGGATCTTG  2672
                 |||||||     ||     ||||||  |||||||   |||||||   |||  ||||| ||||||  |||
Db   2675  GATGTTCTAGTACACATCCTAATAAAATAGCTTTATCGGCGGCTTATCGTCATCGTGATGCTT  2734

Qy   2673  TTCGTAGTAACCCCGACTGTACGACAACACTGCGAATTAGCCGGTGATTCTTGGAAAACCT  2732
                 ||||||         |||||  |||||||| ||  ||||||| |||||||   ||||||||
Db   2735  ATCGCACCATCTCTGGTACTGAGACAACACGCTCCTATCCCATCAAGACATGACAACAG  2794

Qy   2733  TCGGTACGAATTTGGCAAGACAAGCTTTAGTCCTTCGTGCGAGGGAACCATTTTGCTTTA  2792
                 |||||      |||||||||||||  ||||||| |||| |||| ||||||||||  ||||
Db   2795  ATGCCTTTCATTTAGCAAGCATGGAGTTGTGGTTAGAGGATCTATGTATGCTTCTCTAA  2854

Qy   2793  ACTCAAATTTGAAGCCTTAGCCAATTTCTTTTGAATTGCTGGGTCATCTCGCAATT  2852
                 ||       |||||  ||     ||| |:  |||| ||||| ||   ||||  ||||||
Db   2855  CAAGTAATATAGAGAGTATATGGCCATGGAAGATATGAGTATCCGAGATGCTTCTCGAGGCT  2914

Qy   2853  ACAATGTAGACTTAGGAGGCAAAATACCAATTCTAA  2887
                 ||||  | | :   |||  ||  :  || |||| |||||
Db   2915  ATGGTTTGAGTGCAGGNAGTAAAGTCYGGTTCTAA  2949
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Search completed: December 16, 2003, 17:29:33
Job time : 896 secs

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                    Copyright (c) 1993 - 2003 Compugen Ltd.
                        GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on:    December 16, 2003, 12:16:53 ; Search time 5962 Seconds
                                         (without alignments)
                               12229.693 Million cell updates/sec

Title:         US-09-428-122-1
Perfect score: 3000
Sequence:      1 cgctcttacctagtagagt.......tgtttgctaaaacacttc 3000

Scoring table: IDENTITY NUC
               Gapop 10.0 , Gapext 1.0

Searched:      22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters:    45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
     1:  em_estba:*
     2:  em_esthum:*
     3:  em_estin:*
     4:  em_estmu:*
     5:  em_estov:*
     6:  em_estpl:*
     7:  em_estro:*
     8:  em_htc:*
     9:  gb_est1:*
    10:  gb_est2:*
    11:  gb_htc:*
    12:  gb_est3:*
    13:  gb_est4:*
    14:  gb_est5:*
    15:  em_estfun:*
    16:  em_estom:*
    17:  em_gss_hum:*
    18:  em_gss_inv:*
    19:  em_gss_vrt:*
    20:  em_gss_fun:*
    21:  em_gss_mam:*
    22:  em_gss_mus:*
    23:  em_gss_pro:*
    24:  em_gss_rod:*
    25:  em_gss_phg:*
    26:  em_gss_vrl:*
    27:  gb_gss1:*
    28:  gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match	Length	DB	ID	Description
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c	2	49.4	1.6	334	9	AU076383	AU076383 AU076383
c	3	46.8	1.6	585	9	AU263143	AU263143 AU263143
c	4	46.8	1.6	1201	13	BX336919	BX336919 BX336919
c	5	46.2	1.5	853	10	BF265090	BF265090 HV_CEa001
c	6	45.4	1.5	843	29	BZ643413	BZ643413 OGAOW57TM
c	7	45.4	1.5	1201	13	BX376097	BX376097 BX376097
c	8	44.8	1.5	391	9	AU263574	AU263574 AU263574
c	9	44.8	1.5	720	29	AG088699	AG088699 Pan trogl
c	10	44.6	1.5	592	28	AZ972038	AZ972038 2M0245E13
c	11	44.4	1.5	1025	29	CNS014J2	CNS014J2 Drosophil
c	12	44	1.5	450	12	BM881804	BM881804 rb14b09.y
c	13	44	1.5	498	10	BG602722	BG602722 EST501812
c	14	44	1.5	593	10	BG602721	BG602721 EST501811
c	15	44	1.5	735	12	BM160527	BM160527 EST563050
c	16	44	1.5	767	12	BM657645	BM657645 170006874
	17	43.8	1.5	596	29	FR0019514	FR0019514 F.rubripe
	18	43.8	1.5	820	28	BH051138	BH051138 RPCI-24-3
c	19	43.6	1.5	574	28	AZ526815	AZ526815 260PbA10
	20	43.2	1.4	716	12	BM627037	BM627037 170006684
	21	43.2	1.4	1101	29	AL052689	AL052689 Drosophil
c	22	43.2	1.4	1201	13	BX394744	BX394744 BX394744
c	23	42.8	1.4	783	29	CNS00AIS	CNS00AIS Drosophil
	24	42.8	1.4	1201	29	CNS0167M	CNS0167M Drosophil
c	25	42.6	1.4	1177	13	BX338151	BX338151 BX338151
c	26	42.4	1.4	240	9	AU072820	AU072820 AU072820
	27	42.4	1.4	1101	29	CNS0039G	CNS0039G Drosophil
c	28	42.2	1.4	660	28	AZ567761	AZ567761 238PvG08
	29	42	1.4	900	28	AQ744776	AQ744776 HS_5506_A
c	30	42	1.4	1201	13	BX337161	BX337161 BX337161
	31	41.8	1.4	516	10	BF954368	BF954368 QV2-NN004
	32	41.8	1.4	712	13	BX416727	BX416727 BX416727
c	33	41.8	1.4	998	13	BX436885	BX436885 BX436885
	34	41.6	1.4	509	12	BM316139	BM316139 fw70a01.x
	35	41.6	1.4	553	9	AW019090	AW019090 fd59g04.x
	36	41.6	1.4	1101	29	CNS00KF8	CNS00KF8 Drosophil
	37	41.4	1.4	480	29	BZ643398	BZ643398 OGAOW57TC
	38	41.4	1.4	926	28	BH156551	BH156551 ENTTD75TR
c	39	41.4	1.4	948	13	BX414840	BX414840 BX414840
c	40	41.4	1.4	1101	29	CNS017NE	CNS017NE Drosophil
	41	41.4	1.4	1201	13	BX384793	BX384793 BX384793
	42	41.2	1.4	703	12	BM602748	BM602748 170006870
	43	41.2	1.4	1201	13	BX462660	BX462660 BX462660
	44	41	1.4	529	10	BE225902	BE225902 i21c12.x
c	45	41	1.4	735	29	CNS04NSM	AL299119 Tetraodon

ALIGNMENTS

```
RESULT 1
CNS01509/c
LOCUS       CNS01509              923 bp    DNA     linear    GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN14B20 of DroBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL105699
VERSION     AL105699.1   GI:5617836
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM    Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 923)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
```

FEATURES
    source   pBeloBAC11.
                    Location/Qualifiers
                    1..923
                    /organism="Drosophila melanogaster"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:7227"
                    /clone="BACN14B20"
                    /clone_lib="DrosBAC"
                    /plasmid="pBeloBAC11"
                    /note="end : SP6"
BASE COUNT   245 a   142 c   100 g   315 t   121 others
ORIGIN

Query Match   1.7%; Score 50.6; DB 29; Length 923;
Best Local Similarity 34.5%; Pred. No. 1.7;
Matches 129; Conservative 66; Mismatches 178; Indels 1; Gaps 1;

Qy   29 TTTCTTGACTTGTTTCTCCTATTGGTGTATCTCTAAAATATTAAATTCAAAATCAAAGT 88
          ||||||||||||||:.|||||| :.||||||||||||| ||:||:||||||:||||||
Db   909 TTTTTTTTTTTTTTAAAWTWYAWTTTTATAITTTWAAATAITTAATAKAAWTTTTTTTT 850

Qy   89 ATATATTTACAATGAAGTCTTCTTCTTCCCCCAAG-TTTGTATTTTCTACATTTGCTATTTT 147
          |||:|:||:..:|| :|||||||| |||||||||| || ||||||||||| .:||||||||
Db   849 TTWTWWTTTWWWAWTAADTTTTAWTKHYWHATGBTKYYTYTTTBTTTTAGGKGGTTT 790

Qy   148 CCCTTTGTCTATGATTGCTACCGAGACAGTTTTGGATTCAAGTGCGAGTTTCGATGGGAA 207
          :||::||||:.:.::::.:||||:||||||.|:.||.|.:||:.:||:.:.|||:|||||
Db   789 YCMRKADNSNNHMMMMHMMASSMSSSVCAAAKAGAYNCGWGMRRKRAMWHNVGAA 730

Qy   208 TAAAAATGGTAATTTTTCAGTTCGTGAGAGTCAGGAGAGATGCTGGAACTACCTACCTATT 267
          |||||:..::|||||.:|.||.|||.|:.:||.|:|:|:||:.:||||||:||.:|||||
Db   729 AAAARMAAAAWAAVVAANDKNCSGGNAGGGSGGBBSRGAATMGCGGACACAKTTBYATT 670

Qy   268 TAAGGGAAAATGTCACTCTAGAAAAATATTCCTGAACAGGCACAGCAATCACAAAAAGCTG 327
          ||||||||||||||:..:.:.||::||:.||||||.:|.|:.:.||.:||.:||||||||
Db   669 MGGAMACAAMAAAAAAAAAAAAAAAGCAAGWKATAAGTCCTWHAAAATCAAAAGGAA 610

Qy   328 TTTTAACAACACTAAGGGCGATTTGACTTTCACAGGTAACGGGAACTCTCTATTGTTCCA 387
          |||:.:.:. |:.||.| ::.:|| | ||:.|||:.:||||||||:.||:||||||||||
Db   609 ATMWABNBKBKTBKKBAAAATATTGTCATTGAATCCATWWTTGGAAAAGGAKGGGGTTCTA 550

Qy   388 AACGGTGGATGCAG 401
          .:|||||||||||
Db   549 AGAGTKGGGGAAG 536

RESULT 2
AU076383/c
LOCUS   AU076383   334 bp   mRNA   linear   EST 27-JUL-1999
DEFINITION   AU076383 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
             discoideum cDNA clone SSA686, mRNA sequence.
ACCESSION   AU076383
VERSION   AU076383.1 GI:5607281
KEYWORDS   EST.
SOURCE   Dictyostelium discoideum
ORGANISM   Dictyostelium discoideum
             Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
REFERENCE   1 (bases 1 to 334)
AUTHORS   Urushihara,H.
TITLE   Developmental cDNA in Dictyostelium discoideum (1999)
JOURNAL   Unpublished
COMMENT   Contact: Hideko Urushihara
             Institute of Biological Sciences
             University of Tsukuba
             1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
             Tel: 81-298-53-4664
             Fax: 81-298-53-6614
             Email: hideko@biol.tsukuba.ac.jp
             PROJECT = Dictyostelium discoideum cDNA project in Japan.
FEATURES
    source   Location/Qualifiers
                    1..334
                    /organism="Dictyostelium discoideum"
                    /mol_type="mRNA"

                    /strain="AX4"
                    /db_xref="taxon:44689"
                    /clone="SSA686"
                    /dev_stage="slug"
                    /clone_lib="Dictyostelium discoideum SS (H.Urushihara)"
BASE COUNT   173 a   30 c   38 g   93 t
ORIGIN

Query Match   1.6%; Score 49.4; DB 9; Length 334;
Best Local Similarity 48.1%; Pred. No. 2.6;
Matches 140; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

Qy   29 TTTCTTGACTTGTTTCTCCTATTGGTGTATCTCTAAAATATTAAATTCAAAATCAAAGT 88
          ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db   325 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAATTTATATTTTTATT 266

Qy   89 ATATATTTACAATGAAGTCTTCTTCTTCCCCAAGTTGTATTTGTATTTTCACATTTGCTATTTTC 148
          |||||||.||||||||||||||| |||||||||| |||||||||||||
Db   265 TTTTTTTTTTTTTTTTTTATTTTTATTTTTTTTTTCTTAAAATTTTCTTCAGTAATTGGT 206

Qy   149 CCTTTGTCTATGATTGCTACCGAGACAGTTTTGGATTCAAGTGCGAGTTTCGATGGGAAT 208
          |||||||||||||||| |||||||||:|||||||||||||||||||||||||||||||||
Db   205 CTATTTTTGAGATATTCTGCTACACCTTTATTAGATTCGAAATGTTCTTTCAAAGAAATCT 146

Qy   209 AAAAATGGTAATTTTTCAGTTCGTGAGAGTCAGGAGAGATGCTGGAACTACCTACCTATTT 268
          |||||||||||.||||||||||||.|||||||||||:|.:||||||||:|||||||:||||
Db   145 AAATGTGGAACTTACCATTGTATAAGATCATGATCAGCAGCAAATGGTAAAACAATAACCAATG 86

Qy   269 AAGGGAAATGTCACTCTAGAAAAATATTCCTGAACAGGCACAGCAATCACA 319
          |||||||||||||||||:||||||||:.||||||:|||.||||||||||||
Db   85 TATTCATAAGCAACATAACATATAAATCAGCCAAGTGTAAGAATTACCA 35

RESULT 3
AU263143/c
LOCUS   AU263143   585 bp   mRNA   linear   EST 09-MAY-2002
DEFINITION   AU263143 VS Dictyostelium discoideum cDNA clone VSE486 3', mRNA
             sequence.
ACCESSION   AU263143
VERSION   AU263143.1 GI:20519690
KEYWORDS   EST.
SOURCE   Dictyostelium discoideum
ORGANISM   Dictyostelium discoideum
             Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
REFERENCE   1 (bases 1 to 585)
AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
             Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE   Population analysis of cDNAs from unicellular and multicellular
             stages of Dictyostelium discoideum
JOURNAL   Unpublished
COMMENT   Contact: Hideko Urushihara
             Institute of Biological Sciences
             University of Tsukuba
             1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
             Tel: 81-298-53-4664
             Fax: 81-298-53-6614
             Email: hideko@biol.tsukuba.ac.jp.
FEATURES
    source   Location/Qualifiers
                    1..585
                    /organism="Dictyostelium discoideum"
                    /mol_type="mRNA"
                    /strain="AX4"
                    /db_xref="taxon:44689"
                    /clone="VSE486"
                    /sex="mat A"
                    /dev_stage="vegetative"
                    /clone_lib="VS"
BASE COUNT   250 a   73 c   81 g   181 t
ORIGIN

Query Match   1.6%; Score 46.8; DB 9; Length 585;
Best Local Similarity 47.9%; Pred. No. 11;
Matches 135; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

```
Qy    74  ATTCAAAATCAAAGTATATATTTTACAATGAAGTCTTCTTCCCCAAGTTGTATTTCT  133
          ||::|:.|:..::.:| ||||            |||:||||::::|||||||||||||
Db   906  ATWAWWTWAWWWAATWTYTYTTTTTTTTTTTTTTTTTTYYTTTTTCCTTHCTYYTTTTTTTTTTTTTTT  965

Qy   134  ACATTTGCTATTTCCCTTGTCATGATTGCTACCGAGACAGTTTGGATTCAAGTGCG  193
          |||||       ||:::|||||||
Db   966  TTTTTTTTATATTTYHHTTTTTTTTTTTTTTATTWAAATAMCCTCCCTTTTTTTWTWTWWWAT  1025

Qy   194  AGTTTCGATGGGAATAAAAATGGTAATTTTCAGTT  229
          ||||||||       ||.|:||||
Db  1026  ATTAAAAAWTTTTTWWHWTTTTMTHTTTTTTTTTT  1061
```

RESULT 5
BF265090/c
LOCUS   BF265090   853 bp   mRNA   linear   EST 23-OCT-2001
DEFINITION   HV_CEa0011D22f Hordeum vulgare seedling green leaf EST library
             HVcDNA0004 (Blumeria challenged) Hordeum vulgare subsp. vulgare
             cDNA clone HV_CEa0011D22f, mRNA sequence.
ACCESSION   BF265090
VERSION   BF265090.3   GI:16334636
KEYWORDS   EST.
SOURCE   Hordeum vulgare subsp. vulgare
  ORGANISM   Hordeum vulgare subsp. vulgare
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
             ; Triticeae; Hordeum.
REFERENCE   1 (bases 1 to 853)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D.,
             Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
             ,D.W., Fenton,R.D., Oates,R. and Main,D.
  TITLE   Development of a genetically and physically anchored EST resource
             for barley genomics: Blumeria infected incompatible (Mla13)
             seedling leaf cDNA library
  JOURNAL   Unpublished
COMMENT   On Nov 17, 2000 this sequence version replaced gi:13261889.
             Contact: Wing RA
             Clemson University Genomics Institute
             Clemson University
             100 Jordan Hall, Clemson, SC 29634, USA
             Tel: 864 656 7288
             Fax: 864 656 4293
             Email: rwing@clemson.edu
             Total hq bases = 280
             Seq primer: AATTAACCCTCACTAAAGGG
             High quality sequence stop: 831.
FEATURES   Location/Qualifiers
     source   1..853
                     /organism="Hordeum vulgare subsp. vulgare"
                     /mol_type="mRNA"
                     /cultivar="CI16155 (Mla13)"
                     /db_xref="taxon:112509"
                     /clone="HV_CEa0011D22f"
                     /tissue_type="seedling green leaf"
                     /lab_host="TJC121"
                     /clone_lib="Hordeum vulgare seedling green leaf EST
                     library HVcDNA0004 (Blumeria challenged)"
                     /note="Vector: lambdaZAP; Site 1: EcoR1; Site 2: Xho1;
                     C.I. 16155 (Mla13) plants were greenhouse grown in the R
                     Wise lab at Iowa State University, Ames, IA; 7 day old
                     green seedlings were challenged with isolate A27 (AvrMla13
) of Blumeria graminis f. sp. hordei, and leaves were
                     harvested 20 and 24 hr post-inoculation and snap frozen;
                     uninoculated leaves were harvested 20 hr post-inoculation
                     (Wei, Wise). In the TJ Close lab at the University of
                     California, Riverside, total RNA was prepared from each
                     sample pool, equal quantities of all three RNA pools were
                     combined, poly(A) RNA was purified from the mixture, one
                     cDNA library was made, and 1 million pfu were in vivo
                     excised to give pBluescript SK(-) cDNA phagemids (Choi,
                     Close). Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
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Qy   38  TTGTTTCCTATTGGTGTATCTCTTAAAATATTAAATTCAAAATCAAAGTATATATTT  97
         ||||||                ||::|                |||||||||||||
Db  584  TTGTTGTTGTTGTGTTGTTTACTTTTTTTTTTTTTTAATTTTATATTTTTTATTTTT  525

Qy   98  ACAATGAAGTCTTCTTCCCCAAGTTGTATTTTCTACATTGCTATTTCCCTTGTCT  157
         ||||||       |                     |||||||||||||||
Db  524  TTTATTTTTTTATTTTTTCTTAAATTTTTCTTCAGTAATTGGTCTATTTTTG  465

Qy  158  ATGATTGCTACCGAGACAGTTTGGATTCAAGTGCGGAGTTTCGATGGGAATAAAAATGGT  217
         ||||||                     |||||||||||||||||
Db  464  AGATATTCTGCTACACCTTTATTAGATTCGAAATGTTCTTTCAAAGAATCTAAATGTGGG  405

Qy  218  AATTTTTCAGTTCGTGAGAGTCAGGAAGATGCTGGAACTACCTACCTATTTAAGGGGAAAT  277
         |||||||||||||                     ||||||||||||||||||||
Db  404  AACTTACCATTGTATAAGAGATCAGCAGCAAATGGTAAAACATAACCAATGTATTCATAA  345

Qy  278  GTCACTCTAGAAAATATTCCTGGAACAGAGGCACAGCAATCACA  319
         |||||||       |||||||||||||||
Db  278  GCAACATAAAACATATAAATCAGCCAAGTGTAAGAATTACCA  303
```

RESULT 4
BX336919
LOCUS   BX336919   1201 bp   mRNA   linear   EST 02-MAY-2003
DEFINITION   BX336919 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
             clone CS0DI033YL20 5-PRIME, mRNA sequence.
ACCESSION   BX336919
VERSION   BX336919.1   GI:30345558
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
COMMENT   Contact: Genoscope
             Genoscope - Centre National de Sequencage
             BP 191 91006 EVRY cedex - France
             Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
             Library was constructed by Life Technologies, a division of
             Invitrogen. This sequence belongs to sequence cluster 2019.r For
             more information about this cluster, see
             http://www.genoscope.cns.fr/
             cgi-bin/cluster.cgi?seq=CS0DI033DF10QP1&cluster=2019.r. Contact :
             Feng Liang Email : fliang@lifetech.com URL :
             http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
             Faraday Avenue Genoscope sequence ID : CS0DI033DF10QP1.
FEATURES   Location/Qualifiers
     source   1..1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI033YL20"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT   317 a   228 c   196 g   375 t   85 others
ORIGIN
Query Match   1.6%;   Score 46.8;   DB 13;   Length 1201;
Best Local Similarity   39.44%;   Pred. No. 12;
Matches   85;   Conservative   36;   Mismatches   95;   Indels   0;   Gaps   0;
```

```
Qy   14  TAGAGGTTGAGTGAATTTCTGACTTGTTCTCCCTATTGGTGTATCTCTTAAAATATTAA  73
         :|::||||       .::||:||       |||||||||||||
Db  846  WATWBBTTTYTTAWWTWWTTTTTWTWTWTTTTTTTTTTTTTTTTTTTTACCTTTTTTYAAAAAATATAA  905
```

sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT   343 a   180 c   169 g   141 t   20 others
ORIGIN

Query Match   1.5%;   Score 46.2; DB 10; Length 853;
Best Local Similarity   57.8%;   Pred. No. 16;
Matches   78;   Conservative   0;   Mismatches   57;   Indels   0;   Gaps   0;

Qy   29 TTTCTTGACTTGTTCTCCCTATTGGTGTATCTCTTAAAATATTAAATTCAAAATCAAAGT 88
Db 808 TTTTTTTATTTGTTTTGTTTTTAATATNTNAGGTTTATAATATATNTTTAAAGTTGTTATTTTTATT 749

Qy   89 AATATATTTTACAATGAAGTCTTCTTTCCCAAGTTTGTATTTTCTACATTGCTATTTTC 148
Db 748 ATNTTTTGTGTGAATTTTTTTTTTTTTATTAAGTTTTTTTATTTTTTNTTTTC 689

Qy 149 CCTTTGTCATGAAT 163
Db 688 CTTTTATCTATATTT 674

RESULT 6
BZ643413/c
LOCUS   BZ643413   843 bp   DNA   linear   GSS 29-JAN-2003
DEFINITION OGAOW57TM ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa011lJ17,
            genomic survey sequence.
ACCESSION   BZ643413
VERSION   BZ643413.1 GI:28104915
KEYWORDS   GSS.
SOURCE   Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 843)
AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick
            ,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek
            ,R.W., Nunberg,A., Robbins,D. and Lakey,N.
TITLE   Consortium for Maize Genomics
JOURNAL   Unpublished
COMMENT   Other GSSs: OGAOW57TC
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TR
            Class: sheared ends.
FEATURES   Location/Qualifiers
     source 1..843
             /organism="Zea mays"
             /mol_type="genomic DNA"
             /strain="B73"
             /db_xref="taxon:4577"
             /clone="ZMMBMa011lJ17"
             /clone_lib="ZM_0.7_1.5_KB"
             /note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
             methylation filtered genomic DNA library"
BASE COUNT   281 a   125 c   279 g   158 t
ORIGIN

Query Match   1.5%;   Score 45.4; DB 29; Length 843;
Best Local Similarity   49.8%;   Pred. No. 24;
Matches   115;   Conservative   0;   Mismatches   116;   Indels   0;   Gaps   0;

Qy 692 GCCATTCAGACTTCCGATGCCCTTACCATTACTGGAAACCAAGGAGAAGTCTCTTTTTCT 751
Db 552 GCTACTGCTGCTACTGCTGCTGCTACTGCTGCTGCTACTGCTGCTACTACTACTACTACT 493

Qy 752 GACAATACTTCTTCTGGATTCTGGAGCTGCAATTTTACAGAAGCCTCGGTGACTATTTCT 811
Db 492 GCTACTACTGCTGCTACTGCTGCTCGCAACTGCTACTGCTGCTACTGCTACTACTACTACT 433

Qy 812 AATATGCTAAAGTTCCTTATTGACAATAAGGTCACAGGAGCGAGCTCCTCAACACG 871
Db 432 GCTGCTGCTACTACTGCTACTACTGCTACTACTACTGCTCGTACTACTACTACTACTACT 373

Qy 872 GGGGATATGTCAGGAGGTGCTATCTGCTCTTATAAAACTAGTACAGATACT 922
Db 372 GCTCCTACTACTGCTACTGCTACTGCTTCTACTACTACTGCTACT 322

RESULT 7
BX376097/c
LOCUS   BX376097   1201 bp   mRNA   linear   EST 08-MAY-2003
DEFINITION BX376097 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC022YM12 5-PRIME, mRNA sequence.
ACCESSION   BX376097
VERSION   BX376097.1 GI:30434756
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1201)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE   Full-length cDNA libraries and normalization
JOURNAL   Unpublished
COMMENT   Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 2866.f
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DC022BG06Q91.
FEATURES   Location/Qualifiers
     source 1..1201
             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="CS0DC022YM12"
             /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
             /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
             /note="1st strand cDNA was primed with a NotI-oligo(dT)
             primer. Five prime end enriched, double-strand cDNA was
             digested with Not I and cloned into the Not I and EcoR V
             sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT   79 a   152 c   66 g   270 t   634 others
ORIGIN

Query Match   1.5%;   Score 45.4; DB 13; Length 1201;
Best Local Similarity   8.8%;   Pred. No. 26;
Matches   52;   Conservative   236;   Mismatches   299;   Indels   1;   Gaps   1;

Qy 841 TAAGGTCACAGGAGCGAGCTCCTCAACACACGCGGGGGATATGTCAGGAGGTGCTATCTGTGC 900
Db 1032 TMTMKTMMMMMMMMMMMMMMMVKKKMMMMMKKHMHMHMMKKHMMHKTMTNTKW 973

Qy 901 TTATAAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAG 960
Db 972 MKTKTMMMMMMMMMMMVKKKMMKKMMMMKKMMMMNYMMMTGMMMMGKHMVMVMVMMMMMMM 913

Qy   961 CAACAATACATCGACAACAGACGGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTC 1020
                :::: |:::::|| ||| ||:| :   :: |:::| |::.|
Db   912 GMMMMKTMMMKMMMGGKGGTMGGGMGGGVMMMVGMRGGGVMMMGTGKKTMGKWNMMGKMMGM 853

Qy   1021 CGGAGGACTTACCCTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCTAAAGGTGG 1080
                ||:||| :.|:::: |||||
Db   852 MGNGTDNMKTWTMKMMMKHMTWTKGNGKTMHGKMMNMMVKMKTMMNVGAAAAAAADAGGG 793

Qy   1081 AGCCATAGCTATCGAAGATAGTGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGT 1140
                |||:|: |||||: |:   :||::|||::|:||:||
Db   792 AAAAAAAGAAAAAKAGAKAGAGKHMNKNMGKTMGTMMGTGKMMGKMGTMHMTMKMVMMM 733

Qy   1141 CTTTTTAGGGAATACAGTCACTTCTACTACTCCTCGGGACGAATAGAGTAGTATCGACTT 1200
                :|::: :|:::: : |::::|::   :|: |:|::.|:|::|::|||::::
Db   732 MMMMMMKKGKMMMMKMGKMMMKMMKMMMTMTGTMMMTMTM-MGKKKTMMTMKNBNK 674

Qy   1201 AGGAACGAGTGCAAAGATGCACAGCTTTGCGTTCTGCTGCTGAGAGCCATCTACTTCTA 1260
                :: |::| :|: ::|:: : :::::| :||: :|::::::
Db   673 MKKAGKKMNNANMKKNNKNKNAMNNNGKMNMNNNGKMMNMMKKKTKKKNNMKKNKNMKNMNM 614

Qy   1261 TGATCCCATAACTACAGATCATCCACAACAGTTACAGATGTCTTAAAAGTTAATGAGAC 1320
                :: : : :::   : ::::   :: ::
Db   613 KMGKMMGKAKAANNMKMMNNNKNMMNNNKNMMMKKMKMNKNKMKNMNNNNKKKKKM 554

Qy   1321 TCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCCACGAGAAAAGTTATC 1380
                : :   :::::   :::   :::   :::
Db   553 MKMNNMNGKKKMQKNNNNNAGKMKMKMMMMMMMNMMNNMNMMKKNNNNNMMKMMNN 494

Qy   1381 AGAGACAGAGGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACA 1428
                : :|:   :: : ::   :|:|||::|
Db   493 MNNNMMAMAMMMGNNNGKKMNNMMMKMGNGMMNANMMMAKKNAAAMNA 446

RESULT 8
AU263574/c
LOCUS   AU263574   391 bp   mRNA   linear   EST 10-MAY-2002
DEFINITION AU263574 vs Dictyostelium discoideum cDNA clone VSD160 5', mRNA
            sequence.
ACCESSION   AU263574
VERSION   AU263574.1 GI:20522372
KEYWORDS   EST.
SOURCE   Dictyostelium discoideum
  ORGANISM Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1 (bases 1 to 391)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE   Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished
COMMENT   Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES   Location/Qualifiers
     source   1..391
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSD160"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="IVS"
BASE COUNT   184 a   40 c   48 g   115 t   4 others
ORIGIN
Query Match   1.5%;   Score 44.8;   DB 9;   Length 391;
Best Local Similarity   46.7%;   Pred. No. 29;
Matches 136;   Conservative 0;   Mismatches 155;   Indels 0;   Gaps 0;

Qy   29 TTTCTTGACTTGTTCTCCTATTGGTGTATCTCTTAAAAATATTAAATTCAAAATCAAAGT 88
                ||||||||||||||||||||||||||||||||
Db   386 TTTTNAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAANTTTTAANTTAAATTTTANT 327

Qy   89 ATATATTTACAATGAAGCTCTTCTTCCCCAAGTTGTATTTCTACATTGGCTATTTTC 148
                ||||||||||||
Db   326 TTTTAATTTTTAATTTTTAATTTTTCTTAAATTTTTCTTTCAGTAATTGGT 267

Qy   149 CCTTGTCTATGATTGCTACCGGAGACAGTTTGGATTCAAGTGCGAGTTCGATGGGGAAT 208
                ||:||:
Db   266 CTATTTTTGAGATATTCTGCTACACCTTTATTAGATTCGAAATGTTCTTTCAAAGAATCT 207

Qy   209 AAAAAATGGTAATTTTTCAGTTGCTGGAGTCAGGAAGATGCTGGAACTACCTACCTATTT 268
                :: ||::|: |:|||
Db   206 AAATGTGGGAACTTACCATTGTATAAGAATCAGCAGCAAATGTAAAACATAACCAATG 147

Qy   269 AAGGGAAATGTCACTCTAGAAAAATATTCCTGAACAGCACAGGCACACGCAATCACA 319
                :: |||
Db   146 TATTCATAAGCAACATAAACATATAAATCAGCCAAAGTGTAAGAATTACCA 96

RESULT 9
AG088699/c
LOCUS   AG088699   720 bp   DNA   linear   GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-087L18.F, genomic survey sequence.
ACCESSION   AG088699
VERSION   AG088699.1 GI:16640501
KEYWORDS   GSS.
SOURCE   Pan troglodytes (chimpanzee)
  ORGANISM Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE   BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 720)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (B-mail:chimpbee@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT   Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
            PRIMERS
            Sequencing: -21M13
            LIBRARY
            Vector   : pKS145
            R.Site 1   : SacI
            R.Site 2   : SacI.
FEATURES   Location/Qualifiers
     source   1..720
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="PTB-087L18.F"
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT   284 a   139 c   119 g   168 t   10 others
ORIGIN
Query Match   1.5%;   Score 44.8;   DB 29;   Length 720;
Best Local Similarity   55.0%;   Pred. No. 32;
Matches 88;   Conservative 0;   Mismatches 72;   Indels 0;   Gaps 0;

Qy   7 TACCTAGTAGAGGTTGAGTGAATTTCTGACTTGTTCTCCTATTGGTGTATCTCTTAAA 66

Db   311 ||| || ||| ||||||| ||||||| ||||||| |||||| || ||| | || |||||||||||
          TATGTATTTGTTTTTGTTTTTGTTTGTTTGTTTGTTTGTTTTCATTCTCCTTAAC 252

Qy   67 ATATTAAATTCAAAATCAAAAGTATATATATTTTACAATGAAGTCTTCTTCCCCAAGTTTGT 126
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   251 AGAGTCATTTGCAGAGCAAAAGTTTTAAATGTTGATGTAGTTTGATTTCTCAAAATTTTC 192

Qy   127 ATTTTCTACATTTGCTATTTTCCCTTTGTCTATGATTGCT 166
          ||||| ||||||| |||||||
Db   191 ATTTATGGATCATGTTTTTGCTCCTAATGTCTAAGATTGTT 152

RESULT 10
AZ972038/c
LOCUS   AZ972038   2M0245E13R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0245E13 R, genomic survey sequence.   592 bp   DNA   linear   GSS 27-APR-2001
ACCESSION   AZ972038
VERSION   AZ972038.1 GI:13843265
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 592)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE   Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished
COMMENT   Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0245 row: E column: 13
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 592.
FEATURES   Location/Qualifiers
     source   1..592
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0245E13"
                     /sex="female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells

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BASE COUNT   222 a   92 c   114 g   164 t
ORIGIN   and selected for ampicillin resistance."

Query Match   1.5%; Score 44.6; DB 28; Length 592;
Best Local Similarity 53.8%; Pred: No.35;
Matches   92; Conservative   0; Mismatches   79; Indels   0; Gaps   0;

Qy   62 TTAAAATATTAAATACAAAATCAAAATCAAAGTATATATTTACAATGAAGTCTTCTTCCCCAAG 121
          |||| | |||||| ||||||| |||||||||||||||||||||||||||||||||||
Db   433 TTGTAACATAATTGAAATCAGAAAGTATTTTGTCTTTAACTTCGTTTCGTTTTCCTTTTCAAG 374

Qy   122 TTTGTATTTTCTACATTTGCTATTTCCCTTTGTCTATGATTGCTACCGAGACAGTTTG 181
          |||||||| |||||| | ||||||||| ||||||||||
Db   373 ATTGTTTTTTGTCCATTTGGAGCCTTGTATGGTTCCATATTTATTTTAGAATTACTTTG 314

Qy   182 GATTCAAGTGCGAGTTTCGATGGGAATAAAAATGGTAATTTTTCAGTTCGT 232
          ||||||||||||||||||| |||||||||||||||||
Db   313 GACTGGAGATATAGCTCAGAGGGTAAGAGAACTGACTCCTCTTCTGAAGGT 263

RESULT 11
CNS01AJ2
LOCUS   CNS01AJ2   Drosophila melanogaster genome survey sequence   1025 bp   DNA   linear   GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC
            BACNl1l1 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL104216
VERSION   AL104216.1 GI:5618827
KEYWORDS   GSS.
SOURCE   Drosophila melanogaster (fruit fly)
  ORGANISM Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 1025)
  AUTHORS   Genoscope.
  TITLE   Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT   Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES   Location/Qualifiers
     source   1..1025
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACNl1l11"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : T7"

BASE COUNT   148 a   88 c   6 g   522 t   261 others
ORIGIN

Query Match   1.5%; Score 44.4; DB 29; Length 1025;
Best Local Similarity 42.6%; Pred. No. 42;
Matches   52; Conservative   29; Mismatches   41; Indels   0; Gaps   0;

Qy   27 AATTTCTTGACTTGTTTCTCCTATTGGTGTATCTCTAAAATATTAAAATTCAAAATCAAA 86
          ::|::|:|:||| ::|::||| :::::|||::|:::::|||:||::|::
Db   600 MACHWTTYTAWMWTTAWYMWTWTTTTWTTTTWTMMACMAACMAATWWATTCACAATMMAA 659

Qy   87 GTATATATTTTACAATGAAGTCTTCTTCCCAAGTTGTATTTCTACATTTGCTATTT 146
          :|||:|:|::|:| |::|||:|||||||:|||::
Db   660 ATWTATWTWTYACATTTTTTYTTTTTTTYCAMTTCRTWATTATTATATTTWTWTYTTA 719

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Qy    147 TC 148
          :|:|
Db    720 YC 721

RESULT 12
BM881804/c
LOCUS       BM881804           450 bp    mRNA    linear   EST 25-APR-2002
DEFINITION  rb14b09.y1 Meloidogyne incognita egg pAMP1 Bird Meloidogyne
            incognita cDNA 5', mRNA sequence.
ACCESSION   BM881804
VERSION     BM881804.1  GI:19265548
KEYWORDS    EST.
SOURCE      Meloidogyne incognita (southern root-knot nematode)
ORGANISM    Meloidogyne incognita
            Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
            Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
REFERENCE   1  (bases 1 to 450)
AUTHORS     McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.
            , Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.
            , Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R.
            , Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
            ,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.
            , Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
            Wilson,R.
TITLE       The Washington Univ. Nematode EST Project, 1999
JOURNAL     Unpublished
COMMENT     Contact: McCarter JP
            The Washington Univ. Nematode EST Project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            The library was constructed by David Bird (david_bird@ncsu.edu).
            DNA Sequencing by: Washington University Genome Sequencing Center
            Seq primer: -40RP from Gibco
            High quality sequence stop: 402.
FEATURES             Location/Qualifiers
     source          1..450
                     /organism="Meloidogyne incognita"
                     /mol_type="mRNA"
                     /db_xref="taxon:6306"
                     /dev_stage="egg"
                     /lab_host="DH10B"
                     /clone_lib="Meloidogyne incognita egg pAMP1 Bird"
                     /note="Vector: pAMP1 (Gibco); Site_1: NotI; Site_2: SalI;
                     The library was provided by Dr. David Bird at North
                     Carolina State University, Raleigh, NC
                     (david_bird@ncsu.edu) The cDNA was made by using Dynabead
                     oligo-dT priming (Dynal). PCR based library using a
                     modified protocol from the SMART PCR cDNA Synthesis Kit
                     from Clontech. Directionally cloned into the UDG sites of
                     pAMP1."
BASE COUNT    193 a     29 c     61 g    167 t
ORIGIN

Query Match           1.5%;  Score 44;  DB 12;  Length 450;
Best Local Similarity 53.5%;  Pred. No. 45;
Matches  92;  Conservative  0;  Mismatches  80;  Indels  0;  Gaps  0;

Qy    56  TATCTCTTAAAATATTAAATTCAAAATCAAAGTATATATTTTACAATGAAGTCTTCTTTC  115
          ||||| ||||||||  |||  ||| |  | ||||| |||| ||  ||||||||||||||
Db   316  TATTTTGAGCATTCAAAACCAAAATCTCAAACCAAATTCTACTAAAATAATTTCTTCTCC  257

Qy   116  CCCAAGTTTGTATTTTCTACATTTGTATTTTCCCTTTGTCTATGATTGCTACCGAGACA  175
          ||||| ||| |||  ||||| | |||||| ||||| || |||| |||  |||||||
Db   256  AATATTTTGTTTAGTTCTTCCATTATTTGTTTCTTTAATTTATTTTATAGTTGCATAAACT  197

Qy   176  GTTTTGGATTCAAGTGCGAGTTCGATGGGAATAAAAATGGTAATTTTCAG  227
          |||||| |||| |||  | |||||| |||||||||||||||||| |
Db   196  TCTTTGAAATGTTCAAATCGTTAGAATCAACAAAAATTGTAAAAATTTTAG  145
```

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RESULT 13
BG602722/c
LOCUS       BG602722           498 bp    mRNA    linear   EST 14-AUG-2001
DEFINITION  EST501812 Plasmodium yoelii sporozoite cDNA Plasmodium yoelii cDNA
            clone PYCDJ76, mRNA sequence.
ACCESSION   BG602722
VERSION     BG602722.1  GI:15152736
KEYWORDS    EST.
SOURCE      Plasmodium yoelii
ORGANISM    Plasmodium yoelii
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 498)
AUTHORS     Kappe,S.H.I., Gardner,M.J., Brown,S.M., Ross,J., Matuschewski,K.,
            Ribeiro,J.M., Adams,J.H., Quackenbush,J., Cho,J., Carucci,D.J.,
            Hoffman,S.L. and Nussenzweig,V.
TITLE       Exploring the transcriptome of the malaria sporozoite stage
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9895-9900 (2001)
MEDLINE     21396555
PUBMED      11493695
COMMENT     Contact: Malcolm J. Gardner
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208
            Email: gardner@tigr.org
            Request for clones, please contact: Stefan Kappe,
            kappes01@popmail.med.nyu.edu Michael Heidelberger Division,
            Department of Pathology New York University School of Medicine.
FEATURES             Location/Qualifiers
     source          1..498
                     /organism="Plasmodium yoelii"
                     /mol_type="mRNA"
                     /strain="17XNL"
                     /db_xref="taxon:5861"
                     /clone="PYCDJ76"
                     /dev_stage="sporozoites from salivary gland"
                     /lab_host="E. coli TOP10"
                     /clone_lib="Plasmodium yoelii sporozoite cDNA"
                     /note="Vector: pCR4; TA cloning; Plasmodium yoelii
                     sporozoite cDNA library from salivary gland sporozoites 14
                     days post-infection"
BASE COUNT    220 a     55 c     60 g    163 t
ORIGIN

Query Match           1.5%;  Score 44;  DB 10;  Length 498;
Best Local Similarity 56.1%;  Pred. No. 46;
Matches  83;  Conservative  0;  Mismatches  65;  Indels  0;  Gaps  0;

Qy    15  AGAGGTTGAGTGAATTTCTTGACTTGGTGTTCTCCCATTGGTGTATCCTTAAAATATTAAA  74
          |||||| |||| ||||| ||| || || ||| ||||||| |||||||||||||||
Db   209  AGTGGTCTATTTATCTTTGTATTTTTTTAGCTCTTCTACATTCTTCAAATATTTTT  150

Qy    75  TTCAAAATCAAAGTATATATTTTACAATGAAGTCTCTTTCCCCAAGTTGTTGTATTTTCTA  134
          |||  ||||||||  |||||||||||||||| |||||||||||
Db   149  TATCAAATATACTACTTTTTTTTTTTTATTAAGTATATTTTTGCTAATTTCGTTTTTCGT  90

Qy   135  CATTTGCTATTTTCCCTTTGTCTATGAT  162
          ||||| |||||||| |||||||||||||
Db    89  TTATCGTTTCTTATATACTTTCTTTCAT  62

RESULT 14
BG602721/c
LOCUS       BG602721           593 bp    mRNA    linear   EST 14-AUG-2001
DEFINITION  EST501811 Plasmodium yoelii sporozoite cDNA Plasmodium yoelii cDNA
            clone PYCDJ76, mRNA sequence.
ACCESSION   BG602721
VERSION     BG602721.1  GI:15152735
KEYWORDS    EST.
SOURCE      Plasmodium yoelii
ORGANISM    Plasmodium yoelii
```

REFERENCE   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
             1 (bases 1 to 593)
AUTHORS   Kappe,S.H.I., Gardner,M.J., Brown,S.M., Ross,J., Matuschewski,K.,
             Ribeiro,J.M., Adams,J.H., Quackenbush,J., Cho,J., Carucci,D.J.,
             Hoffman,S.L. and Nussenzweig,V.
TITLE   Exploring the transcriptome of the malaria sporozoite stage
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9895-9900 (2001)
MEDLINE   21396555
PUBMED   11493595
COMMENT   Contact: Malcolm J. Gardner
             Department of Eukaryotic Genomics
             The Institute for Genomic Research
             9712 Medical Center Drive, Rockville, MD 20850, USA
             Tel: 301 838 3519
             Fax: 301 838 0208
             Email: gardner@tigr.org
             Request for clones, please contact: Stefan Kappe,
             kappes01@popmail.med.nyu.edu Michael Heidelberger Division,
             Department of Pathology New York University School of Medicine.
FEATURES   Location/Qualifiers
     source   1..593
                     /organism="Plasmodium yoelii"
                     /mol_type="mRNA"
                     /strain="17XNL"
                     /db_xref="taxon:5861"
                     /clone="PYCDJ76"
                     /dev_stage="sporozoites from salivary gland"
                     /lab_host="E. coli TOP10"
                     /clone_lib="Plasmodium yoelii sporozoite cDNA"
                     /note="Vector: pCR4; TA cloning; Plasmodium yoelii
                     sporozoite cDNA library from salivary gland sporozoites 14
                     days post-infection"

BASE COUNT   261 a   72 c   70 g   190 t
ORIGIN

Query Match   1.5%;   Score 44; DB 10; Length 593;
Best Local Similarity   56.1%;   Pred. No. 47;
Matches   83;   Conservative   0; Mismatches   65; Indels   0; Gaps   0;

Qy   15 AGAGGTTGAGTGAATTCTTGACTTGTTCTCCCATTGGTGTATCTCTTAAAATATTAAA 74
            ||||| |||||||||| | || || | ||| || | | ||| | ||||
Db   209 AGTGGTCTATTTTATCTTGTATTTTTTTTTAGCTCTTTTACATTTCTTCAAATATTTTT 150

Qy   75 TTCAAAATCAAAGTATATATTTACAATGAAGTCTTCTTTCCCCAAGTTGTATTTTCTA 134
            |||| ||| ||| | | ||| ||| ||| || || | || | || ||||
Db   149 TATCAAATATACTACTTTTTTTTTTATTAGTAATTAAGTTATTTTTGCTAATTCGTTTTTTCGT 90

Qy   135 CATTTGCTATTTTCCCTTGTCTATGAT 162
            ||||| || ||| || || | ||||
Db   89 TTATCGTTTTTCTTATACTTTTCTTTCAT 62

RESULT 15
BM160527/c
LOCUS   BM160527   735 bp   mRNA   linear   EST 04-DEC-2001
DEFINITION EST563050 PyBS Plasmodium yoelii yoelii cDNA clone PYCJS47 5' end,
            mRNA sequence.
ACCESSION   BM160527
VERSION   BM160527.1 GI:17306208
KEYWORDS   EST.
SOURCE   Plasmodium yoelii yoelii
  ORGANISM Plasmodium yoelii yoelii
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1 (bases 1 to 735)
AUTHORS   Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
            Fraser,C.M. and Carucci,D.J.
TITLE   Plasmodium yoelii EST project at TIGR
JOURNAL   Unpublished
COMMENT   Contact: Jane Carlton
            Parasite Genomics Group
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-530-9919

Fax: 301-838-0208
Email: carlton@tigr.org
For clone info, please contact the Malaria Research and Reference
Reagent Resource Center. ATCC
http://www.malaria.mr4.org/mr4pages/index.html
Seq primer: ADF.
FEATURES   Location/Qualifiers
     source   1..735
                     /organism="Plasmodium yoelii yoelii"
                     /mol_type="mRNA"
                     /strain="17XL"
                     /db_xref="taxon:73239"
                     /clone="PYCJS47"
                     /dev_stage="Asexual blood stages"
                     /lab_host="E. coli XL-1 Blue"
                     /clone_lib="PyBS"
                     /note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was
                     collected from BALB/cByJ mice infected with Py17XL
                     parasites, and leukocytes removed by passage over
                     microcrystalline cellulose columns. Total RNA was
                     isolated using the guanidinium isothiocyanate method, and
                     mRNA isolated using oligo(dT)-cellulose chromatography.
                     First strand cDNA synthesis was completed using a 50-base
                     primer and reverse transcriptase in the presence of
                     5-methyl dCTP. After second strand synthesis, uneven
                     termini were treated with Pfu DNA polymerase and EcoRI
                     adaptors ligated to the blunt ends. The sample was cleaved
                     with XhoI and separated on a Sephacryl S-500 column.
                     Size-fractionated cDNA was precipitated and ligated to
                     HybriZAP arms directionally using EcoRI-XhoI cleaved arms.
                     After packaging, the phagemid vector (pAD-GAL4) was
                     excised from the HybriZAP vector and plasmid DNA
                     isolated."

BASE COUNT   313 a   80 c   84 g   258 t
ORIGIN

Query Match   1.5%;   Score 44; DB 12; Length 735;
Best Local Similarity   56.1%;   Pred. No. 49;
Matches   83;   Conservative   0; Mismatches   65; Indels   0; Gaps   0;

Qy   15 AGAGGTTGAGTGAATTCTTGACTTGTTCTCCCATTGGTGTATCTCTTAAAATATTAAA 74
            ||||| |||||||||| | || || | ||| || | | ||| | ||||
Db   202 AGTGGTCTATTTTATCTTGTATTTTTTTTTAGCTCTTTTACATTTCTTCAAATATTTTT 143

Qy   75 TTCAAAATCAAAGTATATATTTACAATGAAGTCTTCTTTCCCCAAGTTGTATTTTCTA 134
            |||| ||| ||| | | ||| ||| ||| || || | || | || ||||
Db   142 TATCAAATATACTACTTTTTTTTTTATTAGTAATTAAGTTATTTTTGCTAATTCGTTTTTTCGT 83

Qy   135 CATTTGCTATTTTCCCTTGTCTATGAT 162
            ||||| || ||| || || | ||||
Db   82 TTATCGTTTTTCTTATACTTTTCTTTCAT 55

Search completed: December 16, 2003, 17:14:31
Job time : 5967 secs

OM nucleic - protein search, using frame_plus_n2p model

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GenCore version 5.1.6

Run on: December 16, 2003, 10:21:33 ; Search time 80.5 Seconds
(without alignments)
11830.552 Million cell updates/sec

Title: US-09-428-122-1
Perfect score: 5409
Sequence: 1 cgctcttacctagtagaggt.........tgtttgctaaaacactttc 3000

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop   6.0 , Fgapext 7.0
Delop   6.0 , Delext   7.0

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 2215726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09428122/runat_16122003_102127_10757/app_query.fasta_1.3143
-DB=A Geneseq_19Jun03 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09428122 @CGN_1_1_104 @runat_16122003_102127_10757 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
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24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4774	88.3	928	21	AAY94327	Chlamydia pneumoni
2	4760	88.0	928	20	AAW88421	Chlamydia pneumoni
3	3865	71.5	746	23	ABB90535	Chlamydia pneumoni
4	2997	55.4	597	20	AAY34611	Chlamydia pneumoni
5	2058	38.0	928	20	AAW88418	Chlamydia pneumoni
6	2048	37.9	928	23	ABB90573	Chlamydia pneumoni
7	2021	37.4	928	21	AAY90237	Chlamydia antigen
8	2006	37.1	918	21	AAY69369	Amino acid sequenc
9	2001	37.0	918	20	AAW88422	Chlamydia pneumoni
10	1993	36.8	914	20	AAW88429	Chlamydia pneumoni
11	1987.5	36.7	885	21	AAY90238	Mature Chlamydia a
12	1986	36.7	928	20	AAW88423	Chlamydia pneumoni
13	1982	36.6	928	23	ABB90542	Chlamydia pneumoni
14	1976	36.5	928	21	AAY90239	Chlamydia antigen
15	1965	36.3	936	21	AAY99842	Chlamydia pneumoni
16	1965	36.3	936	23	ABB90602	Chlamydia pneumoni
17	1946.5	36.0	925	21	AAY99843	Chlamydia pneumoni
18	1940	35.9	930	20	AAY35052	Chlamydia pneumoni
19	1936	35.8	930	23	ABB90548	Chlamydia pneumoni
20	1930	35.7	930	21	AAY90240	Chlamydia antigen
21	1927	35.6	930	20	AAW88424	Chlamydia pneumoni
22	1917.5	35.5	927	20	AAY35054	Chlamydia pneumoni
23	1915	35.4	926	23	ABP56019	Chlamydia psittaci
24	1915	35.4	926	23	ABB98228	Chlamydia polypept
25	1915	35.4	926	24	ABU66284	C. psittaci protei
26	1871	34.6	949	20	AAY35060	Chlamydia pneumoni
27	1855	34.3	928	20	AAW88417	Chlamydia pneumoni
28	1855	34.3	928	21	AAY90236	Chlamydia antigen
29	1855	34.3	928	23	ABB90583	Chlamydia pneumoni
30	1832	33.9	945	21	AAY69368	Amino acid sequenc
31	1811	33.5	945	20	AAW88428	Chlamydia pneumoni
32	1659.5	30.7	839	23	ABP56002	Chlamydia psittaci
33	1659.5	30.7	839	23	ABB98211	Chlamydia polypept
34	1659.5	30.7	839	24	ABU66267	C. psittaci protei
35	1580.5	29.2	841	23	AAY92818	Chlamydia pneumoni
36	1577.5	29.2	841	21	AAY92818	C. pneumoniae CPN1
37	1575.5	29.1	841	20	AAW88420	Chlamydia pneumoni
38	1572.5	29.1	643	20	AAY35056	Chlamydia pneumoni
39	1442.5	26.7	922	23	ABB90546	Chlamydia pneumoni
40	1437.5	26.6	922	21	AAY95548	Chlamydia pneumoni
41	1430.5	26.4	922	20	AAW88419	Chlamydia pneumoni
42	1417.5	26.2	922	20	AAY34597	Chlamydia pneumoni
43	1383.5	25.6	1407	23	ABB90541	Chlamydia pneumoni
44	1377.5	25.5	973	21	AAY96274	Chlamydia POMP91B
45	1377.5	25.5	973	23	ABB90527	Chlamydia pneumoni

ALIGNMENTS

RESULT 1
AAY94327
ID   AAY94327 standard; Protein; 928 AA.
XX
AC   AAY94327;
XX
DT   11-AUG-2000 (first entry)
XX
DE   Chlamydia pneumoniae 98kD putative outer membrane protein.
XX
KW   Chlamydia; antigen; vaccine; infection; outer membrane protein.
XX
OS   Chlamydia pneumoniae.
XX
PN   WO20026237-A2.
XX
PD   11-MAY-2000.
XX

PF 29-OCT-1999; 99WO-GB03579.
XX
PR 29-OCT-1998; 98US-0106070.
PR 01-MAR-1999; 99US-0122066.
PR 27-OCT-1999; 99US-0428122.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Murdin AD, Oomen RP, Dunn PL;
XX
DR WPI; 2000-365569/31.
DR N-PSDB; AAA27021.
XX
PT Novel Chlamydia 98 kDa putative outer membrane protein antigen, used
PT for vaccination and protection against Chlamydia infection -
XX
PS Claim 6; Fig 1; 93pp; English.
XX
CC The present sequence is the 98kDa putative outer membrane protein from
CC Chlamydia pneumoniae. The genomic sequence was amplified using two
CC PCR primers. The 5' primer contains a NotI restriction site, a ribosome
CC binding site, an initiation codon and a sequence close to the 5' end of
CC the 98kDa putative outer membrane protein coding sequence. The 3' primer
CC contains the sequence encoding the C-terminal sequence of the putative
CC outer membrane protein and a BsrGI restriction site. The stop codon was
CC excluded and an additional nucleotide was inserted to obtain an in-frame
CC C-terminal fusion with the Histidine tag. The PCR product was cloned
CC into a eukaryotic expression vector (pCA-Myc-His) by restricting both
CC the vector and the PCR product with NotI and BamHI and performing a
CC ligation reaction. This expression vector was injected intramuscularly
CC and intranasally into mice, which were subsequently inoculated with
CC Chlamydia pneumoniae. The chlamydial lung titers of the immunised mice
CC were lower than those of the controls. Thus the 98kDa putative outer
CC membrane protein can be used as a vaccine to provide protection against
CC Chlamydia infections, especially Chlamydia pneumoniae infections.
CC The present polypeptide may also be administered orally to treat
CC Chlamydia infection.
XX
SQ Sequence 928 AA;

Alignment Scores:
Pred. NO.:   0   Length: 928
Score: 4774.00   Matches: 928
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 88.26%   Indels: 0
DB: 21   Gaps: 0

US-09-428-122-1 (1-3000) x AAY94327 (1-928)

Qy 101 ATGAAGTCTTCTTTCCCCAAGTTTGTATTTTCTACATTTGCTATTTTCCCTTTGTCTATG 160
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Db   1 MetLysSerSerPheProLysPheValPheSerThrPheAlaIlePheProLeuSerMet 20

Qy 161 ATTGCTACCGAGACACAGTTTTTGGATTCAAGTGCGGAGTTTCGATGGGAATAAAAATGTAAT 220
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 IleAlaThrGluThrGlnPheLeuAspSerSerAlaSerPheAspTrpAsnLysAsnGlyAsn 40

Qy 221 TTTTCAGTTCGTGAGAGTCAGGAAGATGCTGGAACTACCTACCTATTTAAGGGAAATGTC 280
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 PheSerValArgGluSerGlnGluAspAlaGlyThrThrTyrLeuLysGlyAsnVal 60

Qy 281 ACTCTAGAAAATATTCCTGGAACAGGCACAGCAATCACAAAAAGCTGTTTAACACACT 340
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Db   61 ThrLeuGluAsnIleProGlyThrGlyThrAlaIleThrLysSerCysPheAsnAsnThr 80

Qy 341 AAGGGCGATTTGACTTTGCACAGTAACGGGAACTCTCATTGTTCCAAACGGTGGATGCA 400
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 LysGlyAspLeuThrLeuHisSerAsnGlyAsnSerLeuLeuPheGlnThrValAspAla 100

Qy 401 GGGACTGTTAGCAGGGGGCTGCGTTGTTAACGACGCAGCCTGGTAGATAAATCTACCACGTTTATA 460
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 101 GlyThrValAlaAlaGlyAlaAlaValAlaAsnSerSerValValAspLysSerThrThrPheIle 120

Qy 461 GGGTTTTCTTCGCTATCTTTATTGCTCTCCTGGAAGTTCGTAATACACCGGCAAGGA 520
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 GlyPheSerSerLeuSerPheIleAlaSerProGlySerSerIleThrArgLysLysGly 140

Qy 521 GCCGTTAGCTGCTCACGGTAGCTGAGTTGACAAAAATGTCAGTTGCTTCTCAGC 580
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 141 AlaValSerCysSerThrGlySerLeuThrLysAsnValSerLeuLeuPheSer 160

Qy 581 AAAAACTTTCAACGGATAATGGGGTGTATCACCGCAAAAACTCTTTCATTAACAGGG 640
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Db 161 LysAsnPheSerThrAspAsnGlyGlyAlaIleThrAlaLysThrLeuSerLeuThrGly 180

Qy 641 ACTACAATGTCAGCTCGTTTTCTGAAAATACCTCCTCAAAGAAGGGGAGCCATTCAG 700
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Db 181 ThrThrMetSerAlaLeuPheSerGluAsnThrSerSerLysGlyGlyAlaIleGln 200

Qy 701 ACTTCCGATGCCCTTACCATTACTGGAAACCAAGGAGGAGTCTCTTTTCTGACAATACT 760
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Db 201 ThrSerAspAlaLeuThrIleThrGlyAsnGlnGlyGlyValSerPheSerAspAsnThr 220

Qy 761 TCTTCGGATTCTGGAGCTGCAATTTTACAGAAGCCTCGGTGACTATTCTAATAATGCT 820
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 221 SerSerAspSerGlyAlaAlaIlePheThrGluAlaSerValThrIleSerAsnAsnAla 240

Qy 821 AAAGTTTCCTTTATTGACAATAAGGTCACAGGAGGCGAGCTCCTCAACACGGGGATATG 880
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Db 241 LysValSerPheIleAspAsnLysValThrGlyGlyAlaSerSerThrArgGlyAspMet 260

Qy 881 TCAGGAGGTGCTATCTGTGCTTATAAAACTAGTACAGATACTAAGGTCACCCTCACTGGA 940
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 261 SerGlyGlyAlaIleCysAlaTyrLysThrSerThrAspThrLysValThrLeuThrGly 280

Qy 941 AATCAGATGTTACTCTTCAGCAACATACATGACAACAGCGGGAGGAGCTATCTATGTG 1000
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 281 AsnGlnMetLeuLeuPheSerAsnAsnThrSerThrThrAlaGlyAlaIleTyrVal 300

Qy 1001 AAAAAGCTCGAACTGGCTTCCGGAGACTTACCCTATTCAGTAGAAATAGTGTCAATGGA 1060
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 LysLysLeuGluLeuAlaSerGlyGlyLeuPheSerArgAsnSerValAsnGly 320

Qy 1061 GGTACAGCTCCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCC 1120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 321 GlyThrAlaProLysGlyGlyAlaIleAlaIleGluAspSerGlyGluLeuSerLeuSer 340

Qy 1121 GCCGATAGTGGTGACATTGTCTTTAGGGAATACAGTCACTCTACTACTCCCTGGGACG 1180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 341 AlaAspSerGlyAspIleValPheLeuValPheLeuGlyAsnThrValThrSerThrProGlyThr 360

Qy 1181 AATAGAAGTAGTATCGACTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTGCT 1240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 AsnArgSerIleAspLeuGlyThrSerAlaLysMetThrAlaLeuArgSerAlaAla 380

Qy 1241 GGTGAGAGCCATCTACTTCTCATGATCCCATAACTACAGGATCATCCACAACAGTTACAGAT 1300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 381 GlyArgAlaIleTyrPheTyrAspProIleThrThrGlySerThrThrValThrAsp 400

Qy 1301 GTCTTAAAGTTAATGAGACTCCGGCAGATTCGCACTACAATATACAGGGAACATCATC 1360
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Db 401 ValLeuLysValAsnGluThrProAlaAspSerAlaLeuGlnTyrThrGlyAsnIleIle 420

Qy 1361 TTTCACAGGAGAAAAGTTATCAGAGACAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAG 1420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 PheThrGlyGluLysGlyLeuSerGluThrGluAlaAlaAspSerLysAsnLeuThrSerLys 440

Qy 1421 CTACTACAGCCTGTAACCTCTTTCAGGAGGTACCTCTATCTTTAAAACATGGAGTGGACTCTG 1480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 441 LeuLeuGlnProValThrSerPheGlnGlyValThrLeuSerLeuLysHisGlyValThrLeu 460

Qy 1481 CAGACTCAGGCATTCACTCAACAGGCAGATTCTGCTCGAAATGACGTAGGAACTACT 1540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 461 GlnThrGlnAlaPheThrGlnGlnAlaAspSerArgLeuGluMetAspValGlyThrThr 480

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Db   841 AspCysGlnAspAlaThrTyrAsnLeuThrLeuGlyTyrThrValAspLeuValArgSer  860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2681 AACCCGACTGTACGACACACTGCGAATTAGCGGTGATTCTTGGAAAACCTTCGGTACG   2740
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Db   861 AsnProAspCysThrThrLeuArgIleSerGlyAspSerTrpLysThrPheGlyThr    880
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Qy  2741 AATTGGCAAGACAAGCTTAGTCCTTCGTGCAGGGAACCATTTTGCTTAACTCAAT     2800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   881 AsnLeuAlaArgGlnAlaLeuArgArgAlaGlyAsnHisPheCysPheAsnSerAsn    900
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Qy  2801 TTTGAAGCCTTAGCCAATTTCTTTGAATTGCGTGGGTCATCTCGCAATTACCAATGTA   2860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 PheGluAlaPheSerGlnPheSerPheGluLeuArgGlySerSerArgAsnTyrAsnVal  920
         ||||||||||||||||||||||||||||
Qy  2861 GACTTAGGAGGACAAAATACCAATTC  2884
         |||||||||||||||||||||||
Db   921 AspLeuGlyAlaLysTyrGlnPhe   928
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RESULT 2
AAW88421
ID   AAW88421 standard; Protein; 928 AA.
XX
AC   AAW88421;
XX
DT   26-APR-1999 (first entry)
XX
DE   Chlamydia pneumoniae surface exposed protein Omp8.
XX
KW   Omp8; outer membrane protein 8; surface exposed protein; antigen;
KW   infection; diagnosis; vaccine; atherosclerosis; asthma.
XX
OS   Chlamydia pneumoniae.
XX
PN   WO9858953-A2.
XX
PD   30-DEC-1998.
XX
PF   19-JUN-1998;   98WO-DK00266.
XX
PR   23-JUN-1997;   97DK-0000744.
XX
PA   (BIRK/) BIRKELUND S.
PA   (CHRI/) CHRISTIANSEN G.
XX
PI   Birkelund S,   Christiansen G,   Knudsen K,   Madsen A;
PI   Mygind P;
XX
DR   WPI; 1999-105610/09.
DR   N-PSDB; AAX06820.
XX
PT   Species-specific test for identifying mammals infected with
PT   Chlamydia pneumoniae - comprises detecting antibodies specific for
PT   outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT   these proteins
XX
PS   Claim 7; Page 53-55; 115pp; English.
XX
CC   This polypeptide comprises the novel 90.0 kDa surface exposed
CC   protein Omp8 of the human respiratory pathogen Chlamydia
CC   pneumoniae. Its amino acid sequence was deduced from DNA (see
CC   AAX06820) isolated from a C. pneumoniae expression library. The
CC   invention provides 12 novel surface exposed proteins, Omp4-Omp15
CC   (see AAW88417-28), and nucleic acid sequences encoding them (see
CC   AAX06816-27). A new species specific test is claimed that is used
CC   to identify mammals (including humans) infected with Chlamydia
CC   pneumoniae. The test comprises detecting antibodies specific for
CC   Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC   membrane proteins, especially by PCR. The proteins are also used
CC   in the diagnosis of C. pneumoniae infection in mammals. The
CC   nucleic acids and proteins can also be used in the immunization of
CC   mammals, the nucleic acids being particularly useful as DNA
CC   vaccines for effecting in vivo expression of antigens. The

```
Qy  1541 CTAGAACCTGCTGATACGTAGCACCATAAACAATTGGTCATTAACATCAGTTCTATAGAC  1600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 LeuGluProAlaAspThrSerThrIleAsnAsnLeuValIleAsnIleSerSerIleAsp   500
Qy  1601 GGTGCAAAGAGGCAAAAATAGAAACCAAAGCTACGTCAAAAAATCTGACTTATCTGA     1660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501 GlyAlaLysLysAlaLysIleGluThrLysAlaThrSerLysAsnLeuThrLeuSerGly   520
Qy  1661 ACCATCACTTATTGGACCCGACGGGCACGTTTTATGAAAATCATAGTTTAAGAAATCCT   1720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521 ThrIleThrLeuLeuAspProThrGlyThrPheTyrGluAsnHisSerLeuArgAsnPro   540
Qy  1721 CAGTCCTACGACATCTTAGAGCTCAAAGCTTCTGGAACTGTAACAAGCACCGCAGTGACT  1780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GlnSerTyrAspIleLeuGluLeuLysAlaSerGlyThrValThrSerThrAlaValThr   560
Qy  1781 CCAGATCCTATAATGGGTGAGAAATTCCATTACGGCTATCAGGGAACTTGGGGCCCAATT  1840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   561 ProAspProIleMetGlyGluLysPheHisTyrGlyTyrGlnGlyThrTrpGlyProIle   580
Qy  1841 GTTTGGGGACAGGGGCTTCTACGACTTCAACCTTCAACTGACTAAAACTGCTATATT    1900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   581 ValTrpGlyThrGlyAlaSerThrThrAlaThrPheAsnThrSerThrGlyTyrIle    600
Qy  1901 CCTAATCCCGAGCGTATCGGCTCTTAGTCCCTAATAGCTTATGGAATGCATTTATAGAT  1960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 ProAsnProGluArgIleGlySerLeuValProAsnSerLeuTrpAsnAlaPheIleAsp   620
Qy  1961 ATTAGCTCTCCATTATCTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGACCGTGCT   2020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   621 IleSerSerLeuHisTyrLeuMetGluThrAlaAsnGluGluGlyLeuGlnGlyAspArgAla 640
Qy  2021 TTTTGGTGTGCTGGATTATCTAACTTCTTCCATAAGGATAGTACAAAAACCACGACGCCGGG 2080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   641 PheTrpCysAlaGlyLeuSerAsnPheHisLysAspSerThrLysThrArgArgGly    660
Qy  2081 TTTCGCCATTGAGTGGCCGGTTATGTCATAGGAGGAAAACCTACTACTTGTTCAGATAAG  2140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 PheArgHisLeuSerGlyGlyTyrValIleGlyGlyLysAsnLeuHisThrCysSerAspLys 680
Qy  2141 ATTCTTAGTGCTGCATTTGTCAGCTCTTGGAAGAGATAGAGACTACTTTGTAGCTAAG   2200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   681 IleLeuSerAlaAlaPheValSerGlnLeuPheGlyLysArgAspArgAspTyrPheValAlaLys 700
Qy  2201 AATCAAGGTACAGTCTACGGAGGAAACTTCTATTACCAGCACAACGAAACCTATATCTCT  2260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   701 AsnGlnGlyThrValTyrGlyGlyAsnPheTyrTyrGlnHisAsnGluThrTyrIleSer   720
Qy  2261 CTTCCTTGCAAACTACGGCCTTGTTCGTTCGTTCTATGTTCCTACAGAGATTCCTGTTCTC 2320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 LeuProCysLysLeuArgProCysSerLeuSerTyrValProThrGluIleProValLeu   740
Qy  2321 TTTTCAGGAAACCTTAGCTACACCCATACGGATAACGATCTGAAAACCAAGTATACAACA  2380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   741 PheSerGlyAsnLeuSerTyrThrHisThrAspAsnAspLeuLysThrLysTyrThrThr   760
Qy  2381 TATCCTACTGTTAAAGGAAGCTGGGGGGAATGAATGATGAGTTTCGGTTGGAAGGA     2440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   761 TyrProThrValLysGlySerTrpGlySerAspAspGluPheArgLeuGluGlyGlyArg   780
Qy  2441 GCTCCGATTGCTTAGAGAAGTGCTCTATTGAGCAGTACATGCCCCTTCATGAAATTG    2500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 AlaProIleCysLeuAspSerAlaLeuProPheGluGlnTyrMetProPheMetLysLeu   800
Qy  2501 CAGTTTGTCTATGCACATCAGGAAGGTTTAAAGAACAGGAACAGAAGCTCGTGAATTT   2560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   801 GlnPheValTyrAlaHisGlnGlyGluGlyPheLysGluGlyLeuThrGluAlaArgGluPhe 820
Qy  2561 GGAAGTAGCCGTCTTGTGAATCTCGGATCCCATTCGGATCCGATTTGATAAGGAAATCA  2620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   821 GlySerSerArgLeuValAsnLeuAlaLeuProIleArgPheAspLysGluSer       840
Qy  2621 GACTGCCAAGATGCAAGCTACAATCTAACTCTTGGTTATACTGTGGATCGTTCCTAGT   2680
```

CC   vaccines may also prevent atherosclerosis and bronchial asthma,
CC   which are possibly associated with C. pneumoniae.
XX
SQ   Sequence   928 AA;

Alignment Scores:
Pred. No.:   0   Length: 928
Score: 4760.00   Matches: 925
Percent Similarity: 99.68%   Conservative: 0
Best Local Similarity: 99.68%   Mismatches: 3
Query Match: 88.00%   Indels: 0
DB: 20   Gaps: 0

US-09-428-122-1 (1-3000) x AAW88421 (1-928)

Qy   101 ATGAAGTCTTCTTCCCAAGTTGTGATTTTCTACATTTGCTATTTTCCCTTGTCTATG 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MetLysSerSerPheProLysPheValPheSerThrPheAlaIlePheProLeuSerMet   20

Qy   161 ATTGCTACGGAGACAGTTTTGGATTCAAGTGCGGAGTTCGATGGGAATAAAAATGGTAAT 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   21 IleAlaThrGluThrValLeuAspSerSerAlaGluPheAspGlyAsnLysAsnGlyAsn   40

Qy   221 TTTTCAGTTCGTGAGAGTCAGGAAGATGCTGAGAACTACCTACCTATTTAAGGGAAATGTC 280
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   41 PheSerValArgGluSerGlnGluAspAlaGluAsnTyrLeuPheLysGlyAsnVal   60

Qy   281 ACTCTAGAAAAATATTCCTGGAACAGGCACAGCAATCACAAAAAGCTGTTTTAACACACT 340
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ThrLeuGluAsnIleProGlyThrGlyThrAlaIleThrLysSerCysPheAsnAsnThr   80

Qy   341 AAGGGCGATTTGACTTTCACAGGTAACGGCGAACTCTCTATTGTTCCAAACGGTGATGCA 400
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 LysGlyAspLeuThrPheThrGlyAsnGlyGluLeuSerIleValProAsnGlyAspAla 100

Qy   401 GGGACTGTAGCAGGGGCTGCGTGTTAACAGCAGCGGTGGTAGATAAATCTACCACGTTTATA 460
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   101 GlyThrValAlaGlyAlaAlaValAlaAsnSerSerValValAspLysSerThrThrPheIle 120

Qy   461 GGGTTTTCTTCGCTATCTTTAATTGCGTCTCCTCCGGAAGTTCGATAACTACCGGCCAAGGA 520
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GlyPheSerSerLeuSerPheIleAlaSerProGlySerSerIleThrThrGlyGlnGly 140

Qy   521 GCCGTTAGCTGCTCTACGGGTAGCTTGAGTTGACAAAAAATGTCAGTTGCTTCTTCAGC 580
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 AlaValSerCysSerThrGlySerPheGluLeuAspLysAsnValSerLeuLeuPheSer 160

Qy   581 AAAAACTTTTCAACGGATAATGGGCGTGCTATCACCGGCAAAAACTCTTTCATTAACAGGG 640
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   161 LysAsnPheSerThrAspAsnGlyArgAlaIleThrGlyLysAsnSerPheIleAsnGly 180

Qy   641 ACTACCAAATGTCAGCTCTGTTTTCTGAAAAATACCTCCTCAAAGAAGGCGGAGCCATTCAG 700
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ThrThrMetSerAlaLeuPheSerGluLysThrSerSerLysLysGlyGlyAlaIleGln 200

Qy   701 ACTTCCGATGCCCTTACCATTACTGGAAACCAAGGGAAGTCTCTTTTTCTGACAATACT 760
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   201 ThrSerAspAlaLeuThrIleThrGlyAsnGlnGlyLysSerLeuPheSerAspAsnThr 220

Qy   761 TCTTCGGATTCTGAGCTGCAATTTTACAGAAGCCTCCGTGACTATTTCTAATAATGCT 820
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   221 SerSerAspSerGlyAlaAlaIlePheThrGluAlaSerValThrIleSerAsnAsnAla 240

Qy   821 AAAGTTCCTTATTGACATAAGTCACAGGAGCGCCTCCAACACACGGGGGATATG 880
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 LysValSerPheLeuAspAsnLysValThrGlyAlaSerSerSerThrThrGlyAspMet 260

Qy   881 TCAGGAGGTGCTATCTGTCTTATAAAACTAGTACAGATACTAAGGTCACCCCTCACTGGA 940
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   261 SerGlyGlyAlaIleCysLeuTyrLysThrSerThrAspThrLysValThrLeuThrGly 280

Qy   941 AATCAGATGTTACTTCTTCAGCAACAATACAATCGAACAATGCAAAACACGACGCGGG 1000
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   281 AsnGlnMetLeuLeuPheSerAsnAsnThrSerThrThrAlaGlyGlyAlaIleTyrVal 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1001 AAAAAGCTCGAACTGGCTCCGGAGGACTTACCCTATTCAGTAGAAATAGTGTCAATGGA 1060

Db   301 LysLysLeuGluLeuAlaSerGlyLysLeuThrLeuPheSerArgAsnSerValAsnGly 320

Qy 1061 GGTACAGCTCCTAAAGGTGAGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCC 1120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   321 GlyThrAlaProLysGlyGlyAlaIleAlaIleGluAspSerGlyGluLeuSerLeuSer 340

Qy 1121 GCCGATAGTGCTGACATTGTCTTTTAGGGAATACAGTCACTTCACTACTCCTGGGACG 1180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   341 AlaAspSerGlyAspIleValPheLeuGlyAsnThrValThrSerThrThrProGlyThr 360

Qy 1181 AATAGAAGTAGTATCGACTTAGGAACGAGTGCAAAGATGACAGCTTTGGGTTCTGCTGCT 1240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 AsnArgSerSerIleAspLeuGlyThrSerAlaLysMetThrAlaLeuArgSerAlaAla 380

Qy 1241 GGTAGAGCCACTCCACTTCTATGATCCCATAACTACAGGATCATCCACAACAGTTACAGAT 1300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   381 GlyArgAlaThrProLeuTyrAspProIleThrThrGlySerThrValThrThrAsp 400

Qy 1301 GTCTTAAAGTAATGACTCCGGCAGATTCTGCACTACAATATCAGGAACATCATC 1360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   401 ValLeuLysValAsnGluThrProAlaAspSerAlaLeuGlnTyrThrGlyAsnIleIle 420

Qy 1361 TTCACAGGAGAAAAGTATCAGACAGAGACAGAGGCCGCAGATTCTAAAAATCTTACTTCCAAG 1420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 PheThrGlyGluLysSerGluThrGluLeuAlaAlaAspSerLysSerAsnLeuThrSerLys 440

Qy 1421 CTACTACAGCCTGTAACTTCTTCAGGAGTGCTACTCTATCTTAAAACATGGAGTGACTCTG 1480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   441 LeuLeuGlnProValThrSerSerGlyValLeuLeuTyrLeuLysHisLysGlyValThrLeu 460

Qy 1481 CAGACTCAGGCATTCACTCAACAGGCCAGATTCTCGTCTCGAAATGGACGTAGGAACTACT 1540
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   461 GlnThrGlnAlaPheThrGlnGlnAlaArgPheSerSerArgAsnGlyMetAspValGlyTyrThrThr 480

Qy 1541 CTAGAACCTGCTGATACTACAGCCACCATAAACAATTGGTCATTAACATCATCTATAGAC 1600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 LeuGluProAlaAspThrSerThrIleAsnAsnLeuValIleLeuAsnIleSerSerIleAsp 500

Qy 1601 GGTGCAAAGAGGCAAAAATAGAAACCAAAGTCACGTCAAAAAATCTGACTTTATCTGA 1660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   501 GlyAlaLysLysAlaLysIleGluThrLysValThrSerLysLysAsnLeuThrLeuSerGly 520

Qy 1661 ACCATCACTTTATTGGACCCGACGGCACGTTTTATGAAATCATAGTTTAAGAAAATCCT 1720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   521 ThrIleThrLeuLeuAspProThrGlyThrPheTyrGluAsnHisSerSerLeuArgAsnPro 540

Qy 1721 CAGTGCCTACGACATCTTAGAGCTCAAAGCTTCTGGAACGTAACAAGCCGCAGTGACT 1780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GlnSerTyrAspIleLeuGluLeuLysAlaSerGlyThrValThrSerThrAlaValThr 560

Qy 1781 CCAGATCCATAATGGGTGAGAAATTCCATTACCGGCTATCAGGGAACTTGGGGCCCCATT 1840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   561 ProAspProIleMetGlyGluLysPheHisTyrGlyTyrGlnGlyThrThrGlyProIle 580

Qy 1841 GTTTGGGGACCAGGGGCTTCACGGGCTTCAAAGCTTCAACCTTGACTAAAACTGGCTATATT 1900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   581 ValTrpGlyThrGlyAlaSerThrArgAlaThrPheAsnThrArgLysThrGlyTyrIle 600

Qy 1901 CCTAATCCCGAGCGTATCCGTCCTTGAGACCTACCTTATGGAATGCATTATAGAT 1960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 ProAsnProGluArgIleGlySerLeuValProAsnSerLeuTrpAsnAlaPheIleAsp 620

Qy 1961 ATTAGCTCTCCATTATCTTATGGAGACTGCAAACGGTTGCAGAAGGGTTGCAGGGGAGACCGTGCT 2020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   621 IleSerSerIleHisThrTyrLeuMetGluThrAlaAsnGluGlyLeuGlnGlyLysAspArgGlyAla 640

Qy 2021 TTTTGGTGTGCTGGATTATCTAACTTCTTCCATAAGGATAGTACAAAAACACGACGCGGG 2080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   641 PheTrpCysLysAlaGlyLeuSerAsnPheHisHisLysAspSerThrLysSerThrArgArgGly 660

```
Qy  2081 TTTCGCCATTTGAGTGGGCGGTTATGTCATAGAGGAGAAACCTACATACTTGTTCAGATAAG 2140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 PheArgHisLeuSerGlyGlyTyrValIleGlyGlyTyrAsnLeuHisThrCysSerAspLys  680

Qy  2141 ATTCTTAGTGCTGCATTTTGTCAGCTCTTGGAAGAGATAGAGACTACTTGTAGCTAAG 2200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   681 IleLeuSerAlaAlaPheCysGlnLeuPheGlyArgAspArgAspTyrPheValAlaLys  700

Qy  2201 AATCAAGGTACAGTCTACGAGGAGAACTCTCTATTACCAGCACAACGAAACCTATATCTCT 2260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   701 AsnGlnGlyThrValTyrGlyGlyThrLeuTyrTyrGlnHisAsnGluThrTyrIleSer  720

Qy  2261 CTTCCTTGCAAACTACGGCCTTGGTTGTCTTATGTTCCTACAGAGATTCCTGTTCTC 2320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 LeuProCysLysLeuArgProCysSerLeuSerTyrValProThrGluIleProValLeu  740

Qy  2321 TTTTCAGGAAACCTTAGCTACACCCCATACGGATAACGATCTGAAAACCAAGTATACAACA 2380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   741 PheSerGlyAsnLeuSerTyrThrHisTyrAspAsnAspLeuLysThrLysTyrThrThr  760

Qy  2381 TATCCTACTGTTAAAGGAAGCTGGGGAATAGATAGTTCGCTTTAGAATTCGGTGGAAGA 2440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   761 TyrProThrValLysGlySerTrpGlyAsnAspSerPheAlaLeuGluPheGlyGlyArg  780

Qy  2441 GCTCCGATTTGCTTAGATGAAAGTGCTCATTTGAGCAGTACATGCCCTCATGAAAATTG 2500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 AlaProIleCysLeuAspGluSerAlaLeuPheGluGlnTyrMetProPheMetLysLeu  800

Qy  2501 CAGTTTGTCTTATGCACATCAGGAAGGTTTAAAGAACAGGGAACAGAAGCTCGTGAATTT 2560
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   801 GlnPheValTyrAlaHisGlnGluGlyPheLysGlyGlnGlyThrGluAlaArgGluPhe  820

Qy  2561 GGAAGTACAGCCGTCTTGTGAATCTTGGCTTACCTATCGGGATCCGATTTGATAAGGAATCA 2620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   821 GlySerSerArgLeuValAsnLeuAlaLeuProIleGlyIleArgPheAspLysGluSer  840

Qy  2621 GACTGCCAAGATGCAACGTACAATCTAACTCTTGGTTATACTGTTGGTACTCTTGTTCGTAGT 2680
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 AspCysGlnAspAlaThrTyrAsnLeuThrLeuGlyTyrThrValGlyThrLeuValArgSer  860

Qy  2681 AACCCCGACTGTACGACAACACTGGGAATTAGCCGGTGATTCTTGGAAAACCTTCGGTACG 2740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   861 AsnProAspCysThrThrThrLeuArgIleSerArgGlyAspSerTrpLysThrPheGlyThr  880

Qy  2741 AATTTGGCAAGACAAGCTTTAGTCCTTCGTGCAGGAGAACCATTTTTGCTTTAACTCAAAT 2800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   881 AsnLeuAlaArgGlnAlaLeuValLeuArgAlaGlyAsnHisPheCysPheAsnSerAsn  900

Qy  2801 TTTGAAGCCTTAGCCAATTTTCTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTA 2860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 PheGluAlaPheSerGlnPheSerPheGlueuArgGlySerSerArgAsnTyrAsnVal  920

Qy  2861 GACTTAGGAGCAAAATACCAATTC 2884
         ||||||||||||||||||||||||
Db   921 AspLeuGlyAlaLysTyrGlnPhe  928
```

RESULT 3
ABB90535
ID   ABB90535 standard; Protein; 746 AA.
XX
AC   ABB90535;
XX
DT   29-JUL-2002 (first entry)
XX
DE   Chlamydia pneumoniae cp0015 protein, SEQ ID NO:19.
XX
KW   Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KW   human respiratory disease; cardiovascular disease; atherosclerosis;
KW   coronary artery disease; carotid artery stenosis; myocardial infarction;
KW   cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW   strain CWL029.
XX

OS   Chlamydia pneumoniae.
XX
PN   WO0202606-A2.
XX
PD   10-JAN-2002.
XX
PF   03-JUL-2001; 2001WO-IB01445.
XX
PR   03-JUL-2000; 2000GB-0016363.
PR   11-JUL-2000; 2000GB-0017047.
PR   21-JUL-2000; 2000GB-0017983.
PR   07-AUG-2000; 2000GB-0019368.
PR   18-AUG-2000; 2000GB-0020440.
PR   14-SEP-2000; 2000GB-0022583.
PR   10-NOV-2000; 2000GB-0027549.
PR   22-DEC-2000; 2000GB-0031706.
XX
PA   (CHIR-) CHIRON SPA.
XX
PI   Ratti G, Grandi G;
XX
DR   WPI; 2002-154726/20.
DR   N-PSDB; ABL91193.
XX
PT   Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT   medicament for treatment or prevention of infection due to Chlamydia,
PT   preferably Chlamydia pneumoniae, and for diagnostic purposes -
XX
PS   Claim 1; Page 49-50; 364pp; English.
XX
CC   Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
CC   pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
CC   them. The proteins are predicted to be immunogenic and may therefore be
CC   useful in vaccine production and for diagnostic purposes. Chlamydia
CC   pneumoniae is a common cause of respiratory disease in humans, and is
CC   also involved in the development of cardiovascular diseases such as
CC   atherosclerosis, coronary artery disease, carotid artery stenosis,
CC   myocardial infarction, cerebrovascular disease, aortic aneurysm,
CC   claudication and stroke. The proteins and nucleic acids of the invention
CC   may be used in vaccines and pharmaceutical compositions for the
CC   prevention or treatment of chlamydial infections, particularly Chlamydia
CC   pneumoniae infections. The proteins may also be used in the detection of
CC   Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
CC   DNA probe assay or blotting techniques for determining Chlamydia
CC   pneumoniae gene expression. The present sequence represents a
CC   specifically claimed Chlamydia pneumoniae protein of the invention.
XX
SQ   Sequence   746 AA;

Alignment Scores:
Pred. No.:   1.71e-309   Length: 746
Score: 3865.00   Matches: 746
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 71.45%   Indels: 0
DB: 23   Gaps: 0

US-09-428-122-1 (1-3000) x ABB90535 (1-746)

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Qy   647 ATGTCAGCTCTGTTTCTGAAATACCTCCTCAAAGAAGAAGGCGGAGCCATTCAGACTTCC 706
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MetSerAlaLeuPheSerGluAsnThrSerSerLysLysGlyGlyAlaIleGlnThrSer  20

Qy   707 GATGCCCTTACCATTACTGGAAACCAAGGGGAAGTCTCTTTTCTGACAATACTTCCTCG 766
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21 AspAlaLeuThrIleThrGlyAsnGlnGlyGluValSerPheSerAspAsnThrSerSer  40

Qy   767 GATTCTGGAGCTGCAATTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTT 826
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    41 AspSerGlyAlaAlaIlePheThrGluAlaSerValThrIleSerAsnAsnAlaLysVal  60

Qy   827 TCCTTTATTGACAATAGGTCACAGGAGCGAGCTCCTCAACACGGGGGATATGTCAGGA 886
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   61  SerPheIleAspAsnLysValThrGlyAlaSerSerSerThrGlyAspMetSerGly   80

Qy  887  GGTGCTATCTGTGCTTATAAAACTAGTACAGATACTAAGGTCACCCTACACTGAAAATCAG   946
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81  GlyAlaIleCysAlaTyrLysThrSerThrAspThrLysValThrLeuThrGluAsnGln   100

Qy  947  ATGTTACTCTTCAGCACAATACATCGACAACACAGCGGAGGAGCTATCCATGCATGTGAAAAAG  1006
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  101  MetLeuLeuPheSerAlaAsnThrSerThrThrAlaGlyGlyAlaIleSerTyrValLysLys  120

Qy 1007  CTCGAACTGGCTTCCGGAGGACTTACCCTATTCAGTAGAAATAGTGTCAATGGGAGTACA  1066
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  LeuGluLeuAlaSerGlyGlyLeuThrLeuPheSerValGluThrValAlaAsnSerValAlaAsnSerGlyGlyThr  140

Qy 1067  GCTCCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGAT  1126
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  141  AlaProLysGlyGlyAlaIleAlaIleGluAspSerGlyGluLeuSerLeuSerAlaAsp  160

Qy 1127  AGTGGTGACATTGTCTTTTAGGGATACAGTCACTTCTACTACCTCCTGGGACGAAATAGA  1186
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  161  SerGlyAspIleValPheLeuGlyTyrAsnThrValThrSerThrThrProGlyThrAsnArg  180

Qy 1187  AGTAGTAATCGACTTAGGAACGAGTGCAAAGATGACAGCTTGCCTTCTGCTGCTGGTAGA  1246
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  SerSerIleAspLeuGlyThrSerAlaLysMetThrAlaLeuArgSerAlaAlaGlyArg  200

Qy 1247  GCCATCTACTTCTATGATCCCATAACTAACTACAGGATCATCCACAACAGTTACAGATGTCTTA  1306
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  201  AlaIleTyrPheTyrAspProIleThrThrGlySerThrThrValThrAspValLeu  220

Qy 1307  AAAGTTAATAGAGACTCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACA  1366
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  221  LysValAsnArgAspSerGlyArgPheCysThrThrIleTyrArgGlyAsnIleIlePheThr  240

Qy 1367  GGAGAAAGTTATCAGAGACAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTA  1426
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  GlyGluSerTyrGlnArgGlnArgProGlnIleLeuLysIleLeuLeuArgSerTyrTyr  260

Qy 1427  CAGCCGTAACCTCTTTCAGGAGGTACTCCATCTTCTTTAAAAACATGAGTGACCTGCAGAT  1486
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  261  GlnProValThrSerLeuSerGlyTyrSerIlePheLeuLysHisMetSerAspLeuGlnThr  280

Qy 1487  CAGGCATTCACTCAACAGGCAGATTCGTCCTCGAAATGGACTAGGAACTACTCCTAGAA  1546
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  281  GlnAlaPheThrGlnGlnAlaAspSerSerSerArgLeuValAspGlyThrThrLeuGlu  300

Qy 1547  CCTGCTGATACTGACCATAAAACAATTTGGTCATTAAACATCAGTTCTATAGACGCGTGCA  1606
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  ProAlaAspThrSerThrIleAsnAsnAsnLeuValIleSerSerIleSerIleAspSerGlyAla  320

Qy 1607  AAGAAGGCAAAAAATAGAAACCAAAGCTACGTCAAAAAATCTGACTTTATCTGGAACCATC  1666
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  321  LysLysAlaLysIleGluThrLysAlaThrSerLysAsnLeuThrLeuSerGlyThrIle  340

Qy 1667  ACTTTATTGGACCCGACGGGCACGTTTTATGAAAATCATAGTTTAAGAATCCTCAGTCC  1726
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  341  ThrLeuLeuAspProThrGlyThrPheTyrGluAsnHisSerLeuArgAsnProGlnAsnSer  360

Qy 1727  TACGACATCTTAGAGCTCAAAGCTTCAACCTTCAACTGACTGTAACAAGCACCGCAGTGACTCCAGAT  1786
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  TyrAspIleLeuGluLeuLysAlaSerGlyThrValThrSerThrAlaValThrProGlnAsp  380

Qy 1787  CCTATAAATGGGTGAGAAATTCCATTACGGCTATCAGGGAACTGGGGCCCAATTGTTTGG  1846
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  381  ProIleMetGlyValGluLysPheHisTyrArgLeuTyrGlnGlyTrpTrpProIleValTrp  400

Qy 1847  GGGACAGGGGCTTCTACGACTGCAACCTTCAACTGACTAAAAACTGGCTATATTCCTAAT  1906
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  401  GlyThrGlyAlaSerThrThrAlaThrPheAsnTrpThrLysThrTyrIleProAsn  420

Qy 1907  CCCGAGCGTATCGGCGTCCTTAGTCCCTAATGGCATTTATGGAATGCATTTATAGATATTAGC  1966
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  ProGluArgIleGlySerLeuValProAsnSerLeuTrpAsnAlaPheIleAspIleSer  440
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Qy 1967  TCTCTCCATTATCTTATGGAGACTGCAAACGAAGGGTGCAGGGAGGAGACCGTGCTTTTGG  2026
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  441  SerLeuHisTyrLeuMetGluThrAlaAsnGluGlyLeuGlnGlyLeuAspArgAlaPheTrp  460

Qy 2027  TGTGCTGATATCTAACTTCTTCCATAAGGATAGTACAAAAACACGACCGCGGGTTTCGC  2086
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  461  CysAlaGlyLeuSerAsnPhePheHisLysAspSerThrLysThrArgArgGlyPheArg  480

Qy 2087  CATTTGAGTGGGGTTATGTCATAGGAGGAAACCTACACTCTGTTGTTCAGATAAGATTCTT  2146
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  HisLeuSerGlyGlyTyrValIleGlyGlyAsnLeuHisThrCysSerAspLysIleLeu  500

Qy 2147  AGTGCTGCATTTGTCAGCTCTTGGAAGAGATAGAGACTACTTGTAGCTAGAATCAA  2206
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  501  SerAlaAlaPheCysGlnLeuLeuGluGlyArgAspArgAspTyrPheValAlaLysAsnGln  520

Qy 2207  GGTACAGTCTACGGAGGAACTCTCATTACCAGCACAACGAAACCTATATCTCTTTCCT  2266
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  521  GlyThrValTyrGlyGlyThrLeuTyrTyrGlnHisIleAsnGluThrTyrIleSerLeuPro  540

Qy 2267  TGCAAACTACGGCCTTGTCTGTGTCTTATGTTCCTACAGAGATCCTATTCGGTGGAAGAGCTCCG  2326
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  CysLysLeuArgProCysSerLeuSerTyrValProThrGluIleProValLeuPheSer  560

Qy 2327  GGAAACCTTAGCTACCACCCATACGGATAACGATCTGAAAACCAAGTATACAACATATCCT  2386
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  561  GlyAsnLeuSerTyrThrHisThrAspAsnAspLeuLysThrLysTyrThrThrTyrPro  580

Qy 2387  ACTGTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTAGAATTCGGTGGAAGAGCTCCG  2446
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  581  ThrValLysGlySerTrpGlyAsnAspSerPheAlaLeuGluPheAlaSerGluSerAspCys  600

Qy 2447  ATTTGCTTAGATGAAAGTGCTCATTGGACAGTACATGCCCTTCATGAAATTGCAGTTT  2506
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  IleCysLeuAspGluSerAlaLeuProPheGluGlnPheMetProPheMetLysLeuGlnPhe  620

Qy 2507  GTCTTATGCACATCAGGAAGGTTTAAAGAACAGGGAACAGAAGCTCGTGAATTTGAAGT  2566
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  621  ValTyrAlaHisGlnGluGlyPheLysGluGlnGlyThrGluAlaArgGluPheGluGlySer  640

Qy 2567  AGCCGTCTTGTGAATCTTGCCTACCATCGGGATCCGATTGATAAGGAATCAGAGCTGC  2626
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  641  SerArgLeuValAsnLeuAlaLeuProIleGlyIleArgPheAspLysGluSerAspCys  660

Qy 2627  CAAGATGCAACGTACAATCTAACTCTTGGTTATACTCTGGATCTCGTTCGTAGTAACCCCC  2686
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661  GlnAspAlaThrTyrAsnLeuThrLeuGlyTyrThrLeuAspLeuValArgSerAsnPro  680

Qy 2687  GACTGTACGACAACACTGCGAATTAGCGGTGATTCTTGGAAAACCTTCGGTACGAATTTG  2746
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  681  AspCysThrThrThrLeuArgIleSerGlyAspSerTrpLysThrPheGlyThrAsnLeu  700

Qy 2747  GCAAGACAAGCTTTAGTCCTTCGTGCAGGAGAACCATTTTGCTTTAACTCAAATTTGAA  2806
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  701  AlaArgGlnAlaLeuValLeuArgAlaGlyGluProPheCysPheAsnSerAsnPheGlu  720

Qy 2807  GCCTTTAGCCAATTTCTTTTGAATTGGCTGGGTCATCTCGCAATTACAATTACAATGTAGACTTA  2866
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721  AlaPheSerGlnPheSerPheGluLeuArgGlySerSerArgAsnTyrAsnValAspLeu  740

Qy 2867  GGAGCAAAATACCAATTC  2884
         ||||||||||||||||||
Db  741  GlyAlaLysTyrGlnPhe  746
```

DE   Chlamydia pneumoniae transmembrane protein sequence.
XX
KW   Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW   sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW   vaccine; neutralising epitope.
XX
OS   Chlamydia pneumoniae.
XX
PN   WO9927105-A2.
XX
PD   03-JUN-1999.
XX
PF   20-NOV-1998;   98WO-IB01890.
XX
PR   04-NOV-1998;   98US-0107078.
PR   21-NOV-1997;   97FR-0014673.
XX
PA   (GEST) GENSET.
XX
PI   Griffais R;
XX
DR   WPI; 1999-357842/30.
XX
PT   Genome sequence of Chlamydia pneumoniae.
XX
PS   Page 632-633; Disclosure; 1912pp; English.
XX
CC   AAY34584-Y35879 represent the proteins encoded by all the open reading
CC   frames in the complete genome (see AAX91990) of Chlamydia pneumoniae.
CC   C. pneumoniae causes respiratory disease such as pneumonia and
CC   bronchitis and is thought to be a contributing factor in heart
CC   disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC   nodosum or pharyngitis. The polypeptides encoded by the open reading
CC   frames of the C. pneumoniae genome (see AAY34611) can be used in
CC   immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC   nucleotides sequences can also be used as immunogenic compositions,
CC   especially where the vector directs the expression of a neutralising
CC   epitope of C. pneumoniae.
XX
SQ   Sequence   597 AA;

Alignment Scores:
Pred. NO.:   4.85e-238   Length: 597
Score: 2997.00   Matches: 596
Percent Similarity: 99.67%   Conservative: 0
Best Local Similarity: 99.67%   Mismatches: 1
Query Match: 55.41%   Indels: 2
DB: 20   Gaps: 0

US-09-428-122-1 (1-3000) x AAY34611 (1-597)

Qy   544 CTTGAGTTGACAAAAAATGTCAGTTTGCTCCTTCAGCAAAAACTTTCAACGGATAATG 603
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 LeuGluPheAsp-LysAsnValSerLeuLeuPheSerLysAsnPheSerThrAspAsnGl 20

Qy   604 CGGTGCTATCACCGCAAAAACTCTTCATTAACAGGACTACAATGTCAGCTCTTGTTTTC 663
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   20 yGlyAlaIleThrAlaLysThrLeuHisSerLeuThrGlyThrThrMetSerAlaLeuPheSe 40

Qy   664 TGAAAATACCTCCCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTACCATTAC 723
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   40 rGluAsnThrSerLysLysGlyGlyAlaIleGlnThrSerAspAlaLeuThrIleTh 60

Qy   724 TGGAAACCAAGGGAAGTCTCTTTTTCTGACAATACTTCTTCGGATTCTCGGAGCTGCAAT 783
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   60 rGlyAsnGlnGlyLysSerLeuPheSerAspAsnThrSerSerAspSerGlyAlaAlaIl 80

Qy   784 TTTTACAGAGCCTCGGTGACTATTCTAATAATGCTAAAGTTCCTTTATTGACAATAA 843
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80 ePheThrGluAlaSerValThrIleSerAsnAsnAlaLysValSerPheIleAspAsnLy 100

Qy   844 GGTCACAGGAGCGAGCTCCTCAACAACGGGGGATATGTCAGGAGGTGCTATCTGTGCTTA 903
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   100 sValThrGlyAlaSerSerThrThrGlyAspMetSerGlyGlyAlaIleCysAlaTy 120
Qy   904 TAAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAAATCCACTGATGTTACTCTCAGCAA 963
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   120 rLysThrSerThrAspThrLysValThrLeuThrGlyLysAsnGlnMetLeuLeuSerSerAs 140

Qy   964 CAATACATCGACAACAGCGGGAGGAGCATCTCATGTGAAAAAGCTCGAACTGGCTTCCGG 1023
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   140 nAsnThrSerThrThrAlaGlyGlyAlaIleSerGluLysLysLeuGluLeuAlaSerGl 160

Qy   1024 AGGACTTACCCTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCTAAAGGTGGAGC 1083
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   160 yGlyLeuThrLeuPheSerArgAsnSerValAsnGlyGlyThrAlaProLysGlyGlyAl 180

Qy   1084 CATAGCTATCGAAGATAGTGGGAATGGGTTATCCGCCGATAGTGGTGACATTGTCTT 1143
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   180 aIleAlaIleGluAspSerGlyLeuSerLeuSerAlaAspSerGlyAspIleValPh 200

Qy   1144 TTTAGGGAATACAGTCACTTCTACTACTCCTGGGACGAATAGAAGTAGTATCGACTTAGG 1203
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   200 eLeuGlyAsnThrValThrSerThrThrProGlyThrAsnArgSerSerIleAspLeuGl 220

Qy   1204 AACGAGTGCAAAGATGACAGCTTTGGCGTTCTGCTGCTGGTGCTGGTAGAGCCATCTACTTCTATGA 1263
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   220 yThrSerAlaLysMetThrAlaLeuArgSerAlaAlaGlyArgAlaIleTyrPheTyrAs 240

Qy   1264 TCCCATAACTACAGGATCATCCACAACAGTTACAGATGTTCTTAAAAGTAATGAGACTCC 1323
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   240 pProIleThrThrGlySerThrThrValThrAspValLeuLysValAsnGluThrPr 260

Qy   1324 GGCAGATTCTGACTACAATACAGGGAACATCATCTTCACAGGAGAAAAGTTATCAGA 1383
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   260 oAlaAspSerAlaLeuGlnTyrThrGlyAsnIleIlePheThrGlyGluLysSerGl 280

Qy   1384 GACAGAGGCGCAGATTCTAAAAATCTTACTTCTGAAGCTACTACAGCCTGTAACTCTTTC 1443
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   280 uThrGluAlaGlnIleLeuLysAsnLeuThrSerLysSerLeuLeuGlnProValThrLeuSe 300

Qy   1444 AGGAGGTACTCCTATCTTTAAAACATGAGGTGACTGACTCGCAGACTCACTCACTCCAACA 1503
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   300 rGlyGlyThrLeuSerLeuLysHisGlyValThrLeuGlnThrGlnAlaPheThrGlnGl 320

Qy   1504 GGCAGATTCTCGTCTCGAAATGACGTAGGAACTACTCTAGAACCTGCTGATACTAGCAC 1563
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   320 nAlaAspSerArgLeuGluMetAspValGlyThrThrLeuGluProAlaAspThrSerTh 340

Qy   1564 CATAAAACAATTTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGAAGGCAAAAATAGA 1623
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   340 rIleAsnAsnLeuValIleAsnIleSerSerIleAspGlyAlaLysLysAlaLysIleGl 360

Qy   1624 AACCAAAGCTACGTCAAAAAATCTGACTTAATCTGACTTATTGGACCCGAC 1683
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   360 uThrLysAlaThrSerLysAsnLeuThrLeuSerGlyThrIleThrLeuLeuAspProTh 380

Qy   1684 GGGCACGTTTATGAAAATCATAGTTTAAGAAATCCTCAGTCCTACGACATCTTAGAGCT 1743
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   380 rGlyThrPheTyrGluAsnHisSerLeuArgAsnProGlnSerTyrAspIleLeuGluLe 400

Qy   1744 CAAAGCTTCTGGAACTGTAACAAGCACCGCAGTGACTCCAGATCCTATAATGGGTGAGAA 1803
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   400 uLysAlaSerGlyThrValThrSerThrAlaValThrProAspProIleMetGlyGluLy 420

Qy   1804 ATTCCATTACGGCTATCAGGGAACTTGGGGCGCCAATTGTTGGGGACAGCAGGGCTTCTAC 1863
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   420 sPheHisTyrGlyTyrGlnGlyThrTrpGlyProIleValTrpGlyThrAlaSerTh 440

Qy   1864 GACTCGCAACCTTCAACTGGACTAAAACTGGCTAAATTCCTAATCCCGAGCGGTATCGGCTC 1923
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   440 rThrArgAsnLeuGlnLeuAspTyrLysThrGlyTyrTyrIleProAsnProGluArgIleGlySe 460

Qy   1924 TTTAGTCCCTAATAGCTTATCGAATGCATTTATAGATATTAGCTCTTCCATTATCTTAT 1983
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   460 rLeuValProAsnSerLeuTrpAsnAlaPheIleAspIleSerSerLeuHisTyrIleLeuMe 480

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CC   Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC   membrane proteins, especially by PCR.  The proteins are also used
CC   in the diagnosis of C. pneumoniae infection in mammals.  The
CC   nucleic acids and proteins can also be used in the immunization of
CC   mammals, the nucleic acids being particularly useful as DNA
CC   vaccines for effecting in vivo expression of antigens.  The
CC   vaccines may also prevent atherosclerosis and bronchial asthma,
CC   which are possibly associated with C. pneumoniae.
XX
SQ   Sequence   928 AA;

Alignment Scores:
Pred. No.:                                 928
Score:                 1.24e-160           Matches:            444
Percent Similarity:    2058.00             Conservative:       142
Best Local Similarity: 61.68%              Mismatches:         320
Query Match:           46.74%              Indels:              44
DB:                    38.05%              Gaps:                20
                       20

US-09-428-122-1 (1-3000) x AAW88418 (1-928)
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```
Qy      101 ATGAAGTCTCTTTCCCAAGTTTGTATTT---TCTACATTTGCTATTTTC---------- 148
                |||||||| ||          ||||| |   ||| |||    ||||||| |||
Db        1 MetLysSerGlnPheSerTrpLeuValLeuSerThrLeuAlaCysPheThrSerCys  20

Qy      149 CCTTTGTCTATGATTGCTACCGAGACAGTTTTGGATTCAAGTGCGAGTTTCGATGGGAAT 208
                |||||| ||          :||      |||:::
Db       21 SerThrValPheAlaAlaThrAlaGluAsnIleGlyProSerPheAspGlySer  40

Qy      209 AAAAAT--GGTAATTTTCAGTTCGTGAGAGTCAGGAAGATGCTGAACTACCTACCTA 265
                |||| |  |||||||:||||:||       |||
Db       41 ThrAsnThrGlyThrThrProLysAsnThr------ThrThrGlyIleAspTyrThr  58

Qy      266 TTTAAGGGAAATGTCACTCTAGAAAAATATTCCTGGAACAGGACAGCAATCACAAAAAGC 325
                ||:::||||||||:||||:::||||:||:||
Db       59 LeuThrGlyIleAspIleThrLeuGlnAsnLeu---GlyAspSerAlaAlaLeuThrLysGly  77

Qy      326 TGTTTTAACAACACTAAGGGCGATTTGACTTTCACAGGTAACGGTAACGGGAACTCTCATTGTTC 385
                ||:::::||:|||::|||      ||||:||||||||||
Db       78 CysPheSerAspThrThrGluSerPheAlaGlyLyLysGlyTyrSerLeuSerPhe  97

Qy      386 CAAACGGTGGCGGATGCAGGACTGCGGGGCTGCGTTAACAGCAGCGTGGTAGATAAA 445
                |||   :: ::     ::||
Db       98 LeuAsnIleLysSer---SerAlaGluGlyAlaAlaLeu--SerValThrThrAspLys 115

Qy      446 TCTACCACGTTTATAGGGTTTCTGCTATCTTTTATTGCGTCTCCTGGAAGTTCGATA 505
                ||: :: ||||||:|||||||    |:||:||:||
Db      116 AsnLeuSerLeuThrGlyPheSerSerLeuThrPheLeuAlaAlaProSerSerValIle 135

Qy      506 ACTACC----------GGCAAAGGAGCCGTTAGCTGCTCTACGGGTAGTTTGACTTTGACAAA 559
                :||||:          ::|||||||||:||:||||||||||
Db      136 ThrThrProSerGlyLysGlyLysGlyAlaValIleCysGly--GlyAspLeuPheAspAsn 154

Qy      560 AATGTCAGTTGCTCTTCAGCAAAAACTTTCAACGGATAATGGCGGTGCTATCACCGCA 619
                ||| |||||||||||||| :::: ||||| |||||||
Db      155 AsnGlyThrIleLysGlnLeuPheLysGlnAspThrCysGlyAlaIleSerThr 174

Qy      620 AAAACTCTTCATTAACACGGACTACAAATGTCAGCTCGTTTCTGAAAATACCTCCTCA 679
                ||||||||| ||||||        ::|||   |||:||:|||
Db      175 LysAsnLeuSerLeuLysAsnSerThrGlySerIleSerPheGluGlyLysAsnLysSerSer 194

Qy      680 --------AAGGAAGGCGGAGCCATTCAGACTTCCGATGCCCTTACCATTACTTGGAAAC 730
                        :: ||:||||||||||:||| |||:::||||||
Db      195 AlaThrGlyIleLysLysGlyLysGlyAlaIleCysAlaThrGlyThrValAsnIleThrAsnAsn 214

Qy      731 CAAGGGGAAGTCTCTTTTCTGACAATACTTCTTCGGATTCTGGAGCTGCAATTTTACA 790
                ||||| |||||||||||:|||        ||||:::|||
Db      215 ThrAlaProThrLeuPheSerAsnAsnIleAlaAlaGluAlaLeuGlyAlaIleAsnSer 234

Qy      791 GAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTCCTTATTGACAAATAAGGTCACA 850
                |||||||||| |||||| ||::|||        |:::|||
Db      235 ThrGlyAsnCysThrIleThrGlyAsnThrSerLeuValPheSerGluAsnSerValThr 254
```

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Qy     1984 GGAGACTGCAAACGAAGGGGTGCAGGGAGGACCGTGCTTTTTGGTGTGCTGGAATTATCTAA 2043
                ||||||||||||| |||||||||||||||||||||||| |||||||||||||||||||
Db      480 tGluThrAlaAsnGluGlyLeuGlnGlyAsnGlyAspArgAlaPheThrArgAlaGlyLeuSerAs  500

Qy     2044 CTTCTTCCATAAGGATAGTACAAAAACACGACGCGGGTTTCGCCATTGAGTGCGGGTTA 2103
                |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db      500 nPhePheHisLysAspSerThrLysThrArgArgGlyPheArgHisLeuSerGlyGlyTy  520

Qy     2104 TGTCATAGGAGGAGAAACCTACACTGTTCAGATAAGAGATTCTTAGTGCTGCATTTGTCA 2163
                |||||||||||||||||| ||||||||||||||| ||||||||||||||||||||||
Db      520 rValIleGlyGlyAsnLeuHisThrCysSerAspLysIleLeuSerAspLysAlaPheCysGl  540

Qy     2164 GCTCTTTGGAAGAGATAGAGACTACTTGTAGCTAAGAATCA-AGTACAGTCTACGGAG 2222
                ||||| ||||||| ||||||||||| |||||||||||||| |||| ||||||||||
Db      540 nLeuPheGlyArgArgAspTyrPheValAlaLysAsnGlnArgTyrSerLeuArgAr  560

Qy     2223 GAACTCTCATTACCACGACACAACGAAACCTATATCTCTTCCTTGCAAACTACGGCCTT 2282
                |||||||||||||||||||||||||| |||||||||||||||||||| ||||||||||
Db      560 gAsnSerLeuLeuProAlaGlnArgAsnLeuTyrLeuSerSerLeuGlnThrThrAlaLe  580

Qy     2283 GTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCCTTTTTCAGGAAAACCT 2334
                |||||||||||||||||||||||| |||||||||||||||||||||
Db      580 uPheValValLeuCysSerTyrArgAspSerCysSerLeuPheArgLysPro  597
```

```
RESULT 5
AAW88418
ID   AAW88418 standard; Protein; 928 AA.
XX
AC   AAW88418;
XX
DT   26-APR-1999 (first entry)
XX
DE   Chlamydia pneumoniae surface exposed protein Omp5.
XX
KW   Omp5; outer membrane protein 5; surface exposed protein; antigen;
KW   infection; diagnosis; vaccine; atherosclerosis; asthma.
XX
OS   Chlamydia pneumoniae.
XX
PN   WO9858953-A2.
XX
PD   30-DEC-1998.
XX
PF   19-JUN-1998;   98WO-DK00266.
PR   23-JUN-1997;   97DK-0000744.
XX
PA   (BIRK/)  BIRKELUND S.
PA   (CHRI/)  CHRISTIANSEN G.
XX
PI   Birkelund S,  Christiansen G,  Knudsen K,  Madsen A;
PI   Mygind P;
XX
DR   WPI; 1999-105610/09.
DR   N-PSDB; AAX06817.
XX
PT   Species-specific test for identifying mammals infected with
PT   Chlamydia pneumoniae - comprises detecting antibodies specific for
PT   outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT   these proteins
XX
PS   Claim 7; Page 43-45; 115pp; English.
XX
CC   This polypeptide comprises the novel 97.2 kDa surface exposed
CC   protein Omp5 of the human respiratory pathogen Chlamydia
CC   pneumoniae.  Its amino acid sequence was deduced from DNA (see
CC   AAX06817) isolated from a C. pneumoniae expression library.  The
CC   invention provides 12 novel surface exposed proteins, Omp4-Omp15
CC   (see AAW88417-28), and nucleic acid sequences encoding them (see
CC   AAX06816-27).  A new species specific test is claimed that is used
CC   to identify mammals (including humans) infected with Chlamydia
CC   pneumoniae.  The test comprises detecting antibodies specific for
```

```
Qy   851 GGAGCGAGCTCCTCAACAACGGGGGATAATGTCAGGAGGTGCTATCTGTGCTTATAAAACT 910
             ::;||    ||||||||||
Db   255 ----------AlaThrAlaGly------AsnGlyGlyAlaLeu------------------- 263

Qy   911 AGTACAGATACTAAGGTCACCCTCACTGTGCTTGAAATCAGATGTTACTCTTCAGCAACAATACA 970
         ||||||:|||  |:||:;|||||||  ::  |||||:|  |||
Db   264 SerGlyAspAlaAspValThrLeuThrValPheSerValThrPheSerGlyAsnGln 283

Qy   971 TCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTCC------GGA 1024
         :;;  ||:::|||  ||||||||||||
Db   284 AlaValAlaAsnGlyGlyAlaIleTyrAlaLysLysLeuThrLeuAlaSerGlyGlyGly 303

Qy  1025 GGACTTACCCTATTCAGTAGAAATAGTGTCAATGAGGTGCAGCTCCTAAAGGTGGAGCC 1084
         |||       ||   |||||||||
Db   304 GlyGlyIleSerPheSerAsnAlaValGlnGlyThrThrAlaGlyAsnGlyGlyAla 323

Qy  1085 ATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGTCTTT 1144
         ||;::|||  ||||||||||  ::::|:||:|||||||
Db   324 IleSerIleLeuAlaAlaGluGluCysSerLeuSerAlaGluAlaGlyAspIleThrPhe 343

Qy  1145 TTAGGGAATAACAGTCACTTCTACTACTCCT---GGGACGAATAGAAGTAGTATCGACTTA 1201
             ||||||||||| || |||:||
Db   344 AsnGlyAsnAlaIleValAlaThrThrProGlnThrThrLysArgAsnSerIleAsnIle 363

Qy  1202 GGAACGAAGTGCAAAGATGACCAGCTTGCGTTCTCGCTGCTGTAGCCCATCTACTTCTAT 1261
         ||||||:|||||  ||||:|  ||||||  :;  |||||  |||||||
Db   364 GlySerThrAlaLysIleThrAsnLeuArgPheSerGlyHisSerIlePhePheTyr 383

Qy  1262 GATCCCATAACTACAGGATCATCCACAACAGTTACAGATGTCTTAAAAGTTAATGAGACT 1321
         ||||||||||    ::::|||  |||||:|||
Db   384 AspProIleThrAlaAlaAsnThrAlaAlaAspThrLeuAsnLeuAsnLysAla 403

Qy  1322 CCGGCAGATTCTGACTACAATATACAGGAACATCATCTTCACAGGAGAAAAGTTATCA 1381
             :;||||||  ||||||||:|  ||:::|
Db   404 AspAlaGlyAsnSerThrAspTyrSerGlyIleValPheSerGlyGluLysLeuSer 423

Qy  1382 GAGACAGAGGCCGACAGATTCTAAAAATCTTAACTTCACTACTACAGCCTGTAACTCTT 1441
         :::||| ||||||   |||||||||
Db   424 GluAspGluAlaLysValAlaAlaAspAsnLeuThrSerLeuGlnProValThrLeu 443

Qy  1442 TCAGGAGGTACTCTATCTTAAAAACATGAGTGACTCTGCAGACTCAGGCATTCACTCAA 1501
            :;|||||  |||||||  |||||:|||  ;:||||:|||||
Db   444 ThrAlaGlyAsnLeuLeuLysArgGlyValThrAlaLeuAspThrLysGlyPheThrGln 463

Qy  1502 CAGGGCAGATTCTCGTCTCGAAATGGAGAGGAAACATGAGAACTACTCTAGAACCTGCT--GATACT 1558
         ||| :::   :;   |||||||||:::  ||||||||:;  ||||||||| 
Db   464 ThrAlaGlySerSerValIleMetAspAlaGlyThrThrLeuLysAlaSerThrGluGlu 483

Qy  1559 AGCACCATAAACAATTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGAAGGCAAAA 1618
         |||     |||  ::  ||| |||||
Db   484 ValThrLeuThrGlyLeuSerIleProValAspSerLeuGlyLysLeuLysValVal 503

Qy  1619 ATAGAAAACCAAAGCTACGTCAAAAAATCATGACTTTATCTGGAACCATCACTTATTGGAC 1678
         |||;::;||||||  :||  |||||||:|
Db   504 IleAlaAlaSerAlaAlaSerLysAsnValAlaLeuAlaGlyProIleLeuLeuLeuAsp 523

Qy  1679 CCGAGGGCACGTTTTATGAAAATCATAGTTTAAGAAAATCCAGTCCAGCACATCTTA 1738
         |||  :||| ||:||||||
Db   524 AsnGlnGlyAsnAlaTyrGluAsnHisAspSerLeuGlyLysGlyLysGlnThrGln 543

Qy  1739 GAGCTCAAAGCTTCTGGAACTGTACAAGCACCGCAGTGACTCCAGATCCTATAATGGGT 1798
         :::|| ||||||||||||  ::  |||  ;:
Db   544 GlnLeuSerAlaLeuGlyThrAlaThrThrThrAspValProAlaValProThrValAla 563

Qy  1799 GAGAAATTCCATTACGGCTATCAGGAGAACTTGGGCGCCCCAATTGTTGG------- 1846
         |||||:;|| ||||||||||  :;   |||||||||  :|:||
Db   564 ThrProThrHisThrTyrGlyTyrGlnGlyThrTrpGly-- 582

Qy  1847 ---GGGAGCGGGCTTCTACGGACTTCAACTGGACTAAAACTGGCTATATTCCT 1903
                ::  |||   |||||||||:::||
Db   583 AlaSerGlnAlaThrProLysThrAlaThrLeuAlaThrLeuAlaTrpThrLysThrGlyTyrIleProPro 602

Qy  1904 AATCCCGAGCGTATCGGCTTCCTTAGTCCCTAATAGCTTATGGAAATGCATTTATAGATATT 1963
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```
Db   603 AsnProGluArgGlnGlyProLeuValProAsnSerLeuTrpGlySerPheSerAspIle 622

Qy  1964 AGCTCTCCATTATCTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGACCGTGCTTTT 2023
             ::;:::     ||||||||||
Db   623 GlnIleAlaIleGlnIleGlyValIleGluValSerAlaLeuThrCysAspAspArgGlyPhe 642

Qy  2024 TGGTGTGCTGGATTATCTAACTCTTCCATAAGGATAGTACAAAAACACGACGCGGGGTTT 2083
            ||||:|||||||  |||||||
Db   643 TrpAlaAlaGlyValAlaAsnPheLeuAspLysAspLysGlyGlyGluLysArgLysTyr 662

Qy  2084 CGGCCATTGAGTGGCGGTTATGTCATAGGAGGAGAAACCATACTGTTCAGATAAGATT 2143
         ||||||||||||||||||  :;|||
Db   663 ArgHisLysSerGlyValGlyTyrAlaIleGlyValGlyAlaAlaGlnThrCysSerGluAsnLeu 682

Qy  2144 CTTAGTGCTGCATTTGTCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAAT 2203
         ||:::;||||||:||  |||||||||
Db   683 IleSerPheAlaPheCysGlnLeuPheGlySerAspLysAspPheLeuValAlaLysAsn 702

Qy  2204 CAAGGTACAGTCTACGGAGGAACTCTATTACCAGCACAACGAACCTATATCTCTCTT 2263
         |||||||||||  ::;|||||||||
Db   703 HisThrAspThrTyrAlaGlyAlaPheTyrIleGlnHis-------IleThrGlu 718

Qy  2264 CCTTGCAAACTACGGCCTTGTTCGTTGCTTATGTTCCT-----ACAGAGATTCCT 2314
            ||||||||||||  :;     :;|||
Db   719 CysSerGlyPheIleGlyCysLeuLeuAspLysLeuProGlySerTrpSerHisLysPro 738

Qy  2315 GTTCTCTTTTCAGGAAACCTTAGCTACACACCCATACGGATAACGATCTGAAAACCAAGTAT 2374
         :::::;   |||||  |||||
Db   739 LeuValLeuGluGluGlyGlnLeuGlnLeuAlaTyrSerHisValSerAsnAspLeuLysThrLysTyr 758

Qy  2375 ACAACATATCCTACTGTTAAAGGAGGCTGGGGAATGATGAGTTTCGCTTTAGAATTCGGT 2434
         ||  :;|||||||||||||  |||||
Db   759 ThrAlaTyrProGluValLysGlyGlyTrpGlyAsnAlaPheAsnMetLeuGly 778

Qy  2435 GGAAGAGCTCCGATTTGCTTAGATGAAAGTGCTCTATTGGACAGTAGCCCTTCATG 2494
         |||||||||||||||:;||  ||||||||
Db   779 AlaSerSerHisSerTyrProGluTyrLeuHisCysPheAspThrTyrAlaProTyrIle 798

Qy  2495 AAATTGCAGTTTGTCTCATGCACATCAGGAAGGTTTTAAAGAACAGAGAAGCTCGT 2554
         |||       ||:::||||:||||||
Db   799 LysLeuAsnLeuThrTyrIleArgGlnAsnAspSerPheSerGluLysGlyGlyThrGluGlyLysArg 818

Qy  2555 GAATTTGGAAGTAGCCGTCTTGTGAATCTGCCTACCTATCGGATCCGATTGATAAG 2614
         ||||:;|||||||||  :::  ||||||||||
Db   819 SerPheAlaAspSerAsnLeuAsnLeuProIleGlyValIleLysPheGluLys 838

Qy  2615 GAATCAGAGTGCCAAGATGCCAAGTACAATCAATCTAACTCTTGGTTATACTGTGGATCTTGTT 2674
         ||||||||||  ||||||::|||  |||
Db   839 PheSerAspCysAsnAspPheSerTyrAspLeuThrLeuSerTyrValProAspLeuIle 858

Qy  2675 CGTAGTAACCCCGACTGTACGACACACTGGATTCTTGGAAAACCTTC 2734
         |||:::;|| |||||||||:::|||||
Db   859 ArgAsnAspProLysCysThrThrAlaLeuLeuValIleLeuGlyLysTrpGluThrTyr 878

Qy  2735 GGTACGAATTTGGCAAGACAAGCTTTAGTCCTTCCGTGCAGGGAACCATTTTGCTTAAC 2794
         |||||||:;||||||:;|||  :::|||||
Db   879 AlaAlaAsnLeuAlaArgGlnAlaLeuGlnValIleSerGlyAlaSerTrpTyrTrpTyr 898

Qy  2795 TCAAATTTGAAGCCTTTAGCCAATTTCTTTTGAATTGCTTGGTGGTCATCCGCAATTAC 2854
         :::||||||||||||||||  :::|||||
Db   899 ProMetPhePheGluValLeuGlyLeuValPheGluValPheGlyHisGlnPheIleTyr 918

Qy  2855 AATGTGACTTAGGAGGCAAAATACCAATTC 2884
         |||       :;||:||||||
Db   919 AsnValAlaSerLeuGlyLysPheGlnPhe 928
```

RESULT 6
ABB90573
ID   ABB90573 standard; Protein; 928 AA.
XX
AC   ABB90573;
XX

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DT   29-JUL-2002 (first entry)
XX
DE   Chlamydia pneumoniae cp0010 protein, SEQ ID NO:95.
XX
KW   Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KW   human respiratory disease; cardiovascular disease; atherosclerosis;
KW   coronary artery disease; carotid artery stenosis; myocardial infarction;
KW   cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW   strain CWL029.
XX
OS   Chlamydia pneumoniae.
XX
FH   Key            Location/Qualifiers
FT   Peptide        1..25
FT                  /label= Signal_peptide
FT   Protein        26..928
FT                  /note= "Mature protein"
XX
PN   WO2002602606-A2.
XX
PD   10-JAN-2002.
XX
PF   03-JUL-2001; 2001WO-IB01445.
XX
PR   03-JUL-2000; 2000GB-0016363.
PR   11-JUL-2000; 2000GB-0017047.
PR   21-JUL-2000; 2000GB-0017983.
PR   07-AUG-2000; 2000GB-0019368.
PR   18-AUG-2000; 2000GB-0020440.
PR   14-SEP-2000; 2000GB-0022583.
PR   10-NOV-2000; 2000GB-0027549.
PR   22-DEC-2000; 2000GB-0031706.
XX
PA   (CHIR-) CHIRON SPA.
XX
PI   Ratti G, Grandi G;
XX
DR   WPI; 2002-154726/20.
DR   N-PSDB; ABL91231.
XX
PT   Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT   medicament for treatment or prevention of infection due to Chlamydia,
PT   preferably Chlamydia pneumoniae, and for diagnostic purposes -
XX
PS   Claim 1; Page 87-88; Page 364pp; English.
XX
CC   Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
CC   pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
CC   them. The proteins are predicted to be immunogenic and may therefore be
CC   useful in vaccine production and for diagnostic purposes. Chlamydia
CC   pneumoniae is a common cause of respiratory disease in humans, and is
CC   also involved in the development of cardiovascular diseases such as
CC   atherosclerosis, coronary artery disease, carotid artery stenosis,
CC   myocardial infarction, cerebrovascular disease, aortic aneurysm,
CC   claudication and stroke. The proteins and nucleic acids of the invention
CC   may be used in vaccines and pharmaceutical compositions for the
CC   prevention or treatment of chlamydial infections, particularly Chlamydia
CC   pneumoniae infections. The proteins may also be used in the detection of
CC   Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
CC   DNA probe assay or blotting techniques for determining Chlamydia
CC   pneumoniae gene expression. The present sequence represents a
CC   specifically claimed Chlamydia pneumoniae protein of the invention.
XX
SQ   Sequence 928 AA;

Alignment Scores:
Pred. No.:             8.27e-160    Length:              928
Score:                 2048.00      Matches:             442
Percent Similarity:    61.68%       Conservative:        144
Best Local Similarity: 46.53%       Mismatches:          320
                                    Indels:              44
Query Match:           37.86%       Gaps:                20
DB:                    23
```

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US-09-428-122-1 (1-3000) x ABB90573 (1-928)

Qy     101 ATGAAGTCTTCTTCCCCAAGTTTGTATTT--TCTACATTTGCTATTTC--------- 148
           |||||||||| ||  ||       || |    |||
Db       1 MetLysSerGlnPheSerTrpLeuValLeuSerThrLeuAlaCysPheThrSerCys   20

Qy     149 CCTTTGTCTATGATTGCTACCGAGACAGTTTGGATTCAAGTGCCAGTTTCGATGGGAAT 208
           |||||  ::  |||         |||         |::::||||:|||||
Db      21 SerThrValPheAlaAlaThrAlaGluAsnIleGlyProSerPheAspGlySer      40

Qy     209 AAAAAT--GGTAATTTTCAGTTCGTGGAGAGTCAGGAAGATGCTGGAACTACCTACCTA 265
           |||   |  ||    ||:  :: ::  ::
Db      41 ThrAsnThrGlyThrThrProLysAsnThr-----ThrThrGlyIleAspTyrThr    58

Qy     266 TTTAAGGGAAATGTCACTCTAGAAAATATTCCTGAACAGCACAGCAATCACAAAAAGC  325
           ||||||||||||||::::||:::||||:|  |||       ||||||||:|
Db      59 LeuThrGlyAspIleThrLeuGlnAsnLeu--GlyAspSerAlaAlaLeuThrLysGly 77

Qy     326 TGTTTTAACAACACTAAGGGCGATTGGACTTTCACAGTAACGGGAACTCCTATTGTTC  385
           ||||||||||||||::||||||||||||||||  |||||:::||||:|
Db      78 CysPheSerAspThrThrGluSerLeuSerPheAlaGlyLysGlyTyrSerLeuSerPhe 97

Qy     386 CAAACGGTGGATGCAGGGACTGTAGCAGGGGCTGCTGTTAACAGCAGCGTCGTGATAAA 445
           :::   :::      |||||||||||:::::       SerValThrThrAspLys
Db      98 LeuAsnIleLysSer---SerAlaGluGluGluCtGAAsnLeu--SerValThrThrAspLys 115

Qy     446 TCTACCACGTTTATAGGGTTTCTTCGCTATCTTTATTGCGTCTCCTGGAAGTTCGATA  505
           ::  ::  |||||||||||||||||||:::
Db     116 AsnLeuSerLeuThrGlyPheSerLeuThrPheLeuAlaAlaProSerSerValIle   135

Qy     506 ACTACC------GGCAAAGGAGCCGTTAGCTGCTTACGGGTAGCTTGAGTTTGACAAAA 559
           |||||||                                                |||:
Db     136 ThrThrProSerGlyLysGlyAlaValLysCysGly--GlyAspLeuThrPheAspAsn 154

Qy     560 AATGTCAGTTGCTCTTCAGCAAAACTTTCAACGGATAATGGGGGTGCTATCACCGCA  619
           :|||||||||||||||||:::         :::      ||||||||||||||||:::
Db     155 AsnGlyThrIleLeuPheLysGlnAspTyrCysGluGluAsnGlyGlyAlaIleSerThr 174

Qy     620 AAAACTCTTCATTAACAGGACTACAAATGTCAGCTCTGTTTCTGAAAATACCCCTCA   679
           |||  |||||||||                |:::         :::|||||||||||||
Db     175 LysAsnLeuSerLeuLysAsnSerThrGlySerIleSerPheGluGlyAsnLysSerSer 194

Qy     680 --------AAGAAGGGGAGCCATTCAGACTTCCGATGCCTTACCATTACTGGGAAAC  730
                   :::     ||||||||:::|||||||||||||||||||||
Db     195 AlaThrGlyLysLysGlyGlyAlaIleCysAlaAlaThrGlyThrValAspIleThrAsnAsn 214

Qy     731 CAAGGGGAAGTCTCTTTTCTGACAATATCTTCTTCGGATTCTGGAGCTGCAATTTTACA 790
           ||||||||||||:::|||||||||||||||||:::|||||||:::||||| ::
Db     215 ThrAlaProThrLeuPheSerAsnAsnIleAlaGluAlaAlaGlyAlaIleAsnSer   234

Qy     791 GAAGCCTCGGTGCATATTTCTAATAATGCTAAAGTTTCCTTTATTGACAATAAGGTCACA 850
           |||||||:::||||||      |||   :::||||||||||||
Db     235 ThrGlyAsnCysThrIleThrGlyAsnThrSerLeuValPheSerGluAsnValThr   254

Qy     851 GGAGCGAGCTCCTCAACAGCGGGGATGTCAGGAGGTGCTATCTGTGTTATAAAACT 910
           ||||||||||||||||||||||||||:::         :::
Db     255 --------AlaThrAlaGly-----AsnGlyGlyAlaLeu-                  263

Qy     911 AGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAGCAACAATACA 970
           |||||||||||:::||||||||:::|||||||||||||||
Db     264 SerGlyAspAlaAspValThrIleSerGlyAsnGlnSerValThrPheSerGlyAsnGln  283

Qy     971 TCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAGTCGAACTGGCTTCC-----GGA 1024
           ::                                            :::
Db     284 AlaValAlaAsnGlyGlyAlaIleTyrAlaLysLysLeuThrLeuaSerGlyGlyGly  303

Qy    1025 GGACTTACCCTATTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCTAAAGGTGGAGCC 1084
           |||||||:::::::                   |||||||||||||||||||||||||||
Db     304 GlyValSerProPheLeuThrIleIleValGlyThrThrAlaGlyAsnGlyAlaGlyAla  323

Qy    1085 ATAGCTATCGAAGATAGTGGGAATTGAGTTTATCCCCGATAGTGGTGACAATTGTCTTT 1144
           |||||||||                  |||||||::::::
Db     324 IleSerIleLeuAlaAlaGlyGluCysSerLeuSerAlaGluAlaGlyLeuThrLeuGlyGly 343
```

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Qy  2204  CAAGGTACAGTCTACGGAGGAGAACTCTTATTACCAGCACACAACGAAACCTATATCTCTT  2263
                ||||
Db   703  HisThrAspThrTyrAlaGlyAlaPheTyrIleGlnHis----------IleThrGlu   718

Qy  2264  CCTTGCAAACTACGGCCTTGTTCGTTGTCTTATGTTCCT--------ACAGAGATTCCT   2314
                :::     |||          ||:::
Db   719  CysSerGlyPheIleGlyCysLeuLeuAspLysLeuProGlySerTrpSerHisLysPro  738

Qy  2315  GTTCTCTTTTCAGGAAACCTTAGCTACCACCCATACGATAACGATCTGAAAACCAAGTAT  2374
                :::::     |||||||||||        ||||:::::||:||||
Db   739  LeuValLeuGluGlyGlnLeuAlaTyrSerHisValSerAsnAspLeuLysThrLysTyr  758

Qy  2375  ACAACATATCCTACTGTTAAAGGAAGCTGGGGAATGATAGTTGCTTTAGAATTCGGT     2434
                |||||||||:::||||||||||     ||:
Db   759  ThrAlaTyrProGluValLysGlySerTrpGlyMetIleValAlaLeuGluPheGly     778

Qy  2435  GGAAGAGCTCCGATTTGCTTAGATGAAGAAGTGCTCATTTGAGCAGTACATGCCCTTCATG 2494
                :::                    |||||||:::
Db   779  AlaSerSerHisSerTyrProGluTyrLeuHisCysPheAspThrTyrAlaProTyrIle  798

Qy  2495  AAATTGCAGTTTGTCTATGCACATCAGGAAGGTTTAAAGAACAGGGAACAGGAAGCTCGT  2554
                |||||                             :::::||||
Db   799  LysLeuAsnLeuThrTyrIleArgGlnAspSerPheSerGlyGlyThrGluGlyThrArg  818

Qy  2555  GAATTTGGAAGTAGCCGTCTTGTGAATCTTGCCTTACCTATCGGGATCCGATTTGATAAG  2614
                |||||||||          |||||:::
Db   819  SerPheAspAspSerAsnLeuPheAsnLeuSerLeuProIleGlyIleValLysPheGluLys 838

Qy  2615  GAATCAGACTGCCAAGATGCAACGTACAATCTAACTCCTTGGTTATACTGTGGATCTTGTT 2674
                |||||||          :::||||||||||||
Db   839  PheSerAspCysAsnAspPheSerTyrAspLeuThrLeuSerTyrValProAspLeuIle  858

Qy  2675  CGTAGTAACCCCGACTGTAGGACAACACTGGGATTAGCGGTGAGTGATTCTTGGAAAACCTTC 2734
                ||||:::||||||||||          :::|||
Db   859  ArgAsnAspProLysCysThrThrAlaLeuValIleSerGlyAlaSerTrpGluThrTyr  878

Qy  2735  GGTACGAATTTGGCAAGACAAGCTTTAGTCTTCGTGCAGGAACCATTTTTGCTTTAAC    2794
                |||          :::||||||||||||
Db   879  AlaAsnAsnLeuAlaArgGlnAlaLeuGluGlnValAlaArgGlyAlaGlySerHisTyrAlaPheSer 898

Qy  2795  TCAAATTTTGAAGCCTTAGCCAATTTCTTTTGAATTGCGTGGGTCATCTCGCAATTAC     2854
                ||||          |||:::||
Db   899  ProMetPheGluValLeuGlyGlnPheValPheGluValAlaArgGlySerSerArgIleTyr 918

Qy  2855  AATGTAGACTTAGGAGCAGAAAAATACCAATTC                          2884
                ||||||          |||||:::|||
Db   919  AsnValAspLeuGlyLysLysPheGlnPhe                              928
```

```
Qy  1145  TTAGGGAATACAGTCACTTCTACTACTCCT---GGGACGAATAGAAGTAGTATCGACTTA  1201
                |||||    :::||    ||||:||||
Db   344  AsnGlyAsnAlaIleValAlaLeuThrThrProGlnThrThrLysArgAsnSerIleAspIle 363

Qy  1202  GGAACGAGGTGCAAAGATGACAGCTTTGCCGTTCTCGCTGCTGGTAGAGCCATCTACTTCTAT 1261
                |||:::|||||          |||:
Db   364  GlySerThrAlaLysIleThrAlaAsnLeuArgAlaIleSerGlyHisSerIlePhePheTyr  383

Qy  1262  GATCCCATAACTACGGATCATCCACAACAGTTACAGATGTCTTAAAGTTAATGAGACT   1321
                ||||||          :::|||||
Db   384  AspProIleThrLeuAlaAsnThrAlaAlaAspSerThrLeuAsnLeuAsnLeuLysAla  403

Qy  1322  CCGGCAGATTCTGCACTACAATATCAGGGAACATCATCTTCACAGGAGAAAAGTTATCA  1381
                |||          :::||||||||:::||
Db   404  AspAlaGlyAsnSerThrAspTyrSerGlySerIleValPheSerGlyGluLysLeuSer 423

Qy  1382  GAGACAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGTACTACAGCCTGTAACTCTT  1441
                ||||||||:::          ||||||||
Db   424  GluAspGlyGluAlaLysValAlaAlaAspAsnLeuThrSerLysTyrTyrSerLeuThrLeu 443

Qy  1442  TCAGGAGGTACTCTATCTTTAAAAACATGGAGTGACTCTGCAGACTCAGGCATTCACTCAA  1501
                :::          |||||||||||
Db   444  ThrArgGlyAsnLeuValLeuValGlyValThrLeuAspThrLysLysGlyPheThrGln  463

Qy  1502  CAGGGCAGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAACCTGCT---GATACT 1558
                ||||||          |||:::
Db   464  ThrAlaGlySerSerValIleMetThrAspAlaGlyThrThrLeuLysValAlaSerThrGluGlu 483

Qy  1559  AGCACCATAAACAATTGGTCATTAACAACAGTTCTATAGACGGTGCAAAGAAGGCAAAA  1618
                |||||:::          ||||||||||
Db   484  ValThrLeuThrGlyLeuSerIleProValAspSerLeuGlyGluGlyLysLysValVal  503

Qy  1619  ATAGAAACCAAAGCTACGTCAAAAATCTGACTTTATCTGAACCATCACTTATTGGAC     1678
                |||          :::|||
Db   504  IleAlaAlaSerAlaAlaSerLysAsnValAlaAlaLeuSerGlyIleProIleLeuLeuAsp 523

Qy  1679  CCGACGGGCACGTTTTATGGAAAATCATAGTTTAAGAAATCCTCAGTCCTACGACATCTTA  1738
                ||||||          :::||
Db   524  AsnGlnGlyAsnAlaTyrGluAsnHisAspLeuGlyLysThrGlnAspPheSerPheVal  543

Qy  1739  GAGCTCAAAGCTTCTGGAACTGTAACAAGCACCGCAGTGACTCCCAGATCCTATAATGGGT 1798
                :::||          ||:::|||
Db   544  GlnLeuSerAlaLeuGlyThrValThrSerThrAlaValProAlaValProThrValAla  563

Qy  1799  GAGAAATTCCATTACGGCTATCAGGGAACTTGGGCGCCAATTGTTTGG---------    1846
                |||||||||||||||
Db   564  ThrProThrHisTyrGlyTyrGlnGlyThrTrpGly---MetThrTrpValAspAspThr 582

Qy  1847  ---GGGACAGGGGCTTCTACCACTGGGTATCCGCAACCTTCAACTGGACTAAAACTGGCTATATTCCT 1903
                |||:::     ||||:::|||
Db   583  AlaSerThrProLysThrAlaThrLeuAlaThrHisLeuAlaThrArgAlaThrTrpAsnGlyTyrLeuPro 602

Qy  1904  AATCCCGAGGGTATCGGCTCTTTAGTCCCTAATAGTGTTATGGAATGCATTTTATAGATATT 1963
                ||||||          :::||:::|||
Db   603  AsnProGluArgGlnGlyProLeuValProAsnSerLeuTrpProValSerPheSerAspIle 622

Qy  1964  AGCTCCTCCATTATCTTATGGAGACTGCAAACGAGAGGGTTGCAGGAGGACCGTGCTTTT   2023
                |||:::     ::     ||||
Db   623  GlnAlaIleGlnGlyValIleGluArgSerAlaLeuThrLeuCysSerAspArgArgGlyPhe 642

Qy  2024  TGGTGTGCTGGATTATCTAACTTCTTCCATAAGGATAGTACAAAAACACGACGCGGGTTT  2083
                |||          :::||
Db   643  TrpAlaAlaGlyValAlaAsnPheLeuAspLysAspLysLysGlyGluLysArgLysTyr  662

Qy  2084  CGCCATTTGAGTGGCCGTTATGTCATAGGAGAGAAACCTACATACTTGTTCAGATAAGATT 2143
                ||||||:::          ||||||||
Db   663  ArgHisLeuSerGlyGlyTyrGlyTyrAlaIleGlyTyrAlaIleAlaGlnThrCysSerGluAsnLeu 682

Qy  2144  CTTAGTGCTGCATTTGTCAGCTCTTTGGAAGATAGAGACTACTTTGTTGACTAAGAAT   2203
                :::||          ||||||||
Db   683  IleSerPheAlaPheCysGlnLeuProPheGlySerAspPheLeuValAlaAlaLysAsn  702
```

RESULT 7
AAY90237
ID   AAY90237 standard; Protein; 928 AA.
XX
AC   AAY90237;
XX
DT   29-AUG-2000 (first entry)
XX
DE   Chlamydia antigen CPN100635.
XX
KW   Chlamydia antigen; diagnosis; infection; community acquired pneumonia;
KW   therapy; upper respiratory tract disease; bronchitis; sinusitis;
KW   asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma.
XX
OS   Chlamydia pneumoniae.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..43
FT   /note= "signal peptide"
FT   Protein   44..928
FT   /note= "mature CPN100635"
XX
PN   WO200032794-A2.
XX
PD   08-JUN-2000.

```
XX
PF  01-DEC-1999;  99WO-CA01147.
XX
PR  01-DEC-1998;  98US-0110339.
PR  01-DEC-1998;  98US-0110340.
PR  01-DEC-1998;  98US-0110427.
PR  01-DEC-1998;  98US-0110428.
PR  01-DEC-1998;  98US-0110438.
XX
PA  (CONN-) CONNAUGHT LAB LTD.
XX
PI  Murdin AD, Oomen RP, Wang J;
XX
DR  WPI; 2000-412339/35.
DR  N-PSDB; AAA30849, AAA30850.
XX
PT  Nucleic acids encoding polypeptide antigens from Chlamydia useful for
PT  preventing, diagnosing and treating diseases such as community acquired
PT  pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
PT  asthma -
XX
PS  Claim 16; Fig 3; 174pp; English.
XX
CC  This sequence is a Chlamydia antigen of the invention, designated
CC  CPN100635. The nucleic acids (and their complementary sequences) may be
CC  used as diagnostic agents for detecting the presence of nucleic acids
CC  encoding Chlamydia antigens in samples according to standard methods,
CC  and therefore, for diagnosing Chlamydia infections. For example, they may
CC  be used as primers and probes for diagnostic polymerase chain reaction
CC  (PCR) assays. Antisense sequences may be used to down regulate
CC  expression of the proteins and may be used to treat infections. The
CC  nucleic acids may also be used to produce the protein antigens they
CC  encode according to standard recombinant DNA methodologies. The
CC  proteins may then be used as antigens for the production of antibodies
CC  (i.e. as vaccines) for preventing infection by Chlamydia. The
CC  antibodies may also be used as diagnostic reagents for detecting
CC  infections. Chlamydia is a pathogen implicated in the development of
CC  (for example) community acquired pneumonia, upper respiratory tract
CC  disease (especially bronchitis and sinusitis, asthmatic bronchitis,
CC  adult-onset asthma and acute exacerbations of asthma in adults.
XX
SQ  Sequence  928 AA;
```

```
Alignment Scores:
Pred. No.:              1.38e-157      Length:          928
Score:                  2021.00        Matches:         438
Percent Similarity:     61.05%         Conservative:    142
Best Local Similarity:  46.11%         Mismatches:      326
Query Match:            37.36%         Indels:          44
DB:                     21             Gaps:            20
```

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US-09-428-122-1 (1-3000) x AAY90237 (1-928)

Qy  101  ATGAAGTCTTCTTTCCCCAAGTTTGTATTT---TCTACATTGCTATTTC-------  148
              ||||| ||        |||||||| || ||||||||  ||
Db    1  MetLysSerGlnPheSerTrpLeuValLeuSerThrLeuAlaCysPheThrSerCys  20

Qy  149  CCTTTGTCTATGATGCTACCGAGACAGCAGTTTGATTCAAGTGCGAGTTTCGATGGGAAT  208
              |||      ||:
Db   21  SerThrValPheAlaAlaThrAlaGluAsnIleGlyAsnIleGlyProSerPheAspGlySer  40

Qy  209  AAAAAT--GGTAAATTTTCAGTTCGTGAGAGTCGAGGAAGATGCTGGAACTACCTACCTA  265
              |||  ::: :  ::: ::
Db   41  ThrAsnThrGlyThrTyrThrProLysAsnThr------ThrThrGlyIleAspThr  58

Qy  266  TTTAAGGGAAAATGCACTCTAGAAAATATTCCTGAACAGCAGCAATCACAAAAAGC  325
              |||::::|||||
Db   59  LeuThrGlyAspIleThrLeuGlnAsnLeu---GlyAspSerAlaAlaLeuThrLysGly  77

Qy  326  TGTTTTAACACACTAAGGGCGGATTGACTTTCACAGGTAACGGGAACTCTCTATTGTTC  385
              |||||||:::|||
Db   78  CysPheSerAspThrThrGluSerLeuSerPheAlaGlyLysGlyTyrSerLeuSerPhe  97
```

```
Qy  386  CAAACGGTGGATGCAGGAGGGCTGCTGCTGTTAACAGCAGCGTCGTGGTAGATAAA  445
              :::  :::
Db   98  LeuAsnIleLysSer---SerAlaGluGluAlaAlaLeu---SerValThrThrAspLys  115

Qy  446  TCTACCACGTTTATAGGGTTTCTTCCGCTATCTTTATTGCGTCTCCTGGAAGTTCGATA  505
              ::: :::
Db  116  AsnLeuSerLeuThrGlyPheSerSerLeuThrPheLeuAlaLeuAlaProSerSerValIle  135

Qy  506  ACTACC------GGCAAAGGAGCCGTTAGCTGCTCACGGCCGTTGACTTGAGTTGACAAAA  559
              |||||         ||||
Db  136  ThrThrProSerGlyLeuLysGlyAlaValLysCysGly--GlyAspLeuThrPheAspAsn  154

Qy  560  AATGTCAGTTGCTTCTTCAGCAAAAACTTTTGCAGGATAATGGCGGTGCTATCACCGCA  619
              |||:::::::::: ||||
Db  155  AsnGlyThrIleLeuPheLysGlnAspTyrCysGluGluAlaGlyGlyAlaIleSerThr  174

Qy  620  AAAACTCTTTCATTACACAGGACTACAATGTCAGCTCTGTTTTCTGAAAATACCTCCTCA  679
              |||:::|||
Db  175  LysAsnLeuSerLeuLysAsnSerThrGlySerIleSerPheGluGlyLysLysSerSer  194

Qy  680  ------AAGAAAAGGCGGAGCCATTCAGACTTCCGATGCCCATTACCATTACTGACGAAAC  730
              |||||||||||  :::
Db  195  AlaThrGlyLysLysGlyGlyAlaIleCysAlaThrGlyThrValAspIleThrAsnAsn  214

Qy  731  CAAGGGGGAGTCTTCTTTTGACAATACTTCTTCGGATTCTCGGAGCTGCAATTTTACA  790
              |||||||::: :::
Db  215  ThrAlaProThrLeuPheSerAsnAsnIleAlaGluAlaLeuAlaGlyAlaIleAsnSer  234

Qy  791  GAAGCCTCGGTACTATTTCTAATAATGCTAAAGTTTCCTTTATTGACAATAAGGTCACA  850
              |||::: |||
Db  235  ThrGlyAsnCysThrIleThrGlyIleAsnThrSerLeuValPheSerGluAsnSerValThr  254

Qy  851  GGAGCGGAGCTCCTCAACACGGGGATATGTCAGGAGGTGCTATCTGTGTTATAAAACT  910
              |||||||
Db  255  --------AlaThrAlaGly-----AsnGlyGlyAlaLeu--  263

Qy  911  AGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAGCAACAATACA  970
              |||::: |||
Db  264  SerGlyAspAlaAspValThrIleSerGlyAsnGlnAsnSerValThrPheSerGlyAsnGln  283

Qy  971  TCGACAACAGCGGAGGAGCTCATCTATGTGAAAAAGCTCGAACTGGCTTCC------GGA  1024
              :::|||||||  |||
Db  284  AlaValAlaAlaAsnGlyAlaIleGlyAlaIleTyrAlaLysLysLeuThrLeuAlaSerGlyGlyGly  303

Qy 1025  GGACTTACCCTATTCAGTAGAAATAGTGCAATGAGAAATAGTGCAGCTCCTAAAGGTGGAGCC  1084
              |||   |||
Db  304  GlyGlyAsnProPheSerAsnAsnIleValGlnGlyThrThrAlaGlyAsnGlyGlyAla  323

Qy 1085  ATAGCTATCCGAAGATAGTGGGGAATTGAGTTTATCCGCCGGATAGTGGTGCATTGTCTT  1144
              |||:::::: :::|||
Db  324  IleSerIleLeuAlaAlaGlyGluCysSerSerLeuPheSerGluAlaLeuAlaAspHisTyrLeu  343

Qy 1145  TTAGGGAATACAGTCACTTCTACTACTCCT---GGGACGAATAGAAGTAGTATCGGACTTA  1201
              ||| ::
Db  344  AsnGlyAsnAlaAlaIleValAlaThrThrProGlnThrThrLysArgAsnSerIleAspIle  363

Qy 1202  GGAACGAGTGCAAAGATGACAGCTTTGCGTTCGTCGTGCTGTGAGCCATCTACTTCTAT  1261
              |||::::::: |||
Db  364  GlySerThrGlyLysAspHisGluLeuArgAlaIleSerGlyHisSerIlePhePheTyr  383

Qy 1262  GATCCCATAACTACAGGATCATCCACAACAGTTACAGATGTCTTAAAAGTTAATGGACT  1321
              |||   :::::
Db  384  AspProIleThrLeuAsnThrAlaLeuAspSerThrLeuAsnLeuAsnLysAla  403

Qy 1322  CCGGGCAGATTCTGCTACAGTATACAGGGAACATCATCTTCACAGGAGAAAAGTTATCA  1381
              :::::
Db  404  AspAlaGlyAsnSerThrAspTyrArgSerGlyIleValPheSerGlyLeuLeuSer  423

Qy 1382  GAGAGACAGAGCCCGCCGAGAATTCTAAAATCTTACTTGCGAAGCTACTACGCCTGTAACTCTT  1441
              |||||
Db  424  GluAspGluLysValAlaLeuAspAsnLeuThrSerThrLeuLysGlnProValThrThrLeu  443

Qy 1442  TCAGGAGGTACTCTATCTTTAAAACATGAGTAAAACATGGACTCGCAGACTCAGGCATTCACTCAA  1501
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Db    799  LysLeuAsnLeuThrTyrIleArgGlnAspSerPheSerGluLysGlyThrGluGlyArg  818
                                                                    
Qy   2555  GAATTTGGAAGTAGCCGTCTTGTGAATCTTGCCTTACCATCCGGATCCGATTGATAAG  2614
           :::    |||    |||||                    :::    |||::    ||||||
Db    819  SerPheAspAspSerAsnLeuPheAsnLeuSerLeuProIleGlyValLysPheGluLys  838

Qy   2615  GAATCAGACGCCAAGATGCAACGTACAACTCAACTCTTGGTTATACTGTGGATCTTGTT  2674
           |||||    :::||||||          ||:::    :::||||||
Db    839  PheSerAspCysAsnAspPheSerTyrArgAspLeuThrLeuSerTyrValProAspLeuIle  858

Qy   2675  CGTAGTAACCCCGACTGTACGACAACACTGCGAATTAGCCGTGATTCTTGGAAAACCTTC  2734
           |||::::    |||||||          :::    |||||||    |||:::||
Db    859  ArgAsnAspProLysCysThrThrAlaLeuValIleSerGlyAlaSerTrpGluThrTyr  878

Qy   2735  GGTACGAATTGGCAAGACAAGCTTAGTCCTTCGTGCAGGGAACCATTTTGCTTTAAC  2794
           |||    |||||    ||||||    :::    ||||||          ||:::||
Db    879  AlaAsnAsnLeuAlaArgGlnAlaLeuGlySerHisTyrAlaPheSer  898

Qy   2795  TCAAATTTGAAGCCTTAGCCGAATTTCTTTGAGGTTGCGTGGGTCATCTCGCAATTAC  2854
           ||    :::    |||||          |||||||    :::||||||
Db    899  ProMetPheGluValLeuGlyGlnPheValPheGluValArgGlySerSerArgIleTyr  918

Qy   2855  AATGTAGACTTAGGAGCAAAATACCAATTC  2884
           |||::::||||||
Db    919  AsnValAspLeuGlyGlyLysPheGlnPhe  928
```

RESULT 8
AAY69369
ID   AAY69369 standard; Protein; 918 AA.
XX
AC   AAY69369;
XX
DT   19-JUN-2000 (first entry)
XX
DE   Amino acid sequence of the CPN100395 polypeptide.
XX
KW   CPN100395; Chlamydia infection; immune response; vaccine.
XX
OS   Chlamydia pneumoniae.
XX
XX
PN   WO200011183-A2.
XX
PD   02-MAR-2000.
XX
PF   18-AUG-1999;   99WO-IB01449.
XX
PR   20-AUG-1998;   98US-0097187.
PR   20-AUG-1998;   98US-0097188.
PR   20-AUG-1998;   98US-0097189.
PR   20-AUG-1998;   98US-0097190.
PR   20-AUG-1998;   98US-0097195.
PR   20-AUG-1998;   98US-0097196.
PR   20-AUG-1998;   98US-0097197.
PR   27-AUG-1998;   98US-0097191.
PR   17-AUG-1999;   99US-0376770.
XX
PA   (CONN-) CONNAUGHT LAB LTD.
XX
PI   Murdin AD, Oomen RP;
XX
DR   WPI; 2000-224703/19.
DR   N-PSDB; AAZ61509.
XX
PT   Novel antigens and corresponding DNA molecules that can be used to
PT   prevent, treat and diagnose disease caused by Chlamydia infection in
PT   mammals, especially humans -
XX
PS   Claim 19; Fig 15-E; 201pp; English.
XX
CC   AAY69362-69 represent Chlamydia pneumoniae polypeptides. The
CC   polypeptides are present in the bacterial membrane structure, in the
CC   external vicinity of the membrane structure, in the inclusion membrane
CC   structure, in the external vicinity of the inclusion membrane structure,

```
Db    444  ThrAlaGlyAsnLeuValLeuLysArgGlyValThrLeuAspThrLysGlyPheThrGln  463
           :::    |||    ||||||                    |||::    ||||||
Qy   1502  CAGGCAGAATTCTCCTCGTCTATAGGACGTAGGACTACTACTCTAGACCTGCT--GATACT  1558

Db    464  ThrAlaGlySerSerValIleMetAspAlaGlyThrThrLeuLysAlaSerThrGluGlu  483
           |||||||    :::    |||:::    |||||||
Qy   1559  AGCACCATAAACAATTGGTCATTAACATCAGTTCTATAGACGGTGCAAGAAGGCAAAA  1618

Db    484  ValThrLeuThrGlyLeuSerIleProValAspSerLeuGlyLeuGluGlyLysLysValVal  503
           |||::    :::||||||          ||:::    |||||||
Qy   1619  ATAGAAAACCAAAGTACGTCAAAAAATCTGACTTTATCTGGAACCATCACTTATTGGAC  1678

Db    504  IleAlaAlaSerAlaAlaSerGlyLysAsnValAlaLeuSerGlyLysProIleLeuLeuLeuAsp  523
           |||    |||    ||||||    :::    ||||||
Qy   1679  CCGACGGGGCCACGTTTTATGAAAATCATAGTTAAGAAATCCTCAGTCCTACGACATCTTA  1738

Db    524  AsnGlnLysAsnAlaTyrGluAsnHisAspThrGlnLysThrGlnIleAspPheSerPheVal  543
           |||    :::    ||||||          |||:::    ||||||
Qy   1739  GAGCTCAAAGCTTCTGGAACTGTAACAAGCACCGCAGTGACTCCCAGATCCTATAATGGGT  1798

Db    544  GlnLeuSerAlaLeuGlyThrAlaThrThrAspThrAlaValProAlaValProAlaValAla  563
           :::    |||    ||||||    :::
Qy   1799  GAGAAATTCCATTACGGCTATCAGGGAACTTGGGCGCCCAATTGTTTGG-----------  1846

Db    564  ThrProThrHisTyrGlyTyrGlnGlyThrTrpGly--MetThrValAspAspThr  582
           |||    :::    ||||||
Qy   1847  --GGGACAGGGGCTTCTACGACTGCGAACCTTCAACTGGACTAAAACTGGCTATATTCCT  1903

Db    583  AlaSerThrProLysThrAlaThrLeuAlaThrArgThrAsnThrGlyTyrLeuPro  602
           |||    |||    ||||||
Qy   1904  AATCCCGAGCGTATCGGCTCCTTAGTCCCTAATAGCTTATGGAATGCATTTATAGATATT  1963

Db    603  AsnProGluArgGlnGlyTyrProLeuValProAsnSerLeuTrpAsnAlaPheSerAspIle  622
           |||||||          :::    ||||||
Qy   1964  AGCTCTCTCCATTATCTTATTGGAGACTGCAAACGAAGGGTTGCAGGGAGACCGTGCTTTT  2023

Db    623  GlnAlaIleIleGlnHisLysValIleIleGluThrLeuCysSerArgAspArgGlyPhe  642
           :::    |||    ||||||
Qy   2024  TGGTGTGCTGGATTATCTAACTTCTTCCATAAGGATAGTACAAAAAACACGACGCGGGTTT  2083

Db    643  TrpAlaAlaGlyValAlaAsnPheLeuAsnLysLeuAspLysSerGlyGluLysGlyGlyLysTyr  662
           |||    :::    ||||||
Qy   2084  CGCCCATTGAGTGGGGGTTATGTCATAGGAGGAAAACCTACATACTTGTTCAGATAAGATT  2143

Db    663  ArgHisLysSerGlyGlyTyrAlaIleGlyGlyTyrAlaAlaAlaGlnThrCysSerGluAsnLeu  682
           ||||||          :::    |||||||
Qy   2144  CTTAGTGCTGCATTTGTCAGCTCCTTGGAGAGATAGAGACTACTTTGTAGCTAAGAAT  2203

Db    683  IleSerPheAlaPheCysGlnLeuPheGlySerAspLysPheLeuValAlaLysAsn  702
           :::    |||    ||||||
Qy   2204  CAAGGTACAGTCTACGGAGGAACTCCTATTACCAGCACAACGAAACCTATATCTCTCTT  2263

Db    703  HisThrAspThrTyrAlaGlyPheTyrIleGlnHis----------IleThrGlu  718
           ||||||          :::||
Qy   2264  CCTTGCAAACTACGGCCTTGTTCGTTGTGTCTATGTTCCT------ACAGAGATTCCT  2314

Db    719  CysSerGlyPheIleGlyLeuCysLeuLeuAspLysLeuProGlySerTrpSerHisLysPro  738
           :::    |||    ||||||
Qy   2315  GTTCTCTTTTCAGGAAACCTTAGCTACACACCCATACGGATAACGATCTGAAAACCAAGTAT  2374

Db    739  LeuValLeuGluGluGlnLeuAlaTyrSerHisValSerAsnAspLeuTyrThrLysTyr  758
           :::    |||    ||||||
Qy   2375  ACAACATATCCTACACTGTTAAAAGGAAGCTGGGGAAGATGAATAGTTTCGCTTTAGAATTCCGGT  2434

Db    759  ThrAlaTyrProGluValGlySerTrpGlyValPheAsnAlaPheAsnMetMetLeuGly  778
           |||    :::    ||||||
Qy   2435  GGAAGAGCTCCGATTCCTTTAGATGAGTGCTCTATTTGAGCAGTACATGCCCTTCATG  2494

Db    779  AlaSerSerHisSerTyrProGluTyrLeuHisCysPheAspThrTyrArgAlaProTyrIle  798
           :::    |||    ||||||
Qy   2495  AAATTGCAGTTTGTCTATGCACATCAGGAAGGTTTAAAGAACAGGGAACAGAAGCTCGT  2554
```

CC   and in the cytoplasm of the infected cell. The polypeptides may be
CC   used to prevent, treat and detect the presence of Chlamydia infection
CC   and/or the presence of Chlamydia in a sample. The polypeptides may
CC   also be used to induce an immune response in a mammal. The vaccine
CC   vector comprising the polynucleotides is used to induce an immune
CC   response in a mammal. Antibodies directed against the polypeptides
CC   may also be used therapeutically to treat and/or prevent a Chlamydia
CC   infection.
XX
SQ   Sequence   918 AA;

Alignment Scores:
Pred. No.:   918
Score: 2.37e-156   Matches: 432
Percent Similarity: 61.39%   Conservative: 150
Best Local Similarity: 45.57%   Mismatches: 316
Query Match: 37.09%   Indels: 50
DB: Gaps: 20

US-09-428-122-1 (1-3000) x AAY69369 (1-918)

Qy   101 ATGAAGTCCTCTTCTCCCAAGTTGTATTTCTACATTTGCTATTTCCCTTTGTCTATG 160
                ||||:::|||||| ::| ||||||||||||| ||
Db   1 MetArgSerPheSerLeuLeuIleSerSerLeuLeuAlaPheProLeuLeuMet   20

Qy   161 ATT----------GCTACCGGACAGTTTGGATTCAAGTGCCGAGTTTCGATGGGAAT 208
                          || ::: ||| |||||||:::|||:::
Db   21 SerValSerAlaAspAlaAlaAspLeuThrLeuGlySerArgAspSerTyrArgAsnGlyAsp 40

Qy   209 ---AAAAATGGTAATTTTCAGTTCGTGAGAGTTCAGGAAGATGCT---GGAACTACCTAC 262
                   ||||||||||||||| || ||| |||||||||||||||
Db   41 ThrSerThrThrGluPheThrProLysAlaAlaThrSerAspAlaSerGlyThrThrTyr 60

Qy   263 CTATTTAAGGGAAATGTCACTCTAGAAAAATATTCCTGGAACAGCAGCAATCACAAAA 322
                ::: ||||||||||||||| |||||||||||
Db   61 IleLeuAspGlyAspValSerIleSerGln--AlaGlyLysIleThrSerLeuThrThr 79

Qy   323 AGTCGTTTTAACACACTAGGGCCGATTTGACTTTCACAGGTAACGGAACTCCTATTG 382
                :::|||||| |||||| |||::: |||||
Db   80 SerCysPheSerAsnThrAlaGlyAsnGlyThrPheLeuGlyAsnGlyPheSerLeuHis 99

Qy   383 TTCCAAACGGTGCGATGCAGGGACTGTAGCAGGGCTGCTGTTAACAGCAGCTGGTGAGAT 442
                || ::: || ||||||||||| :::::
Db   100 PheAspAsnIleIleSerSerThrValAlaGlyValValSerAsnThrAlaAlaSer 119

Qy   443 AAAATCTACCACCGTTTATAGGGTTTCTTGCTATCTTTTTATTGCCGTCTCCTGGAAGTTCG 502
                ||| :::||| :::|||||| ||
Db   120 GlyIleThrLysPheSerGlyPheSerThrLeuArgMetLeuAlaLeuAlaProArg------ 137

Qy   503 ATAACTACCGCAAAGGAGGAGCCCGGTTAGCTGCTCTCACGGGTAGCTTGAGTTTGACAAAAAAT 562
                :::|| |||||| |||||||::: ||||||
Db   138 ---ThrThrGlyLysGlyAlaIleLeuLysIleLysAsnGly--LeuValPheGluSerIle 155

Qy   563 GTCAGTTGCTTGCTTCAGCAAAAACTTTTCAACGGATAATGGCGGTGCTATCACCCGCAAA 622
                || :::|| ||||||||| ||| |||
Db   156 GlyAsnLeuAspLeuAsnGluAsnSerGluAsnGlyLysGlyAlaIleLeuAsnThrLys 175

Qy   623 ACTCTTTTCATTACAACAATACTTCTTCGGATTCTGCAGCTACAGTGTCAGCTGCTGAAAATACCTCCTCAAAG 682
                ||||||| :::::|| |||||| |||
Db   176 ThrLeuSerLeuThrThrGlySerThrAlaThrThrGlyGlyValAlaIleSerArgGlyAlaIleSerGlyIle 195

Qy   683 AAAGGCCGAGCCATTCAGACTTCCGATGCCGTTAGCGTTGTTGACAAAACCAAGGGAAGTC 742
                ::||||| ||||||| |||||| :::
Db   196 GlnGlyGlyAlaIleLeuAlaIleLysTyrAlaSerGlyAspSerValIleSerGluSerSerVal 215

Qy   743 TCTTTTTCTGACAAATACTTTCTTCGGAATTCTGGAGCTGCAATTTTACAGAGCCTCGGTG 802
                ||||||| ::: ||||| ||||||
Db   216 SerPheGlyAsnAsnSerAlaThrThrSerGlyGlyAlaIleSerGlyAlaIleGlyAsnLeu 235

Qy   803 ACTATTTCTAATAATGCTAAAGTTCCTTTATTGACAATAAGGTCACAGCGAGCTCC 862
                :::|| ::: ||| :::
Db   236 ValIleSerAsnAsnGlnAsnIlePheAspGlyCysLysLysAlaThr--------- 251

Qy   863 TCAACACGGGGGATATGTCAGGAGGTGCTATCTGTGCTTATAAA------ACTAGTACA 916
                ::::||||| |||||| :::
Db   252 ---------------ThrAsnGlyGlyAlaIleIleAspCysAsnLysAsnLysAsnPro 266

Qy   917 GATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAGCAACAACAATACATCGACA 976
                |||::::|||||| :::|||||| ::::||
Db   267 AspProIleLeuThrLeuSerGlyAsnGluSerLeuHisPheLeuAsnAsnThrAlaGly 286

Qy   977 ACAGCGGGAGGAGCTATCTATGTGAAAAAAGCTCGAACTGGCTCCGGA---GGACTTACC 1033
                ||||||||||||||||||:::::||||||||| :::||
Db   287 AsnSerGlyAlaGlyAlaIleTyrThrLysLeuValLeuSerGlyArgGlyLeuVal 306

Qy   1034 CTATTCAGTAGAAATAGTGTCAATGAGGTACAGCTCCTAAAGGTGGAGCCATAGCTATC 1093
                |||||| || ::: ||||||
Db   307 LeuPheSerAsnLysAlaLeuAlaAlaAsnAlaThr--ProLysGlyGlyAlaIleAlaIle 325

Qy   1094 GAAGATAGTGGGGAATGAGTTTATCCGGCGATAGTGTGACATTGTCTTTTTAGGGAAT 1153
                |||||| :::|| |||::: ||||||
Db   326 LeuAspSerGlyGlyIleIleSerGlyAlaAspLeuAspLeuAsnIleIlePheGluGlyGlyAsn 345

Qy   1154 ACAGTCACTTCACTACT-------------CCTGGGACGAATAGAAGTAGTAGTATCGGACTTAGGA 1204
                |||||| |||||||
Db   346 Thr---ThrSerThrThrGlySerProAlaSerValThrArgAsnAlaIleAspLeuAla 364

Qy   1205 ACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTGGAAGCCATCTACTTCTATGAT 1264
                ||||||| :::   ::|||||| :::
Db   365 SerAsnAlaLysPheLeuAsnLeuArgLeuAlaThrArgGlyAsnLysValIlePheTyrAsp 384

Qy   1265 CCCATAACTACAGGATCATCCACAACAGTTACAGATGTCTTAAAAGTTAATAGACTCCG 1324
                ||| ::: |||::: ||||||
Db   385 ProIleThr--------SerSerGlyAlaThrAspLysLeuSerLeuAsnLysAlaAsp 401

Qy   1325 GCAGATTCTGCACTACAATATACAGGGACAACATCATCCTCCAGAGAAGAAAGTTATCAGAG 1384
                |||||||||||| :::|||||| |||||||||
Db   402 AlaGlySerGlyAsnThrTyrIleValPheSerGlyLysLysLeuSerGlu 421

Qy   1385 ACAGAGGCCCGAGATTCTAAAAATCTAACTTACTTCGAAGCTACTACAGCCTGTAACTCTTTCA 1444
                ||||||| ::: |||||| :::
Db   422 GluGluLeuLysLysProAspAsnLeuLysSerThrPheThrGlnAlaValGluLeuAla 441

Qy   1445 GGAGGTACTCTATCTTTAAAACATGGAGTGACTCTGCAGACTCAGGCATTCACTCAACAG 1504
                |||||| :::|| ||||||||||||
Db   442 AlaGlyAlaLeuValLeuLysAspGlyValThrValAlaLaAsnThrIleThrGlnVal 461

Qy   1505 GCAGATTCTGCTCTCGAAATGGACGTAGGAGAACTACTCTGAA---CCTGCTGATACTAGC 1561
                ||||||::::|| ||||||||| :::
Db   462 GluGlySerLysValMetAspGlyValGlyThrArgPheGluAlaSerArgAlaGluGlyVal 481

Qy   1562 ACCATAAAACAATTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGAAGGCAAAAATA 1621
                |||||| ::: |||||| |||
Db   482 ThrLeuAsnGlyLeuAlaIleAsnIleAspSerArgLeuAspSerLeuAspAspGlyAlaIleIle 501

Qy   1622 GAAACCAAAGCTACGTCAAAAAATCTGACTTTATCTGAACCATCACTTATTGGACCCG 1681
                |::   :::|||||||||||| :::||
Db   502 LysAlaThrAlaAlaSerArgValAlaLeuSerGlyProIleMetLeuValAlaAspAla 521

Qy   1682 ACGGGACACGTTTATGAAAATCATAGTTTAAGAAAATACCTCCTCTAGAG 1741
                ||| :::|||||| :::::|||
Db   522 GlnGlyAsnTyrTyrGlyTyrGlnGlyAsnTrpAsn---IleValTrpValAspAspAlaThr 541

Qy   1742 CTCAAAGCTTCTGAACTGTAACACAGCACCCGAGTGACTCCTATAATGGTGGAG 1801
                |||||| |||:::|| |||||||
Db   542 LeuSerAlaGlnGlyThrMetThrThrThrAspIleProIleLeuAsnThr 561

Qy   1802 AAATTCCATTACGGCTATCAGGGACTTGGGGCCCAATTGTTGG-------GGGACA 1852
                ::: ||| :::||
Db   562 ThrAsnHisTyrGlyTyrGlnGlyAsnTrpAsn---IleValTrpValAspAlaThr 580

Qy   1853 GGGGCTTCTACGGCTGCAACCTCACTGGACTAAAACTGGCTATATTCCTAATCCCGAG 1912
                ::   :::
Db   581 AlaLysThrLysAsnAlaThrLeuThrTrpThrGlyTyrGlyTyrIleLysProAsnProGlu 600

Qy   1913 CGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCATTATGAATATTAGCTCTCTC 1972

DT   26-APR-1999 (first entry)
XX
DE   Chlamydia pneumoniae surface exposed protein Omp9.
XX
KW   Omp9; outer membrane protein 9; surface exposed protein; antigen;
KW   infection; diagnosis; vaccine; atherosclerosis; asthma.
XX
OS   Chlamydia pneumoniae.
XX
PN   WO985953-A2.
XX
PD   30-DEC-1998.
XX
PF   19-JUN-1998;   98WO-DK00266.
XX
PR   23-JUN-1997;   97DK-0000744.
XX
PA   (BIRK/) BIRKELUND S.
PA   (CHRI/) CHRISTIANSEN G.
XX
PI   Birkelund S, Christiansen G, Knudsen K, Madsen A;
PI   Mygind P;
XX
DR   WPI; 1999-105610/09.
DR   N-PSDB; AAX06821.
XX
PT   Species-specific test for identifying mammals infected with
PT   Chlamydia pneumoniae - comprises detecting antibodies specific for
PT   outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT   these proteins
XX
PS   Claim 7; Page 56-58; 115pp; English.
XX
CC   This polypeptide comprises the novel 96.7 kDa surface exposed
CC   protein Omp9 of the human respiratory pathogen Chlamydia
CC   pneumoniae. Its amino acid sequence was deduced from DNA (see
CC   AAX06821) isolated from a C. pneumoniae expression library. The
CC   invention provides 12 novel surface exposed proteins, Omp4-Omp15
CC   (see AAW88417-28), and nucleic acid sequences encoding them (see
CC   AAX06816-27). A new species specific test is claimed that is used
CC   to identify mammals (including humans) infected with Chlamydia
CC   pneumoniae. The test comprises detecting antibodies specific for
CC   Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC   membrane proteins, especially by PCR. The proteins are also used
CC   in the diagnosis of C. pneumoniae infection in mammals. The
CC   nucleic acids and proteins can also be used in the immunization of
CC   mammals, the nucleic acids being particularly useful as DNA
CC   vaccines for effecting in vivo expression of antigens. The
CC   vaccines may also prevent atherosclerosis and bronchial asthma,
CC   which are possibly associated with C. pneumoniae.
XX
SQ   Sequence 918 AA;

Alignment Scores:

Pred. No.:	918
Score:	6.12e-156 Length: 918
	2001.00 Matches: 433
Percent Similarity:	61.28% Conservative: 151
Best Local Similarity:	45.44% Mismatches: 309
Query Match:	36.99% Indels: 60
DB:	20 Gaps: 21

US-09-428-122-1 (1-3000) x AAW88422 (1-918)

```
Qy    101 ATGAAGTCTTCTTCCCCAAGTTGTATTTCTATTTCCCTTTGTCTATG 160
          ||| ::::                   ::: ||:::    |||||||||
Db      1 MetArgSerPheSerLeuLeuIleSerSerSerLeuAlaPheProLeuLeuMet  20

Qy    161 ATT----------GCTACCGAGACAGTTTGGATTCAAGTGCCAAGTTTCCGATGGGAAT 208
          ||:::         ::|          ||:  |::|::  :||  :::|||||||||||
Db     21 SerValSerAlaAspAlaAspLeuThrLeuGlyTyrSerArgAspSerTyrAsnGlyAsp  40

Qy    209 ---AAAAATGGTAATTTTCAGTTCGTGAGAGTCAGGAAGATGCT---GGAACTACCTAC 262
                     ||||||||           ::: :::      ||||||||||
```

Db   601 ArgGlnGlyProLeuValProAsnSerLeuTrpGlySerPheValAspValArgSerIle 620

Qy   1973 CATTATCTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGACCGTGCTTTTTGGTGTGCT 2032

Db   621 GlnSerLeuMetAspArgSerThrSerSerLeuSerSerLeuSerAsnLeuTrpValSer 640

Qy   2033 GGATTATCTAACTTCTTCCATAAGGATAGTACACAAAAAACACGACGCGGGTTCGCCATTTG 2092

Db   641 GlyIleAlaAspPheLeuHisGluAspGlnLysGlyAsnGlnArgSerTyrArgHisSer 660

Qy   2093 AGTGGCGGTTATGTCATAGGAGGAAACCTACATACTTGTTCAGATAAGGATTCTTAGTGCT 2152

Db   661 SerAlaGlyTyrAlaLeuGlyGlyGlyGlyGlyPhePheThrAlaSerGluAsnPheAsnPhe 680

Qy   2153 GCATTTGTCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGGATCAAGGTACA 2212

Db   681 AlaPheCysGlnLeuPheGlyTyrAspLysAspHisLeuValAlaLysAsnHisThrHis 700

Qy   2213 GTCTACGGAGGAACTCTCTATTACCAGCAC--------AACGAAACCTATATCTCTCTT 2263

Db   701 ValTyrAlaGlyAlaMetSerTyrArgHisLeuGlyGluSerLysThrLeuAlaLysIle 720

Qy   2264 CCTTGCAAACTACGGCCTTGTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCCTCTT 2323

Db   721 ------------------LeuSerGlyAsnSerAspSerLeuProPheValPhe 732

Qy   2324 TCAGGAAAACCTTAGCTACACCCATACGGATAACGATCTGAAAACCAAGATACACACATAT 2383

Db   733 AsnAlaAlaArgPheAlaTyrArgGlyHisThrAspAsnAsnMetThrThrLysTyrThrGlyTyr 752

Qy   2384 CCTACTGTTAAAGAAGCTGGGGAATGATAGTTCGCTTAGAATTCGGTGGAAGAGCT 2443

Db   753 SerProValLysGlySerTrpGlyTyrAsnAspAlaPheGlyIleGluCysGlyGlyAlaIle 772

Qy   2444 CCGATTTGCTTAGAT---GAAAGTGCTCTATTTGACAGTACAGCAGTGACCCTCATGAAATTG 2500

Db   773 ProValValAlaSerGlyArgArgSerTrpValAspThrValAspSerPheLeuAsnLeu 792

Qy   2501 CAGTTTGTCTATGCACATCAGGAAGGTTTAAAGAACAGGGAACAGGAGCTCGTGAAATTT 2560

Db   793 GluMetIleTyrAlaHisGlnAsnAsnAspPheLysGluAsnGlyThrGluGlyArgSerPhe 812

Qy   2561 GGAAGTAGCCGTCTTGTGATGAATCTTGCCTTACCTATCCGGATCCGATTGATAAGGAATCA 2620

Db   813 GlnSerGluAspLeuPheAsnLeuAlaValAlaProValGlyIleLysPheGluLysPheSer 832

Qy   2621 GACTGCCAAGATGCAAGTACAACTCAACTAACTCTTGGTTATACGTCGGATCTTGTTCGTAGT 2680

Db   833 Asp------LysSerThrTyrAspLeuSerIleLeuAlaTyrValProAspValIleArgAsn 850

Qy   2681 AACCCCGACTGTACGACACAACACTGCGAATTAGCGGTGATTCTTGAAAACCTTCGTACG 2740

Db   851 AspProGlyCysThrThrThrLeuMetValSerGlyAspSerTrpSerThrCysGlyGlyThr 870

Qy   2741 AATTTGGCAGCAAGCAAGCTTTAGTCCTTCGTGCAGGGAACCATTTTGCTTAAACTTCAAAT 2800

Db   871 SerLeuSerSerArgGlnAlaLeuLeuValArgAlaGlyAsnHisHisAlaPheAlaSerAsn 890

Qy   2801 TTTGAAGCCTTTAGCCAATTTCTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTA 2860

Db   891 PheGluValPheSerGlnPheGluValGluLeuArgGlySerSerArgSerTyrAlaIle 910

Qy   2861 GACTTAGGAGCAAAAATACCAATTC 2884

Db   911 AspLeuGlyGlyLysArgPheGlyPhe 918

RESULT 9
AAW88422
ID   AAW88422   standard; Protein; 918 AA.
XX
AC   AAW88422;
XX

```
Db    41 ThrSerThrThrGluPheThrProLysAlaAlaThrSerAspAlaSerGlyThrThrTyr 60
Qy   263 CTATTTAAGGGAAATGTCACTCTAGAAAAAATATTCCTGGACAGCACAGCAATCACAAAA  322
         :::||:|||||       |||||||:::||:||||
Db    61 IleLeuLeuSerGlyAspValSerIleSerGln---AlaGlyLysGlnThrSerLeuThrThr 79
Qy   323 AGCTGTTTTACCAACACTAAGGGCGATTTGACTTTGCACAGTAACGGCGGAACTCTCATTG  382
         ||||||||:|||||||||||||||||::||||||
Db    80 SerCysPheSerAsnThrAlaGlyAsnLeuThrPheLeuGlyAsnGlyPheSerLeuHis  99
Qy   383 TTCCAAACGGCTGGATGCAGGGGACTGTAGCAGGGGCTCTGTTTAAACAGCAGGTGTAGAT  442
         ||||       :: :||||||||::::::
Db   100 PheAspAsnIleIleSerSerThrValAlaGlyValValValSerAsnThrAlaAlaSer  119
Qy   443 AAAATCTACCACGTTTATAGGGTTTTCTTCGCTATCTTTAATTGCGTCTCCTGGAAGTTCG  502
         ::||       :::|||||||||||
Db   120 GlyIleThrLysPheSerGlyPheSerThrLeuArgMetLeuAlaAlaProArg------  137
Qy   503 ATAACTACCGGCAAAGGAGCCGGTTAGCTGCTTACGGGTAGCTTG--------------  547
         |||||||||||||       |||||
Db   138 ---ThrThrGlyLysGlyValAlaIleLysIleThrAspGlyLeuValPheGluSerIleGly 156
Qy   548 AGTTTGACAAAAAATGTCAGTTTGCTCTCTTCAGCAAAACTTTCAACGGATAATGGCCGT  607
         ::||||       |||||||||||||||
Db   157 AsnLeuAspGlnAsn--------------GluAsnAlaSerSerGluAsnGlyGly  170
Qy   608 GCTATCACCCGCAAAAAACTCTTTCATTACACAGGGACTACAAATGTCAGTCTGTTTCTGAA  667
         |||||||       :::|||||||||||
Db   171 AlaIleLeuAsnThrLysThrLeuSerLeuThrGlySerThrArgPheValAlaPheLeuGly 190
Qy   668 AATACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTACCATTACTGGA  727
         ||||:::::::||||||||||
Db   191 AsnSerSerSerGlnGlnGlyLeuGlyValAlaIleTyrAlaSerGlyValIleSerGlu 210
Qy   728 AACCAAGGGGAAGTCTCTTTTTCTGACATATCTTCGGATTCTGGAGCTGCAATTTTT  787
         |||       :::|||||||||||
Db   211 AsnSerAlaGlyIleLeuSerPheGlyAsnAsnSerAlaThrThrSerGlyGlyAlaIleSer 230
Qy   788 ACAGAAGCCTCGGTGACTATTCTAATAATGCTAAAGTTCCTTATTGACAATAAGGTC  847
         :::||       |||||||||
Db   231 AlaGluGlyAsnLeuValIleSerSerAsnAsnGlnAsnIlePhePheAspGlyCysLysLysAla 250
Qy   848 ACAGGAGGCGAGCTCCTCAACAACGGGGATATGTCAGAGGTGCTATCGTCGTGCTTATAAA  907
         :::||||||||||
Db   251 Thr--------------ThrAsnGlyGlyAlaIleLeuAspCysAsnLys 261
Qy   908 -----ACTAGTACAGATACTAAGGTCACCCTACTAAGCGTGAAATCATGATGTTACTCTTCAGC  961
         |||:::||||||||
Db   262 AlaGlyAlaAsnProAspProIleLeuThrLeuSerGlyAsnGluSerLeuHisPheLeu 281
Qy   962 AACAATACATCGACACAGCGGAGGAGCTATCATGTGAAAAAGCTCGAACTGGCTTCC 1021
         |||||||       :::||||||||
Db   282 AsnAsnThrAlaGlyAsnGlyValGlyAlaIleTyrThrLysLeuValLeuSerSer 301
Qy  1022 GGA--GGACTTACCCTATTCAGTAGAAAATAGTGTCAATGAGGTACAGCTCCTAAAGGT 1078
         ||||||||       |||||||||||
Db   302 GlyArgGlyValGlyValLeuPheSerAsnAsnLysAlaAlaAsnAlaThr---ProLysGly 320
Qy  1079 GGAGCCATAGTAGTGCAAGATAGTGGGAATTGAGTTATCCGCCGATAGTGGTGACATT 1138
         |||||||||||||:::|||
Db   321 GlyAlaIleAlaIleLeuAspSerGlyIleIleSerIleSerAlaAlaAspLeuGlyAsnIle 340
Qy  1139 GTCTTTTTAGGGAATACAGTCACTTCTACTACT------------CCTGGGACGAATAGAAGT 1189
         ||||||||||||:::||||||||
Db   341 IlePheGluGlyAsnThr---ThrSerThrThrGlySerProAlaSerValThrArgAsn 359
Qy  1190 AGTATCGACTTAGGACGAGTAGTGCAAGATGCAGAAGATACAGTTGCGTTGCTCTGCTAGAGCC 1249
         ||:::|||||||       |||||||
Db   360 AlaIleAspLeuAlaSerAsnAlaLysPheLeuAsnLeuArgAlaThrArgArgValAsnLys 379
Qy  1250 ATCTCACTTCATGATCCCATAACTACAGGATCATCCACAACAGTTACAGATGTCTTAAAA 1309
         ||:::|||       ||||:::|||
Db   380 ValIlePheTyrAspProIleThr--------SerSerGlyValAlaThrAspLysLeuSer 396
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Db  1310 GTTAATCAGACTCCGCAGATTCTGCACTACAATATACAGGGAACTCATCTTCACAGGA 1369
         :::||:|||       :::||||:||||
Qy   397 LeuAsnLysAlaAspAlaGlySerGlyAsnThrTyrGluGlyTyrIleValPheSerGly 416
Db  1370 GAAAAGTTATCAGAGACAGAGGCCCGAGATTCTAAAAATCTTACTTCGAAGCTACTACAG 1429
         |||||       |||||||::||||
Qy   417 GluLysLeuSerGluGluSerGlnSerGluLysProAspAsnLeuLysSerThrPheThrGln 436
Db  1430 CCTGTAACTCTTCAGGAGGTACTCTATCTTTAAAACATGGAGGTGACCTGCGAGACTCAG 1489
         |||:::|||       |||||||
Qy   437 AlaValGluLeuAlaAlaGlyAlaLeuValLeuLysValAspValAlaThrValAlaLeuAasn 456
Db  1490 GCATTCACTCAACAGGCAGATTCCGTCTCGAAATGACGTAGGAACTACTCTAGA----- 1546
         ||||||       :::||||:|||
Qy   457 ThrIleThrGlnValGluGlyLysLysValValMetAspGlyGlyThrThrPheGluAla 476
Db  1547 CCTGCTGATACTAGCACCATAACAATTGGTCATTAACATCAGTTCTTATAGACGGTGCA 1606
         ||:::|||       |||||:||
Qy   477 SerAlaGluGlyValThrLeuAsnGlyValLeuAlaIleAsnIleAspSerLeuAspGlyThr 496
Db  1607 AAGAAGGCAAAATAGAAACCAAAGCTACGTCAAAAATCTGACTTTATCTGAACCATC 1666
         ||||||||       :::||||||||
Qy   497 AsnLysAlaIleIleIleLysAlaThrAlaAlaSerLysAspValAlaAlaSerGlyProIle 516
Db  1667 ACTTTATTGGACCCGACGGGCACGTTTTATGAAAAAACATAGTTTAAGAAATCCTCAGTCC 1726
         ||:::|||       ||||:::|||||||
Qy   517 MetLeuValAspAlaGlyAsnTyrTyrGluHisHisAsnLeuSerGlnGlnValVal 536
Db  1727 TACGACATCTTAGAGCTCAAAGCTTCTGGAACTGTAACAAGCACCGACAGTGACTCCAGAT 1786
         ::: :::|||||       :::|||||
Qy   537 PheProLeuIleGluLeuSerArgIleAlaGlnGlyThrMetThrThrAspIleProAspThr 556
Db  1787 CCTATAATGGTGAGAAATTCCATTACGGCTATCGGGAACTTGGGCCCCAATTGTTGG 1846
         ||||||       :::|||||||
Qy   557 ProIleLeuAsnThrThrAsnHisTyrGlyTyrGlnGlyTyrThr---GlyIleIleValTrp 575
Db  1847 --------------GGGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAAAAATCTGGCTAT 1897
         :::|||
Qy   576 ValAspAspAlaThrAlaLysThrAlaThrLeuThrTrpThrLysThrGlyTyr 595
Db  1898 ATTCCTAATCCGAGCGTATCGGCTTCTTAGTCCCTAATAGCTTATGGAATGCATTATA 1957
         ::: |||||:::       :::||||||
Qy   596 LysProAsnProGluArgGlnGlyProLeuValProAsnSerLeuTrpGlySerPheVal 615
Db  1958 GATATTAGCTCTCTCCATTATCTTATGGACTGCAAACGAAGGGTTGCAGGGAGACCGT 2017
         |||||:::|||       ::: :::|||
Qy   616 AspValArgSerIleGlnSerLeuMetAspArgSerThrSerSerLeuSerSerSerThr 635
Db  2018 GCTTTTGGTGTGCTGGATTATCTAACTTCTTCCATAAGGATAGTAGCAAAAACAACGAGC 2077
         |||       :::||||:::|||
Qy   636 AsnLeuTrpValSerGlyIleIleAlaAspPheAlaAspPheAlaAsnLysGlnGlnArg 655
Db  2078 GGGTTTCGCCATTGAGTGGCGGTTATGTCATAGGAGGAGAAACCTACATACTTGTTCAGAT 2137
         ||| ||||       :::||||
Qy   656 SerTyrArgHisSerSerAlaGlyThrTyrAlaLeuGlyTyrGlyPhePheThrAlaSerGlu 675
Db  2138 AAGATTCTTAGTGCTGCATTTTGTCAGCTCTTGGAAGAGAGATAGAGACTACTTTGTAGCT 2197
         |||:::|||       ||||
Qy   676 AsnPhePheAsnPheAlaPheCysGlnLeuPheGlyTyrAspLysAspHisLeuValAla 695
Db  2198 AAGGATTCAAGTACAGTCACGGACGGAACTCTCATTACCAGCAC-------AACGAA 2248
         |||||||       :::|||
Qy   696 LysAsnHisThrValThrTyrAlaGlyAlaMetSerTyrArgHisGluSerLys 715
Db  2249 ACCTAATATCTCTCCTTGCAAACTACGGCCTTGTTCGTTCTTATGTTCCTACCAGAG 2308
         :::|||||       ::: :::|||||
Qy   716 ThrLeuAlaLysIle------------LeuSerGlyAsnSerAspSer 727
Db  2309 ATTCCTGTTCTCTTTTCAGGAAAACCTTAGCTACACCCATAACGGATAACGATCTGAAAACC 2368
         :::|||||       :::|||||
Qy   728 LeuProPheValPheAsnAlaArgPheAlaTyrGlyValHisThrAspAsnMetThrThr 747
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PS   Disclosure; Page 78-80; 115pp; English.
XX
CC   This polypeptide is described as a subsequence of the claimed
CC   novel surface exposed protein Omp5 (see AAW88418) of Chlamydia
CC   pneumoniae, a human respiratory pathogen.  The invention provides
CC   a new species specific test for identifying mammals (including
CC   humans) infected with C. pneumoniae.  The test comprises detecting
CC   antibodies specific for surface exposed proteins Omp4-Omp15 (see
CC   AAW88417-28) or detecting nucleic acid fragments encoding them (see
CC   AAX06816-27), especially by PCR.  The proteins are also used in the
CC   diagnosis of C. pneumoniae infection in mammals.  The nucleic acids
CC   and proteins can also be used in the immunization of mammals, the
CC   nucleic acids being particularly useful as DNA vaccines for
CC   effecting in vivo expression of antigens.  The vaccines may also
CC   prevent atherosclerosis and bronchial asthma, which are possibly
CC   associated with C. pneumoniae.
XX
SQ   Sequence  914 AA;
```

Alignment Scores:

```
Pred. No.:                          Length:           914
Score:                  2.78e-155   Matches:          432
Percent Similarity:     61.22%      Conservative:     141
Best Local Similarity:  36.85%      Mismatches:       319
Query Match:                        Indels:            44
DB:                                 Gaps:              20
```

US-09-428-122-1 (1-3000) x AAW88429 (1-914)

```
Qy   101 ATGAAGTCTTCTTCCCCAAGTTTGTATT---TCTACATTTGCTATTTC--------  148
             ||||||||| ||||                :::  |||  ||| |||
Db     1 MetLysSerGlnPheSerTrpLeuValLeuSerSerThrLeuAlaCysPheThrSerCys   20

Qy   149 CCTTTGCTATGATGCTACCGAGACAGTTTTGGATTCAAGTGCGAGTTTCGATGGGAAT  208
                                 :::   ||||     |||||| ||
Db    21 SerThrValPheAlaAlaThrAlaGluAsnIleGlyProSerPheAspGlySer   40

Qy   209 AAAAAT---GGTAATTTTCAGTTCGTGAGAGTCAGGAAGATGCTGAACTACCTACCTA  265
             ||||||:|:::|||                    ||   :::
Db    41 ThrAsnThrGlyThrThrProLysAsnThr------ThrThrGlyIleAspTyrThr   58

Qy   266 TTTAAGGGAAATGTCACTCTAGAAAAATATCCTGGAACAGCAGGACACAGAATCACAAAAAGC  325
            |||    ||||:|||:|||::||||||     ||| ||  ||||||||
Db    59 LeuThrGlyAspIleThrLeuGlnAsnLeu---GlyAspSerAlaAlaLeuThrLysGlyGly   77

Qy   326 TGTTTTAACACACTAAGGGCGATTGACTTTCACAGTAACGGGAACTCTCTATTGTTC  385
            ||||||||:|:::|||                 ||:|||||
Db    78 CysPheSerAspThrThrGluSerPheAlaGlyLysGlyTyrSerLeuSerPhe   97

Qy   386 CAAACGGTGGATGCAGGGACTGTAGCAGGGGGCTGCTGTTAACAGCAGCGTGTAGATAAA  445
            |||||           :::     ||   |||||||||||:::
Db    98 LeuAsnIleLysSer---SerAlaGluGlyValGlyAlaAlaLeu---SerValThrThrAspLys   115

Qy   446 TCTACCACGTTTATAGGGTTTCTTCGGTCATCTTTTATTGGGTCTCCTGGAAGTTCGATA  505
            :::     ::::  ||||||||       |||||||
Db   116 AsnLeuSerLeuThrGlyPheSerSerLeuThrPheLeuAlaAlaProSerSerValIle   135

Qy   506 ACTACC------GGCAAGAGGAGCCGTTAGCATCCTCACGGGTAGCTTGAGTTTGACAAAA  559
            |||||       |||||||       |||:::
Db   136 ThrThrProSerGlyLysGlyAlaValLysCysGly---GlyAspLeuThrPheAspAsn   154

Qy   560 AATGTCAGTTGCTCTTCAGCAAAACTTTTCAACCGGATAATGGCGATCACCGCA  619
            ||     :::        ||      :::         ::: |||||||||
Db   155 AsnGlyThrIleLeuPheLysGlnAspTyrCysGluGlyAsnGlyAlaIleSerThr  174

Qy   620 AAAACTCTTTCATTAACAGGACTACAATGCACATGTCGTCTGTTTTCTGAAAATACCTCCTCA  679
            |||    ||   |||||||||         |       :::||||
Db   175 LysAsnLeuSerLeuIleAsnSerThrGlySerIleSerProGluGlyAsnGlyAsnSerSer   194

Qy   680 ------AAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTACCATTACTGGAAAC  730
            :::           |||||||||  :::   ::: |||
Db   195 AlaThrGlyLysLysGlyGlyAlaIleGlnThrSerAspAlaThrValAspIleThrAsnAsn   214
```

Left column (continuation of alignment):

```
Qy  2369 AGTATACACAATATCCTACTGTTAAAGGAAGCTGGGAATGATAGTTTCGCTTAGAA  2428
             |||||||||             |||||||||||| :::|||   |||
Db   748 LysTyrThrGlyTyrSerProValLysProGlySerTrpGlyIleAsnAspAlaPheIleGlyGlu  767

Qy  2429 TTCGGTGGAAGAGCTCCGATTGCTTAGAT---GAAAGTGCTCTATTGGAGCAGTACATG  2485
             |||||                 :::    ::: |||
Db   768 CysGlyGlyAlaIleProValValAlaSerGlyArgArgSerTrpValAspThrHisThr  787

Qy  2486 CCCTTCATGAAATGCAGTTGTCTCATGCACATCAGGAAGGTTTTAAAGAACAGGGAACA  2545
             |||||||:::  |||:::  ||| |||||||
Db   788 ProPheLeuAsnLeuGluMetIleTyrAlaHisGlnAsnAspPheLysGluAsnGlyThr  807

Qy  2546 GAAGCTCGTGAATTGGAAGTAGCCGTCTCTGTGAATCTTGCCTTACCTATCGGGATCCGA  2605
             |||     ||||||||||        |||||:::|||::|
Db   808 GluGlyArgArgSerPheGluGlnSerPheAsnLeuPheAsnLeuAlaValProValGlyIleLys  827

Qy  2606 TTTGATAAGGAATCAGACTGCCAAGAGTCAACGTACAAATCAACTCCTTGGTTATACTGTG  2665
             |||  ::::||| ||||||      ::||::::|:::
Db   828 PheGluLysPheSerAsp------LysSerThrTyrAspLeuSerIleAlaTyrValPro  845

Qy  2666 GATCTTGTTCGTGTAGTAACCCGACTGTACGACAACACTGCGGAATTAGCCGGTGATTCTTGG  2725
             |||||:::||| |||||||||||||||      ||:::
Db   846 AspValIleArgAsnAspProGlyCysThrThrLeuMetValSerGlyValAspSerTrp  865

Qy  2726 AAAACCTTCGTACCAGAATTGGCAAGACAAGCTTTAGTCCTTCGTGCAGGGAACCATTTT  2785
             ||||||||:::|||||||||||:::||||||||:::
Db   866 SerThrCysGlyThrSerLeuSerArgGlnAlaLeuLeuValArgAlaGlyAlaGlyAsnHisHis  885

Qy  2786 TGCTTTAACTCAAATTTTGAAGCCTTTAGCCAATTTCTTTGAATTGCCTGGGTCATCT  2845
             |||||                  :::  |||||||||
Db   886 AlaPheAlaSerAsnPheGluValPheSerGlnPheGluValGluValGlyLeuArgGlySerSer  905

Qy  2846 CGCAATTACAAATGTAGACTTAGGAGCAAAAATACCAATTC  2884
             ||||||||||:::     :::   ||||||
Db   906 ArgSerTyrAlaIleAspLeuGlyAlaArgPheGlyPhe  918
```

```
RESULT 10
AAW88429
ID   AAW88429 standard; Protein; 914 AA.
XX
AC   AAW88429;
XX
DT   26-APR-1999  (first entry)
XX
DE   Chlamydia pneumoniae surface exposed protein Omp5.
XX
KW   Omp5; outer membrane protein 5; surface exposed protein; antigen;
KW   infection; diagnosis; vaccine; atherosclerosis; asthma.
XX
OS   Chlamydia pneumoniae.
XX
PN   WO9858953-A2.
XX
PD   30-DEC-1998.
XX
PF   19-JUN-1998;  98WO-DK00266.
XX
PR   23-JUN-1997;  97DK-0000744.
XX
PA   (BIRK/) BIRKELUND S.
PA   (CHRI/) CHRISTIANSEN G.
XX
PI   Birkelund S, Christiansen G, Knudsen K, Madsen A;
PI   Mygind P;
XX
DR   WPI; 1999-105610/09.
DR   N-PSDB; AAX06828.
XX
PT   Species-specific test for identifying mammals infected with
PT   Chlamydia pneumoniae - comprises detecting antibodies specific for
PT   outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT   these proteins
XX
```

Qy   731 CAAGGGGAGTCTCTTTTCTGACAATACTTCTTCGGATTCTGAGCTGCAATTTTACA 790
          ||||||||||| :: ||||||| ||||| ||
Db   215 ThrAlaProThrLeuPheSerAsnIleAlaGlyLeuAlaLeuAlaGlyAlaIleAlaIleAsnSer 234

Qy   791 GAAGCCTCGGTGACTATTCCAATAATGCTAAAGTTCCTTATTGACAATAAGGTCACA 850
          ::: ||| :::::|| ||||||
Db   235 ThrGlyAsnCysThrIleThrGlyAsnThrSerLeuValPheSerGluAsnSerValThr 254

Qy   851 GGAGCCAGCTCCTCAACAACGGGGGATATGTCAGGAGGTGCTATCTGTGCTTATAAAACT 910
          --------------- ||||| |||| |||::::
Db   255 ------AlaThrAlaGly------AsnGlyAlaLeu- 263

Qy   911 AGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAGCAACAATACA 970
          ||| |||||||||||||| ||||||||| ||||||||
Db   264 SerGlyAspAlaAspValThrIleSerGlyAsnGlnSerValThrPheSerGlyAsnGln 283

Qy   971 TCGACAACAGCGGGAGGAGCTATCTATGTGAAAAAGCTGCAACTGGCTTCC------GGA 1024
          :::
Db   284 AlaValAlaAsnGlyAlaIleTyrValAlaLysLysLeuGlnLeuAlaSerGlyGlyGly 303

Qy   1025 GGACTTACCCTATTCAGTAGAAAATAGTGTCAATGAGGTACAGCTCCTAAGGTGGAGCC 1084
          ||||||| ||||| |||||||||||
Db   304 GlyGlyIleSerSerPheSerAsnIleValGlnGlyThrThrAlaGlyAsnGlyAlaAla 323

Qy   1085 ATAGCTATCGAGAATAGTGGGGAATTGAGTTTATCCGCCGATAGTGTGACATTGTCTTT 1144
          ||||||||||||||||| |||:::::::::|||||||
Db   324 IleSerIleLeuAlaAlaGlyGluCysSerLeuSerAlaGluAlaGluAlaGlyAspIleThrPhe 343

Qy   1145 TTAGGGATACAGTCACTTCTACTACTCCT---GGGACGAATAGAAGTAGTATCGACTTA 1201
          |||::::||||||||||
Db   344 AsnGlyAsnAlaIleValAlaThrThrProGlnThrThrLysArgAsnSerIleAspIle 363

Qy   1202 GGAACGAGTGCAAGATGACAGCTTTGCGTTCTGCTGGTAGAGCCATCTACTTCTTAT 1261
          |||||||||/||:::||||
Db   364 GlySerThrThrAlaLysIleThrAlaAsnLeuArgAlaIleSerGlyHisSerIlePhePheTyr 383

Qy   1262 GATCCCATAACTACACAGGATCATCCACACAGGTTACAGATGTCTTAAAAGTTAATGAGACT 1321
          ||:::|| ||| |||
Db   384 AspProIleThrAlaAsnThrAlaAlaAspSerThrAspThrLeuAsnLeuAsnLysAla 403

Qy   1322 CCCGGCAGATTCTGCACTACAGAATATACAGGGAACATCATCTTCACAGGAGAAAAGTTATCA 1381
          |||::::::::||| |||||||||||||||
Db   404 AspAlaGlyAsnSerThrAspTyrSerGlyIleValPheSerGlyGlyGluLysLeuSer 423

Qy   1382 GAGACAGAGGGCCGCAGATTCTAAAAATCTACTTCGAAGCTACTACAGGCCTGTAACTCTT 1441
          ::: ||||
Db   424 GluAspGluAlaLysLeuAlaAspAsnLeuThrSerHisLeuLysGlnProValThrLeu 443

Qy   1442 TCAGGAGGTACTCTATCTTTAAAACATGGAGTGACTCTGCAGCATTCACTCCAA 1501
          ||||| |||||||||
Db   444 ThrAlaGlyAsnLeuValLeuLysArgGlyValThrLeuAspThrLysGlyPheThrGln 463

Qy   1502 CAGGCAGATTCTCGTCTCGAAATGACGTAGGAACTACTCTAGAACCTGCT--GATACT 1558
          |||||| :::   :::
Db   464 ThrAlaGlySerSerValIleMetAspThrAspAlaAlaGlyThrThrLeuLysAlaSerThrGluGlu 483

Qy   1559 AGCACCATAAACAATTTGGTCATTAACATCAGTTCTATAGACGGTGCAAGAAGGCAAAA 1618
          |||||| |||||||||
Db   484 ValThrLeuThrGlyLeuSerIleProValAspSerLeuGluGlyLysLysValVal 503

Qy   1619 ATAGAACCAAAGCTACGTCAAAAATCTGACTTATCCTGGAACCATCACTTATTGGAC 1678
          ||::::::||||||:::::
Db   504 IleAlaAlaSerAlaAlaSerLysAsnValAlaLeuAlaSerGlyProIleLeuLeuLeuAsp 523

Qy   1679 CCGGAGCCGCACGTTTTATGAAAATCATAGTTAAGAAAATCCTCAGTCCTACGACATCTTA 1738
          ||||||| ::::   :::
Db   524 AsnGlnGlyAsnAlaAlaTyrGluAsnHisAspLeuGlyLysThrGlnAspPheSerPheVal 543

Qy   1739 GAGCTTCAAAGCTTCTGGAACTGTACCAAGCACCGGACTGACTCCAGAATCCTATAATGGGT 1798
          ||:::::::|||||||::::
Db   544 GlnLeuLeuSerAlaLeuGlyThrAlaThrThrAspValProAlaValProThrValAla 563

Qy   1799 GAGAAAATTCCATTACCGGCTATCAGGGAACTTGGGGCCCAATTGTTGG-------- 1846

Qy   564 ThrProThrHisTyrGlyTyrGlyIleGlyThrTrpGly--MetThrTrpValAspAspThr
          ||||||||||||| ::: ||| |||
Db   1847 ---GGGACAGGGGCTTCTACGACTGCAACCTTCAACTGGACTAAAACTGGCTATATTCCT 1903

Db   583 AlaSerThrProLysThrLysThrLeuAlaThrLeuAlaThrArgThrArgAsnThrArgLeuPro 602
          ||| ::: ||::::|||
Qy   1904 AATCCCGGAGCTATCGGCTCTTAGTCCCTAATAGCTTATCGGAATGCATTATAGATATT 1963

Db   603 AsnProGlyArgGlnGlyProLeuValProAsnSerleuThrProGlyAsnSerPheSerPheIle 622
          |||||||||||
Qy   1964 AGCTCTCCATTATCTTATGGAGACTGCAAATCAGAAGGGTTGCAGGGAGACCGTGCTTTT 2023

Db   623 GlnAlaIleGlnGlyValIleGluArgSerAlaLeuThrLeuCysSerAspArgGlyPhe 642
          :::::   :::||||||||||||
Qy   2024 TGGTGTGCTGGATTATCTAACCTTCTTCCATAAGGATAGTACAAAAAACACGACGCGGGTTT 2083

Db   643 TrpAlaAlaGlyValAlaAlaAsnPheLeuAspLysLysGlyGluLysArgLysTyr 662
          :::::::::|||||| |||
Qy   2084 CGCCATTTGAGTGGCGGTTATGTCATAGGAGGAAAACCTACACTTGTTCAGATAAGAATT 2143

Db   663 ArgHisLysSerGlyGlyTyrAlaIleGlyGlyTyrAlaAlaGlnThrCysSerGluAsnLeu 682
          |||||||||||||||| ::::: ||||||
Qy   2144 CTTAGTGCTGCATTTGTCAGCTCTTTGGAAGAGACTTTGGTAGCTACTAGCTAAGAAT 2203

Db   683 IleSerPheAlaPheCysGlnLeuPheGlySerAspLysAspPheLeuValAlaLysAsn 702
          :::||| ||| ||||||||||
Qy   2204 CAAGGTACAGTCTACGGAGGAACTCTTATTACCAGCACAACGAAACCTATATCTCTCTT 2263

Db   703 HisThrAspThrThrTyrAlaGlyAlaPheTyrIleGlnHis----------IleThrGlu 718
          :::||||||||||||||||||
Qy   2264 CCTTGCAAACTACGGCCTTGTTCGTTGCTTCTTATGTTCCT---ACAGAATTCCT 2314

Db   719 CysSerGlyPheIleGlyPheCysLeuLeuAspLysProGlySerTrpSerHisLysPro 738
          :::
Qy   2315 GTTCTCTTTCAGGAAACCTTAGCTACACCATACGACTACGGATAACGATCTGAAAAACCAAGTAT 2374

Db   739 LeuValLeuGluGlyGlnLeuAlaTyrSerHisValSerAsnAspLeuLysThrLysTyr 758
          |||||||||||||||||||
Qy   2375 ACACACATATCCTACTGTTAAAGGAAGCTGGGGGAATGAGTTTCGCTTTAGAATTCGGT 2434

Db   759 ThrAlaTyrProGluValLysGlyValLysGlyAsnAsnAlaPheAsnMetLeuGly 778
          ||| :::||||||||||||
Qy   2435 GGAAGAGCTCCGATTTGCTTAGATGAAGAGTGCTCTATTTGAGCAGTAGCATGCCCTTCATG 2494

Db   779 AlaSerSerHisSerTyrProGluTyrLeuHisCysPheAspThrTyrAlaProTyrIle 798
          :::
Qy   2495 AAATTGCAGTTGTCTATGCACATCAGGAAGGTTTAAAGAGGTTCTTGGAAAAACCTTC 2554

Db   799 LysLeuLeuAsnLeuThrTyrIleArgGlnAspSerPheSerGlyValThrGluGlyArg 818
          ::: ||||||||
Qy   2555 GAATTGGAAGTAGCCGTCTTGTGAATCTTTGCCTTACCCATTGGATCCGATTTGATAAG 2614

Db   819 SerPheAspAspSerAsnLeuPheAsnLeuSerLeuProIleGlyValLeuLysProGluLeuLys 838
          :::   :::
Qy   2615 GAATCAGACTGCCAAGATGCCAAGATGCAACGTACAATCTAACTCTTGTTATACTGTGGATCTTGTT 2674

Db   839 PheSerAspCysAsnAspPheSerTyrAspLeuThrLeuSerTyrValProAspLeuIle 858
          |||
Qy   2675 CGTAGTAACCCCGACTGTACGACAACACTGCGAATTAGCGGTGATTCTTGGAAAACCTTC 2734

Db   859 ArgAsnAspProLysCysThrThrThrAlaLeuValIleSerGlyAlaSerTrpGluThrTyr 878
          |||||:::::   :::
Qy   2735 GGTACGAATTTGGCAAGACAAGCTTTAGTCTTGCGTCGCAGGGAACCATTTTGCTTTAAC 2794

Db   879 AlaAlaAsnAsnAlaLeuArgGlnAlaLeuLeuGlnValAlaArgAlaGlySerHisTyrAlaAlaPheSer 898
          :::::::::   :::
Qy   2795 TCAAATTTGAAGCCTTAGCCAATTTCTTTTGAATTGCGTGGGTCA 2842

Db   899 ProMetPheGluValLeuGlyGlnPheGluValPheGluAlaValProThrValAla 914

RESULT 11
AAY90238

```
ID   AAY90238 standard; Protein; 885 AA.
XX
AC   AAY90238;
XX
DT   29-AUG-2000  (first entry)
XX
DE   Mature Chlamydia antigen CPN100635.
XX
KW   Chlamydia antigen; diagnosis; infection; community acquired pneumonia;
KW   therapy; upper respiratory tract disease; bronchitis; sinusitis;
KW   asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma.
XX
OS   Chlamydia pneumoniae.
XX
PN   WO200032794-A2.
XX
PD   08-JUN-2000.
XX
PF   01-DEC-1999;  99WO-CA01147.
XX
PR   01-DEC-1998;  98US-0110339.
PR   01-DEC-1998;  98US-0110340.
PR   01-DEC-1998;  98US-0110427.
PR   01-DEC-1998;  98US-0110428.
PR   01-DEC-1998;  98US-0110438.
XX
PA   (CONN-) CONNAUGHT LAB LTD.
XX
PI   Murdin AD, Oomen RP, Wang J;
XX
DR   WPI; 2000-412339/35.
DR   N-PSDB; AAA30849, AAA30850.
XX
PT   Nucleic acids encoding polypeptide antigens from Chlamydia useful for
PT   preventing, diagnosing and treating diseases such as community acquired
PT   pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
PT   asthma -
XX
PS   Claim 16; Fig 3; 174pp; English.
XX
CC   This sequence is a Chlamydia antigen of the invention, designated
CC   CPN100635. The nucleic acids (and their complementary sequences) may be
CC   used as diagnostic agents for detecting the presence of nucleic acids
CC   encoding Chlamydia antigens in samples according to standard methods,
CC   and therefore, for diagnosing Chlamydia infections. For example, they may
CC   be used as primers and probes for diagnostic polymerase chain reaction
CC   (PCR) assays. Antisense sequences may be used to down regulate
CC   expression of the proteins and may be used to treat infections. The
CC   nucleic acids may also be used to produce the protein antigens they
CC   encode according to standard recombinant DNA methodologies. The
CC   proteins may then be used as antigens for the production of antibodies
CC   (i.e. as vaccines) for preventing infection by Chlamydia. The
CC   antibodies may also be used as diagnostic reagents for detecting
CC   infections. Chlamydia is a pathogen implicated in the development of
CC   (for example) community acquired pneumonia, upper respiratory tract
CC   disease (especially bronchitis and sinusitis, asthmatic bronchitis,
CC   adult-onset asthma and acute exacerbations of asthma in adults.
XX
SQ   Sequence    885 AA;
```

Alignment Scores:

```
Pred. No.:           7.81e-155     Length:        885
Score:               1987.50       Matches:       420
Percent Similarity:  62.12%        Conservative:  136
Best Local Similarity: 46.93%      Mismatches:    302
Query Match:         36.74%        Indels:        37
DB:                  21            Gaps:          16
```

```
US-09-428-122-1 (1-3000) x AAY90238 (1-885)

Qy    251 GGAACTACCTACCTATTTAAGGGAAATGTCACTCTAGAAAATATTCCTGGAACAGGCACA 310
          |||   |||||||      |||||||||||||:::||||||:::        |||
Db     11 GlyIleAspTyrThrLeuThrGlyAspIleThrLeuGlnAsnLeu--GlyAspSerAla 29
```

```
Qy    311 GCAATCACAAAAAGCTGTTTAACAACACTAAGGGCCGATTGACTTTCACAGGTAACGGG 370
          ||||   ||||||| ::::|||||   |:::||| |||   |||
Db     30 AlaLeuThrLysGlyCysPheSerAspThrThrGLuSerLeuSerPheAlaGlyLysGly 49
```

```
Qy    371 AACTCTCTATTGTTCCAAACGGTGGATGCAGGAGTCGTAGCAGGGGCGTCGTTAACAGC 430
          |||||       ::: ::: :::   |||| ::: ||| ::: ||| ||
Db     50 TyrSerLeuSerPheLeuAsnIleLysSer---SerAlaGluGlyAlaAlaLeu---Ser 67
```

```
Qy    431 AGCGTGTAGATAAATCTACCACGTTTATAGGGTTTCCTGCTATCTTTTATTGGTGTCT 490
          |||| |:::| ::::  ||||||||||||||||:::|||||||||:::
Db     68 ValThrThrAspLysAsnLeuSerLeuThrGlyPheSerSerLeuThrPheLeuAlaAla 87
```

```
Qy    491 CCTGGAAGTTCGATAACTACC------GGCAAAGGAGCCGTTAGCTGCTCCTACGGGTAGC 544
          |||   |||  ||||||||||       ||   |:::||||||||||  ||
Db     88 ProSerSerValIleThrThrProSerGlyLysGlyLysAlaValLysCysGly---GlyAsp 106
```

```
Qy    545 TTGAGTTGACAAAAAATGTCAGTTTGCTCTTCAGCAAAAACTTTTCAACCGATAATGGC 604
          |||:::                :::|||||::::        :::||||  |||
Db    107 LeuThrPheAspAsnAsnGlyThrIleLeuPheLysGlnAspTyrCysGluGluAsnGly 126
```

```
Qy    605 GGTGCTATCACCGCAAAAACTCTTTCATTACAGGGACTACAATGTCAGCTCGTTTTCT 664
          ||||| |||||          |||||| ::: |||
Db    127 GlyAlaIleSerThrLysAsnLeuLysAsnSerThrGlySerIleSerPheGlu 146
```

```
Qy    665 GAAAATACCCCTCA--------AAGAAAGGCGAGCCATTCAGACTTCCGATGCCCTT 715
          ||| |||:::::: ||         |||   :::   :::  |||
Db    147 GlyAsnLysSerSerAlaThrGlyLysLysGlyLysGlyAlaIleCysAlaThrGlyThrVal 166
```

```
Qy    716 ACCATTACTGGAAACCAAGGGAGTCTCTTTTCTGACAATACTTCTTCCGGATTCTGGA 775
          ||| |||||||||||||                ||||| ||| :::||
Db    167 AspIleThrAsnAsnThrAlaProThrLeuPheSerAsnAsnIleAlaGluAlaAlaGly 186
```

```
Qy    776 GCTGCAATTTTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTCCTTTATT 835
          |||||| |:::                ::: :::   :::   :::
Db    187 GlyAlaIleAsnSerThrGlyThrIleThrGlyAsnCysThrLeuThrSerLeuValPheSer 206
```

```
Qy    836 GACAATAAGGTCACAGGAGCGAGCTCCTCAACAACGGGGATATGTCAGGAGGTGCTATC 895
          ::::|||  |||          |||||||||         :::|||
Db    207 GluAsnSerValThr--------------AlaThrAlaGly-----AsnGlyGlyAlaLeu 220
```

```
Qy    896 TGTGTCTTATAAAACTAGTACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTC 955
          ||| |||      |||||| |||   ::: |||||||::::||
Db    221 -------------------SerGlyAspAlaAspValThrIleSerGlyAsnGlnSerValThr 235
```

```
Qy    956 TTCAGCAACAATACATCGACACAGCGGAGGAGCTATCTATGTGAAAAAGCTCGAACTG 1015
          ||||||||                |||||| ||||| |:::|||||
Db    236 PheSerGlyAsnGlnAlaValAlaAsnGlyGlyAlaIleThrTyrAlaLysLysLeuThrLeu 255
```

```
Qy   1016 GCTTCC------GGAGGACTTACCCTATTCAGTAGAAAATAGTGTCAATGGAGGTACCAGCT 1069
          |||||       || ||| ||||||||| |||  |||||||:::|||||| |||
Db    256 AlaSerGlyGlyGlyAsnGlyGlyAsnProPheSerAsnAsnIleValGlnGlyThrThrAla 275
```

```
Qy   1070 CCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGGGAATTGAGTTTATCCGCCGATAGT 1129
          ||| |||||| |||||||          :::|||   ||| :::||
Db    276 GlyAsnGlyGlyAlaIleSerIleLeuAlaAlaAlaGlyGluCysSerLeuPheSerGluAla 295
```

```
Qy   1130 GGTGACATTGTCTTTTTAGGGAATACAGTCACTCCTACTACTCCT---GGGACGAATAGA 1186
          |||||| |:::        ||| :::|||||  |||||||||    |||
Db    296 GlyAspHisTyrLeuAsnGlyAsnAlaIleValAlaThrThrProGlnThrThrLysArg 315
```

```
Qy   1187 AGTAGTATCGACTTAGGAACGAGTGCAAAGATGCAGAGCGTTTGCGTTCGTCCTGGTAGA 1246
          ::::||||       |||||:::::: |:::  ::: |||||| ||
Db    316 AsnSerIleAspIleGlySerThrGlyLysAspHisGluLeuArgAlaIleSerGlyHis 335
```

```
Qy   1247 GCCATCTACTTCTATGATCCCATAACTACACAGGATCATCCACAACAGTTACAGATGTCTTA 1306
          |||||||||| ||||||:::        |||||:::||| |||:::
Db    336 SerIlePhePheTyrAspProIleThrAlaLysAsnThrAlaAlaAlaAspSerThrLeu 355
```

```
Qy   1307 AAAGTTAATGAGACTCCGGCAGATTCTGCACTACAATATACAGGGACACATCCTTCACA 1366
          :::|||              |||||| :::  |:::||||||:::::: |||||:::
Db    356 AsnLeuAsnLysAlaAlaAspAlaGlyAsnSerThrAspTyrSerGlySerIleValPheSer 375
```

Qy   1367 GGAGAAAAGTTATCAGAGACAGAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTA 1426
               |||||||||||||||| ::| ||||||| ||||||| :
Db   376 GlyGluLysLeuSerGluAspGluAlaLysGlnAlaLysValAlaAspAsnLeuThrArgLeuLys 395

Qy   1427 CAGCCTGTAACTCTTTCAGGAGTACTCTATCTTTAAAACATGGAGTGACTCTGCAGACT 1486
               ||||||||| ::|||||||| ||| |||||| ||||||||
Db   396 GlnProValThrLeuThrLeuPheArgGlyAsnLeuValLeuGlyValArgGlyValThrLeuAspThr 415

Qy   1487 CAGGCATTCACTCAACAGGCAGAGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAA 1546
               ::: ||||||| | ||| : |||||||| :::|||
Db   416 LysGlyPheThrGlnThrAlaGlySerValIleMetAspAlaAlaGlyThrThrLeuLys 435

Qy   1547 CCTGCT--GATACTAGCACCATAAACAATTGGTCATTAACATCAGTTCATATAGACGGT 1603
                 ::: ||||||||| ||||||||| :: |||||||
Db   436 AlaSerThrGluGluValThrLeuThrGlyLeuSerIleProValAspSerLeuGlyGlu 455

Qy   1604 GCAAAGAGGCAAAAATAGAAACCAAAGTACGTCAAAAAATCTGACTTATCTGGAACC 1663
               |||||| ||||||::::||||||| ||||||| ||||||
Db   456 GlyLysLysValAlaValIleAlaAlaAlaSerLysAsnValAlaLeuSerGlyPro 475

Qy   1664 ATCACTTTATTGGACCCGACACGGGCACGTTTTATGAAAATCATAGTTTAAGAAATCCTCAG 1723
               ||:|||:|::||| |||||||| |||||| :
Db   476 IleLeuLeuLeuAspProAsnGlyAsnAlaTyrGluAsnHisSerLeuGlyLysThrGln 495

Qy   1724 TCCTACGACATCTTAGAGCTCAAAGCTTCTGGAACTGTAACAAGCACCGCAGTGACTCCA 1783
               :::|||||| ||| ||||||||| ||||||||||||:::||
Db   496 AspPheSerPheValGlnLeuSerAlaLeuGlyThrAlaThrThrThrAspValProAla 515

Qy   1784 GATCCTATAATGGGTGAGAAATTCATTACGGCTATCAGGGAACTGGGGCCCAATTGTT 1843
               ||||||||||||||||||| :::|||:::|||||||:::
Db   516 ValProThrValAlaThrProThrHisTyrGlyTyrGlyLeuThrTrpGlyTyr---MetThr 534

Qy   1844 TGG------------GGGACAGGGGCGGTTTCTACGACTGCAACCTTCAACTGGACTAAA 1888
               ||| ||| :::::::|||:::|| |||||||||
Db   535 TrpValAspThrArgAlaSerThrProLysThrLysThrAlaThrTrpThrLeuAlaThrTrpThrAsn 554

Qy   1889 ACTGGCTATATCCTAATCCCGAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAAT 1948
               ||||||||::: ::||||||||||||| |||||||
Db   555 ThrGlyTyrLeuProGluProAsnProGlyGlnGlyProLeuValProAsnSerLeuTrpGly 574

Qy   1949 GCATTTATAGATATTAGTCTCTCCATTATCTTATGGAGACTGCAAACGAAGGGTTGCAG 2008
               :::||| ||:::   :: :::||||
Db   575 SerPheSerAspIleGlnAlaIleGlnAlaIleGlnValIleGluArgSerAlaLeuThrLeuCys 594

Qy   2009 GGGAGACCCGTGCTTTTTGGTGTGCTGGATTATCTAACTTCTCCATAAGGATAGTACAAAA 2068
               |||||||||||||||||| ||||||
Db   595 SerAspArgGlyPheThrTrpAlaAlaGlyValAlaAlaAsnPheLeuAspProLysLysGlyGly 614

Qy   2069 ACACGACGCGGGGTTTCGCCATTTGAGTGGCGGTTATGTCATAGGAGGAAAACCTACATACT 2128
               ::|||| |||||||||||||||||||||||||| :: |||||||
Db   615 GluLysArgLysTyrArgHisLysSerGlyGlyTyrAlaIleGluGlyTyrAlaIleAlaGlnThr 634

Qy   2129 TGTTCAGATAAGATTCTTAGTGTGCTGCATTTGTCAGCTCTTTGAAGAGAGAGATAGAGACTAC 2188
               |||||||::: :::::||| |||:::|| ||||||||||| :::
Db   635 CysSerGluAsnLeuIleSerPheAlaPheCysGlnLeuPheCysGlySerAspLysAspPhe 654

Qy   2189 TTTGTAGCTAAGAATCAAGGTACAGTCTACGGAGGAACTCTCATTACCAGCACACAACGAA 2248
               ||||||||||||||||| ||||| |||||| |||||||||||
Db   655 LeuValAlaLysAsnHisThrAspThrTyrArgAlaGlyAlaPheTyrIleGlnHis------ 672

Qy   2249 ACCTATATCTCTCCTTGCAAACTACGGCCTTGTTCGTTGTCTTATGTTCCT------ 2302
               ::::: |||||||||| ||||||||||
Db   673 ------IleThrGluCysSerSerGlyPheIleIleGlyCysLeuLeuAspLeuProGlySer 690

Qy   2303 --ACAGAGATTCCGTGTCTCTTTCAGGAGAACCTAGCTACACCCCATACGGATAACGAT 2359
               ::: ||||||::::||||||||||
Db   691 TrpSerHisLysProLeuGlyLeuGlyLeuGlyLeuLeuGlyLeuGlnLeuAlaTyrSerHisValSerArgAsnAsp 710

Qy   2360 CTGAAAACCAAGTATCAACAACATATCCCTACTGTAAAGGAAGCTGGGGAATGATAGTTTC 2419
               ||||||| ::: ||||||::| ||||||||||:::
Db   711 LeuLysThrLysTyrThrAlaTyrProGluValLysGlySerTrpGlyValPheGlyAlaAsnAlaPhe 730

Qy   2420 GCTTTAGAATTCGGTGGAAGAGCTCCGATTTGCTTAGATGAAGAAGTTGCTCTCATTGAGCAG 2479

Db   731 AsnMetMetLeuGlyAlaSerHisSerTyrProGluTyrTyrLeuHisCysPheAspThr 750

Qy   2480 TACATGCCCTTCATGAGAATTGCAGTTTGTCATGCACATCAGGAAGGTTTAAAGAACAG 2539
               ||| :::|||||||||||| ||:::|| :::|||||
Db   751 TyrAlaProTyrIleLysLeuAsnLeuThrTyrIleArgGlnAspSerPheSerGluLys 770

Qy   2540 GGAACAGAAGCTCCGTGAATTTGGAAGTAGCGCGTCTTGTGAATCTTCCTTACCTATCGGG 2599
               :::|||||||||| |||| :::|||||||
Db   771 GlyThrGluGlyTyrArgSerPheAspAspSerAsnLeuPheAsnLeuSerLeuProIleGly 790

Qy   2600 ATCCGATTTGATAAGGAATCAGACTGCCAAGATGCAAGATGCAACCAATCAACTCTTGGTTAT 2659
               :::::::::||||||| :|||:::||||| |||:::|||||
Db   791 ValLysPheGluLysPheSerAspCysAsnAspPheSerTyrLeuThrLeuSerTyr 810

Qy   2660 ACTGTGGATCTTCGTTCGTAGTACCCGACTGTACGACAACACTGCGAATTAGCGGTGAT 2719
               ||||||||||||:::::||||| |||| |||||||||
Db   811 ValProAspLeuIleArgAsnAspProLysCysThrThrAlaLeuValIleSerGlyAla 830

Qy   2720 TCTTGGAAAACCTTCGGTACGAATTTGGCAAGACAAGCTTTAGTCCTTCGTCGTGCAGGGAAC 2779
               ||:|||::||| |||:::|||||| |||:::||||||
Db   831 SerTrpGluThrPheTyrAlaAsnAsnLeuAlaArgGlnAlaLeuGlnAlaLeuArgAlaGlySer 850

Qy   2780 CATTTTGCTTAACTCAAATTTGAAGCCTTTAGCCAATTTCTTTTGAATTGCGTGG 2839
               ||| :::::|||||||||||||||||:::||||||
Db   851 HisTyrAlaPheSerProMetPheGluValLeuGlyGlnPheValPheGluValArgGly 870

Qy   2840 TCATCTCCGAATTACAATGTAGACTTAGGAGACAAAATACCAATTC 2884
               ||||||| ||||||||||:::|||||||
Db   871 SerSerArgIleTyrAsnValAspLeuAspLeuGlyLysPheGlnPhe 885

RESULT 12
AAW88423
ID   AAW88423 standard; Protein; 928 AA.
XX
AC   AAW88423;
XX
DT   26-APR-1999 (first entry)
XX
DE   Chlamydia pneumoniae surface exposed protein Omp10.
XX
KW   Omp10; outer membrane protein 10; surface exposed protein;
KW   antigen; diagnosis; infection; vaccine; atherosclerosis; asthma.
XX
OS   Chlamydia pneumoniae.
XX
PN   WO9958953-A2.
XX
PD   30-DEC-1998.
XX
PF   19-JUN-1998;   98WO-DK00266.
XX
PR   23-JUN-1997;   97DK-0000744.
XX
PA   (BIRK/) BIRKELUND S.
PA   (CHRI/) CHRISTIANSEN G.
XX
PI   Birkelund S,   Christiansen G,   Knudsen K,   Madsen A;
PI   Mygind P;
XX
DR   WPI; 1999-105610/09.
DR   N-PSDB; AAX06822.
XX
PT   Species-specific test for identifying mammals infected with
PT   Chlamydia pneumoniae - comprises detecting antibodies specific for
PT   outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT   these proteins
XX
PS   Claim 7; Page 60-62; 115pp; English.
XX
CC   This polypeptide comprises the novel 98.4 kDa surface exposed
CC   protein Omp10 of the human respiratory pathogen Chlamydia
CC   pneumoniae. Its amino acid sequence was deduced from DNA (see

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CC   AAX06822) isolated from a C. pneumoniae expression library. The
CC   invention provides 12 novel surface exposed proteins, Omp4-Omp15
CC   (see AAW8417-28), and nucleic acid sequences encoding them (see
CC   AAX06816-27). A new species specific test is claimed that is used
CC   to identify mammals (including humans) infected with Chlamydia
CC   pneumoniae. The test comprises detecting antibodies specific for
CC   Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC   membrane proteins, especially by PCR. The proteins are also used
CC   in the diagnosis of C. pneumoniae infection in mammals. The
CC   nucleic acids and proteins can also be used in the immunization of
CC   mammals, the nucleic acids being particularly useful as DNA
CC   vaccines for effecting in vivo expression of antigens. The
CC   vaccines may also prevent atherosclerosis and bronchial asthma,
CC   which are possibly associated with C. pneumoniae.
XX
SQ   Sequence  928 AA;

Alignment Scores:
Pred. No.:                        1.06e-154
Score:                            1986.00        Length:        928
Percent Similarity:               60.95%         Matches:       430
Best Local Similarity:            45.26%         Conservative:  149
Query Match:                      36.72%         Mismatches:    327
DB:                                               Indels:         44
                                                 Gaps:           20

US-09-428-122-1 (1-3000) x AAW88423 (1-928)
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Qy  101 ATGAAGTCTTCTTCCCCAAGTTGTATTTTCTACATTGCTATTTTCCCTTGTCTATG 160
            ||||||||||                    ::
Db    1 MetLysSerSerLeuHisTrpPheValIleSerSerLeuAlaLeuProLeuSerLeu 20

Qy  161 ----------ATTGCTACCGGAGACAGTTTGGATTCAAGTGCCGAGTTTCGAT 202
            |||          |||    :::    ||||
Db   21 AsnPheSerAlaPheAlaAlaAlaValAlaValGlyIleGluAsnLeuGlyIleProThrAsnSerPheSer 40

Qy  203 GGGAATAAAAAATGGTAATTTTCAGTTCGTGAGAGTCAGGAAGAATGCT---GGAACTACC 259
            ||||||           :: ::::::      |||        ||||||||
Db   41 Gly------ProGlyThrTyrThrProProAlaGlnThrThrAsnAlaAlaSerGlyThrIle 58

Qy  260 TACCTATTAAGGGAAATGCTACTCTAGAAAAATATTCCTGGAACAGCAGCAAATCACA 319
            ||:::::||||         |||        ||| |||:::   |||
Db   59 TyrAsnLeuThrGlyAspValSerErIleThrAsn--AlaGlySerProThrAlaLeuThr 77

Qy  320 AAAAGCTGTTTTAACACACTAAGGGCGATTTGACTTTCACAGGTAACGGAACTCTCTA 379
            ||||||    |||||          ||||        ||||||||: |||
Db   78 AlaSerCysPheLysSerPheGlnGlyHisGlyTyrHisGlyTyrGlnPhe 97

Qy  380 TTGTTCCAAACGGTGGATGCAGGACTGTAGGCAGGGGCTGCTGTTAACAGCAGCGTGGTA 439
            |||         ||||||    ||||::::     |||:::||||:::
Db   98 LeuLeuGlnAsnIleAspAlaGly------AlaAsnCysThrPheThrAsnThrAlaAla 115

Qy  440 GATAAAATCTACCACGTTTATAGGGGTTTTCTTGCTATCTTTATTGCGTCTCCTGGAAGT 499
            ::::|||||              |||:|||  |||   :::
Db  116 AsnLysSerLeuSerPheSerGlyPhePheSerTyrLeuSerLeuIleGlnThr------Thr 133

Qy  500 TCGATAACTACCGGCAAAGGAGGAGCCGTTAGCTGTCTCACGGGTAGCTTGAGTTTGACAAAA 559
            ||:::        ||||| ||||:::     ||||:::
Db  134 AlaSerPheThrGlyAlaIleAlaLys---SerThrGlyAlaCysSerSerIleGlnSer 152

Qy  560 AATGTCAGTTGCTCTTCAGCAAAAACTTTTCAACGGATAATGGCCGGTGCTATCACCGCA 619
            :::||||||    |||||||:: :::||     |||||||:::
Db  153 AsnTyrSerCysTyrPheGlyGlnAsnPheSerAlaAsnAspAsnGlyAlaAlaLeuGlnGly 172

Qy  620 AAAACTCTTTCATTAACAGGACTACACATGTCAGCTCGTTTTCTGAAAATACCTCCTCA 679
            :::||||||||        ::::||| |||:::||||||
Db  173 SerSerIleSerLeuSer--LeuAsnProAsnLeuThrPheAlaLysAsnLysAsnAlaThr 191

Qy  680 AAGAAAGGCGGAGCCAATTCAGACTTCCCATGCCCATTACCATTACTGGAAACCAAGGGGAA 739
            :::||||||      ||||||::: ||:::||||:::
Db  192 GlnLysGlyGlyAlaAsnSerThrGlyIleThrIleAsnAsnThrLeuAsnAsnSer 211

Qy  740 GTCTCTTTTCTGACAATACTCTTCGGATTCTGGAGCTGCAATTTTACAGAAGCCTCG 799
            ||::::||||||     |||:::|||||||||
Db  212 AlaSerPheSerGluAsnThrAlaAlaAlaAsnGlyGlyAlaAlaIleTyrThrGluAlaSer 231

Qy  800 GTGACTATTTCTAATAATGCTAAAGTTCCTTTATTGACATAAGGTCACAGGAGCCGAGC 859
            |||::::||:::
Db  232 SerPheIleSerSerAsnLysAlaAlaIleSerPheIleAsnAsnSerValThrAlaThrSer 251

Qy  860 TCCTCAACACGGGGGATATGTCAGGAGGTGCTATCTGTGCTTATAAAACTAGTACAGAT 919
            :::       |||||||||
Db  252 Ala------ThrGlyGlyAlaAlaIleTyrCysSerSerThrSerAlaPro 265

Qy  920 ACTAAGGTC---ACCCTCACTGGAAATCAGATGTTACTCTTCAGCAACAATACATCGACA 976
            |||       |||||:: ||
Db  266 LysProValLeuThrLeuSerAspAsnGlyGluLeuAsnPheIleGlyAsnThrAlaIle 285

Qy  977 ACAGCCGGGAGGAGCTATCTATGTGAAAAAGTCGAACTGGCTTCCGGAGGACTTACCCTA 1036
            |||||||||||||||         |||||||||||||
Db  286 ThrSerGlyGlyAlaIleTyrThrAspAsnLeuValLeuSerSerGlyGlyProThrLeu 305

Qy 1037 TTCAGTAGAAATAGTGTCAATGAGGTACAGCTCCTAAAGGTGGAGCCATAGTCATCGAA 1096
            ||||||||||||||||||||||
Db  306 PheLysAsnAsnSerAlaIleAspThrAlaAlaProLeuGlyGlyAlaIleAlaIleAla 325

Qy 1097 GATAGTGGGGAATTGAGTTATTATCCGCCGATAGTGGTGACATTGTCTTTTTGGGGATTACA 1156
            |||||||||||||||||||||||||
Db  326 AspSerGlySerLeuSerLeuSerAlaLeuGlyGlyAlaIleGlyIleThrPheGluGlyAsnThr 345

Qy 1157 GTC------ACTTCTACTACCTCTGGGACGAATAGAAGTAGAAGTGATCGCATTAGGA--- 1204
            |||||||                      :::||
Db  346 ValValLysGlyAlaSerSerSerGlnThrThrThrArgAsnSerIleGlyAsnIleGlyAsn 365

Qy 1205 ACGAGTGCAAAGATGACAGCTTGCGTTCTGCGTCTGCTGAGCCATCTACTTCTATGAT 1264
            |||::: |||||       ||||||::: |||
Db  366 ThrAsnAlaLysIleValGlnLeuValArgAlaSerGlnGlyAsnThrIleTyrPheTyrAsp 385

Qy 1265 CCCATAACTACTACAGGATCATCCACAACAGTTACAGATGTCTTAAAAGTTAATGAGACTCCG 1324
            |||||||||||||||||||||||||
Db  386 ProIleThrThrAsnHisThrAlaAlaLeuAsnSerAspAlaLeuAsnGlyProAsp 405

Qy 1325 GCAGATTTGCCACTACATATACAGGAGAACATCATCTTCACAGGAGAAAAGTTATCAGAG 1384
            :::||       ||||||||||
Db  406 LeuAlaGlyAsnProAlaTyrGlnGlyThrIleValPheSerGlyGlyLysLeuSerGlu 425

Qy 1385 ACAGAGGGCGCAGATTCTAAAAATCTTACTTCGAAGTCTACTACAGCCTGTAACTCTTTCA 1444
            :::|||||||                |||:::||||||
Db  426 AlaGluIleAlaGluIleAlaGluAlaAspAsnLeuLysSerThrIleGlnProLeuThrLeuAla 445

Qy 1445 GGAGGTACTCATCTTTAAAACATGGAGTGGAACCATCACTCCAGGCATTCACTCAACAG 1504
            ||||||||||||:::||||||
Db  446 GlyGlyGlnLeuSerLeuLysSerGlyValThrLeuValAlaLysSerPheSerGlnSer 465

Qy 1505 GCAGATTCTCGTCTCGAAATGGACGTAGGAACTACTCTAGAACCTGCTGATACTAGCACC 1564
            |||||||||||||::::|||||||||
Db  466 ProGlySerThrLeuLeuMetAspValSerTrpAsnAsnProGlnValPheSerCysLeuThr 485

Qy 1565 ATAAACAATTTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGAAGGCAAAAATAGAA 1624
            ||:::||      |||::::|||:::
Db  486 IleAsnAsnLeuValLeuAsnValAspSerLeuLysGluThrHisLysLeuLys 505

Qy 1625 ACCAAAGCTACGTCAAAAAATCTGACTTTATCTGGAACCATCACTACTTTTATTGGACCCGACG 1684
            ||||||||||              :::|||:::
Db  506 AlaThrGlnAlaSerGlnThrValThrLeuSerGlyLeuSerLeuValAspProSer 525

Qy 1685 GGCACGTTTTATGAAAATCATAGTTTAAGAAAATCCTCAGTCTACGACATCTTAGAGCTC 1744
            |||||       ::: :::
Db  526 GlyAsnValTyrGluAspValSerTrpAsnAsnProGlnValPheSerCysLeuThrLeu 545

Qy 1745 AAAGCTTCT------GGAACTGTAACAAGCACCGCAGTGACTCCTGACTCCTATAATGGGT 1798
            ||||||||                |||||||||
Db  546 ThrAlaAspAspProAlaAsnIleHisIleThrAspLeuAlaAlaAspProLeuGluLysLys 565

Qy 1799 GAGAAATTCCATTACGGCTATCAGGGAACTTGGGGCCCAATTGTTGGGGACCAGGGGGCT 1858
            ||||||       :::||||||||||||
Db  566 AsnProIleHisTrpGlyTyrGlnGlyThrTrpAla---LeuSerTrpGlnGlnAspThr 584
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RESULT 13
ABB90542
ID   ABB90542 standard; Protein; 928 AA.
XX
AC   ABB90542;
XX
DT   29-JUL-2002 (first entry)
XX
DE   Chlamydia pneumoniae cp6731 protein, SEQ ID NO:33.
XX
KW   Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
KW   human respiratory disease; cardiovascular disease; atherosclerosis;
KW   coronary artery disease; carotid artery stenosis; myocardial infarction;
KW   cerebrovascular disease; aortic aneurysm; claudication; stroke;
KW   strain CWL029.
XX
OS   Chlamydia pneumoniae.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..26
FT   /label= Signal_peptide
FT   Protein   27..928
FT   /note= "Mature protein"
XX
PN   WO200202606-A2.
XX
PD   10-JAN-2002.
XX
PF   03-JUL-2001; 2001WO-IB01445.
XX
PR   03-JUL-2000; 2000GB-0016363.
PR   11-JUL-2000; 2000GB-0017047.
PR   21-JUL-2000; 2000GB-0017983.
PR   07-AUG-2000; 2000GB-0019368.
PR   18-AUG-2000; 2000GB-0020440.
PR   14-SEP-2000; 2000GB-0022583.
PR   10-NOV-2000; 2000GB-0027549.
PR   22-DEC-2000; 2000GB-0031706.
XX
PA   (CHIR-) CHIRON SPA.
XX
PI   Ratti G, Grandi G;
XX
DR   WPI; 2002-154726/20.
DR   N-PSDB; ABL91200.
XX
PT   Novel Chlamydia pneumoniae protein useful in the manufacture of a
PT   medicament for treatment or prevention of infection due to Chlamydia,
PT   preferably Chlamydia pneumoniae, and for diagnostic purposes -
XX
PS   Claim 1; Page 57; 364pp; English.
XX
CC   Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
CC   pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
CC   them. The proteins are predicted to be immunogenic and may therefore be
CC   useful in vaccine production and for diagnostic purposes. Chlamydia
CC   pneumoniae is a common cause of respiratory disease in humans, and is
CC   also involved in the development of cardiovascular diseases such as
CC   atherosclerosis, coronary artery disease, carotid artery stenosis,
CC   myocardial infarction, cerebrovascular disease, aortic aneurysm,
CC   claudication and stroke. The proteins and nucleic acids of the invention
CC   may be used in vaccines and pharmaceutical compositions for the
CC   prevention or treatment of chlamydial infections, particularly Chlamydia
CC   pneumoniae infection. The proteins may also be used in the detection of
CC   Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
CC   DNA probe assay or blotting techniques for determining Chlamydia
CC   pneumoniae gene expression. The present sequence represents a
CC   specifically claimed Chlamydia pneumoniae protein of the invention.
XX
SQ   Sequence 928 AA;

Alignment Scores:
Pred. No.:   2.25e-154   Length: 928

```
Qy    1859  TCTACG--------ACTGCAACTTCAACTGACTAAAACTGGCTATATTCCTAATCCC  1909
                  :::||       ||||||       |||||||  ||||||  ||||||||
Db     604  AlaThrLysSerLysAlaAlaThrLeuThrTrpPheThrLysThrGlyTyrAsnProAsnPro  604

Qy    1910  GAGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCATTTATAGATATTAGCTCT  1969
            ||||||  |||:||||  |||:||||||       ::|||||||||||||  ||
Db     605  GluArgArgGlyThrLeuValAlaAlaAsnThrLeuTrpGlySerPheValAlaAspValArgSer  624

Qy    1970  CTCCATTATCTTATGGAGACTGCGAAACGAAGGGTTGCAGGAGGACCGTGCTTTTTGGTGT  2029
            ||| :||::| ::||  |||||  ||||:| |||||||||||||||||||||||||||||
Db     625  IleGlnLeuValAlaAlaThrLysValArgGlnSerGlnGluThrArgGlyIleTrpCys  644

Qy    2030  GCTGATTATCTAACTTCTTCCATAAGGATAGTAGTACAAAAACACGAGCGGGGTTTCGCCAT  2089
               :||:|||||  ||||||  ::||||||||       ::|||||||||||||
Db     645  GluGlyIleIleSerAsnPhePheHisLysAsnLysGlyPheArgHis  664

Qy    2090  TTGAGTGGCGGGTTATGTCATAGAGGAGGAAACCTACATACTTGTTCAGATAAGGATTCTTAGT  2149
            ::::|||||||||||||  |||       ||:||:||||
Db     665  IleLeuSerAlaGlyTyrValGlyTyrAlaThrThrLeuAlaThrSerAspAsnLeuIleThr  684

Qy    2150  GCTGCATTTTGTCAGCTCTTTGGAAGAGAGATAGAGACTACTTTGTAGCTAAGAATCAAGGT  2209
            ||||||       :|||||||||       ||||:|||||||||||||
Db     685  AlaAlaPheCysGlnLeuPheGlyLysArgArgAspHisPheIleAsnLysAsnArgAla  704

Qy    2210  ACAGTCTACGGAGGAGAACTCTATTACCAGCACACAACGAAACCTATATCTCTTCCTTGC  2269
            :::     |||     ::|||:|| :::||||||
Db     705  SerAlaTyrAlaAlaSerLeuHisLeuGlnHisLeuLeuAlaThrLeuSerSer  721

Qy    2270  AAACTACGGCCTTGTTCGTTGTCTTATGTTCCT--------ACAGAGATTCCTGTTCTC  2320
            ::::|||||||||||       ||||||||
Db     722  --------ProSerLeuLeuArgTyrLeuProGlySerGluGluGlnProValLeu  738

Qy    2321  TTTTCAGGAAACCTTAGCTACACCCCATACGGATAACGATCTGAAAACCAAGTATACACACA  2380
            |||       :||||:|       |||:||||||
Db     739  PheAspAlaGlnIleSerTyrIleSerTyrLysSerAsnThrMetLysThrTyrThrTyrThrGln  758

Qy    2381  TATCCTCACTGTTAAAGGAAGCTGGGGGAATGATAGTTTCCTTTAGAATTCGGTCGAAGA  2440
            |||||  |||||||||       |||||||
Db     759  AlaProLysGlyGluSerTrpSerTrpTyrAsnAspGlyCysAlaLeuGluLeuAlaSerSer  778

Qy    2441  GCTCCG---ATTTGCTTAGATGAAAGTGTCTCTATTTGAGCAGTACATGCCCTTCATGAAA  2497
            ||||       :: ||||||
Db     779  LeuProHisThrAlaLeuSerHisGluGlyLeuPheHisAlaTyrPheProPheLeuLys  798

Qy    2498  TTGCAGTTTGCTTCTATGCACATCAGGAGAAGGTTTAAAGACAACAGGAACAGAA--GCTCGT  2554
            ::::::     |||||||||||:::     ||||||
Db     799  ValGluAlaSerTyrIleHisGlnAsnSerPheLysGluArgAsnThrLeuValAlaArg  818

Qy    2555  GAAATTTGGAAGTAGCCGTCTTGTGAATCTTGCCTTACCTATCGGGATCCGATTTGATAAG  2614
            ||||||||       ::::||||||||||||
Db     819  SerPheAspSerGlyAspLeuIleAsnValSerValProIleGlyIleThrPheGluArg  838

Qy    2615  GAATCAGACTGCCAAGATGCAACGTACAAATCTAACTCTTGGTTATACTGTGGATCTTGTT  2674
            |||||       |||:||||||       ||:|| ||||||||
Db     839  PheSerArgArgAsnGluArgAlaSerTyrGluAlaThrValIleTyrValAlaAlaAspValTyr  858

Qy    2675  CGTAGTAAACCCGACTGTACGACAACAACTGCGAATTAGCGGTGATTCTTCGGAAAACCTTC  2734
            |||     |||||||||||:::
Db     859  ArgLysAsnProAspCysThrThrAlaLeuLeuLeuAsnAsnThrSerTrpLysThrThrThr  878

Qy    2735  GGTACGAATTGGCAAGACAAGCTTTAGTCCTTCGTTCGGCAGGGAACCATTTTTGCTTTAAC  2794
            ||||||||       ::: ||||||||
Db     879  GlyThrAsnLeuSerArgGlnAlaGlyIleGlyArgAlaGlyTyrIleGlyPheTyrAlaPheSer  898

Qy    2795  TCAAAATTTGAAGCCTTTAGCCAATTTCTTTTGAATTGCGTGGGTCATCTCGCAATTAC  2854
            |||       ||||||||||:|||||||:||
Db     899  ProAsnLeuGluValThrSerAsnLeuSerMetGluIleArgGlySerSerArgSerTyr  918

Qy    2855  AATGTGAGACTTAGGAGGACAAAATACCAATTC  2884
            |||       |||||||||||::
Db     919  AsnAlaAspLeuGlyLeuGlyLysPheGlnPhe  928
```

```
Score:                    1982.00        Matches:        429
Percent Similarity:       60.95%         Conservative:   150
Best Local Similarity:    45.16%         Mismatches:     327
Query Match:              36.64%         Indels:          44
DB:                       23             Gaps:            19

US-09-428-122-1 (1-3000) x ABB90542 (1-928)
```

```
Qy    101  ATGAAGTCTTCTTCCCAAGTTGTATTTTCCTATTTTCCTTGCTATTTCCCTTGTCTATG  160
                |||||||||                ||||    ||:::       ||||||
Db      1  ...MetLysSerLeuHisTrpPheLeuIleSerSerLeuAlaLeuProLeuSerLeu   20

Qy    161  ------------ATTGCTACCGAGACAGCTTTGGATTCAAGTGCCGAGTTTCGAT    202
                        |||          |||    :::         |||||
Db     21  AsnPheSerAlaPheAlaAlaValAlaValGluIleAsnLeuGlyAsnThrAsnSerPheSer   40

Qy    203  GGGAATAAAAAATGGTAATTTTCAGTTCGTGAGAGTCAGGAAGATGCT---GGAACTACC  259
                |||     ::::||                           ::::||
Db     41  Gly------ProGlyThrTyrProProAlaGlnThrThrAsnAlaAspGlyThrIle     58

Qy    260  TACCTATTTAAGGGAAATGTCACTCTAGAAAATATTCCTGAAACAGGCACAGCAATCACA  319
                                                |||:::     |||||||||
Db     59  TyrAsnLeuThrGlyAspValSerIleThrAsn---AlaGlySerProThrAlaLeuThr   77

Qy    320  AAAAGTCTGTTTTAACACACTAAGGGCGATTTGACTTTCACAGGTAACGGAGACTCCTA    379
                |||       |||       ||:::    |||||       ||:::
Db     78  AlaSerCysPheLysGluThrThrGlyAsnLeuSerPheGlnGlyHisGlyTyrGlnPhe   97

Qy    380  TTGTTCCAAACGGTGATGCAGGAGGACTGTAGCAGGGGCTGCTGTTAACAGCAGCTGGTA  439
                 ::||||||                   |||      :::::
Db     98  LeuLeuGlnAsnIleAspAlaGly------AlaAsnCysThrPheThrAsnThrAlaAla  115

Qy    440  GATAAATCTACCACGTTTATAGGGTTTTCTCGCTATCTTTTATTGCGTCTCCTGGAAGT  499
                |||        ::||    ||||||||||         :::       :::
Db    116  AsnLysLeuLeuSerPheSerGlyPheSerTyrLeuSerLeuIleGlnThr------Thr  133

Qy    500  TCGATAACTACCGGCAAAGGAGCGGTTAGCTCTACGGGTAGCTTGACAAAA         559
                |||||||||||:::                |||      |||:::
Db    134  AsnAlaThrThrGlyThrGlyAlaIleLys---SerThrGlyAlaCysSerIleGlnSer  152

Qy    560  AATGTCAGTTGTCTTCTCAGCAAAAAACTTTCAACGGATAATGGCCGTGCTATCACCGCA  619
                                |||||||||        :::
Db    153  AsnTyrSerCysTyrPheGlyAsnPheSerAsnAspAsnGlyGlyAlaLeuGlnGly     172

Qy    620  AAAACTCTTTCATTAACAGGGACTACAATGTCAGCTCGTTTTCTGAAAATACCTCCTCA  679
                :::||||                |||        :::
Db    173  SerSerIleSerLeuSer-----LeuAsnProAsnLeuThrPheAlaLysAsnSerAlaThr  191

Qy    680  AAGAAAGGCGGAGCCATTCAGATCTTCCGATGCCCTTACCATTACTGGAAACCAAGGGGAA  739
                :::||||||||                |||   :::||||
Db    192  GlnLysGlyGlyAlaIleTyrSerPheThrGlyTyrIleThrIleAsnAsnThrLeuAsnSer  211

Qy    740  GTCTCTTTTTCTGACATATCTTCTCCGGATTCTCGGAGCTGCAATTTTTACAGAAGCCTCG  799
                 :::                |||          |||||||
Db    212  AlaSerPheSerGluAsnThrAlaAlaAsnAsnGlyIleGlyAlaIleTyrThrGluAlaSer  231

Qy    800  GTGACTATTTCTAATAATGTCAAATCAGATGTTCCTTATTGACAATAAGGTCACGGAGGCGAGC  859
                |||||        ::||:::       |||||
Db    232  SerPheSerSerAsnLysAlaIleIleSerPheAsnAsnSerValThrAlaThrThrSer  251

Qy    860  TCCTCAACAACGGGGAGATGTCAGGAGGTGCTATCGTGCTTATAAAACTAGTACAGAT  919
                 :::||||||                |||||||       :::||||
Db    252  Ala------------ThrLysGlyGlyGluLeuLysProValLeuAsnThrAlaIle  265

Qy    920  ACTAAGGTC---ACCCTCACTGTGCTAAAAGCTCGAAAAGCTTCCGGAGGACTTACCCTA  976
                 |||||        :::|||||          |||        :::
Db    266  LysProValLeuThrLeuSerAspAsnGlyGluLeuAsnValLeuSerGlyProThrLeu  285

Qy    977  ACAGCGGGAGGAGCTATCTATGTCAATGAGAGGTACACTCCTGGTTATGTCATAGCTATCGAA  1036
                |||                |||       |||      :::
Db    286  ThrSerGlyIleTyrThrAspAsnGlyAsnLeuValLeuSerGlyProThrLeu     305

Qy   1037  TTCAGTAGAAATAGTGTCAATGAGAGCTTCCTAAAGGTCGAGCCATAGCTATCGAA     1096
                 :: ||||           ::.::: :::
```

```
Db    306  PheLysAsnAsnSerAlaIleIleAspThrAlaIleAspThrAlaLeuGlyGlyAlaAlaAlaIleAlaAla  325
                |||                                                  |||||||||||
Qy   1097  GATAGTGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGTCTTTTAGGGAATACA  1156
                |||||||||||      |||                |||||||||:::
Db    326  AspSerGlySerLeuGlyLeuSerAlaAlaLeuGlyLeuGlyAspIleThrGluGlyAsnThr  345

Qy   1157  GTC------ACTTCTACTACTCCTGGGACGAATAGAAGTAGTATCGACTTAGGA---  1204
                |||          :::|||
Db    346  ValValLysGlyAlaSerSerGlnThrThrThrArgAsnSerIleAsnIleGlyAsn  365

Qy   1205  ACGAGTGCAAAGATGACAGCTTGCGTTCTGCTGCTGGTAGACCATCTACTTCTATGAT  1264
                |||||||:::|||||           |||                |||||||
Db    366  ThrAsnAlaLysIleValGlnLeuArgAlaSerGlnGlyAsnThrIleTyrPheTyrAsp  385

Qy   1265  CCCATAACTACAGGACGATCATCCACAACAGTTACAGATGTCTTAAAAGTTAATGAGACTCCG  1324
                |||                |||    :::|||       |||||||
Db    386  ProIleThrThrSerIleThrAlaAlaAlaLeuSerAspAlaLeuAsnLeuAsnGlyProAsp  405

Qy   1325  GCAGATTCTGCACTACAATATACAGGGAACAACATCATCTTCACAGGAGAAAAGTTATCAGAG  1384
                |||||||                |||||||        :::||||
Db    406  LeuAlaGlyAsnProAlaTyrGlnGlyThrIleValIleAspSerGlyValLysSerGlu  425

Qy   1385  ACAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAGCCTGTAACTCTTTCA  1444
                |||                                :::     |||
Db    426  AlaGluIleAlaLysGluIleAlaAspAsnLeuLysSerThrIleGlnProLeuThrLeuAla  445

Qy   1445  GGAGGTACTCTATCTTTAAAACATGGAGTGACTCTGCGACTCCAGGCATTCACTCAACAG  1504
                |||||                                  :::::
Db    446  GlyGlyGlnLeuSerLeuLysSerGlyValThrLeuAlaLysSerPheSerGlnSer  465

Qy   1505  GCAGATTCTCGTCTGCGAAATGACGTAGGAACTACTCTGATACTAGCACC             1564
                |||||||                |||||||||      :::
Db    466  ProGlySerThrLeuMetAspAlaGlyLeuThrGluThrAlaAspGlyIleThr  485

Qy   1565  ATAAAACAATTCGTCATTAACATCAGTTCTATAGACGTGCAAAGAAGCAAAAAATAGAA  1624
                |||||||||      :::||||||                |||      |||||
Db    486  IleAsnAsnLeuValLeuAsnValAspSerLeuLysLysThrLysLysAlaThrLeuLys  505

Qy   1625  ACCAAAGTACGTCAAAAAATCTGACTTTATCTGGAACCATCACTTTATTGGACCGACG  1684
                |||||||||||||      :::|||||                :::||||
Db    506  AlaThrGlnIleAlaSerGlnThrValThrLeuSerGlyLeuSerLeuValLeuAspProSer  525

Qy   1685  GGCACGTTTTATGAAAATCATAGTTTAAGAAAATCCTACGACATCTTAGAGCTC  1744
                |||||||            |||||||                :::
Db    526  GlyAsnValTyrGluAspValSerTrpAsnAsnProGlnValPheSerLeuThrLeu  545

Qy   1745  AAAGCTCT------GGAACTGTAACAGCACCGCAGTGACTCCAGATCCTATAATGGGT  1798
                |||||||                :::||||||
Db    546  ThrAlaAspProAlaAsnIleHisIleThrAspLeuAlaAlaAspProLeuGluLys  565

Qy   1799  GAGAAATTCCATTACGGCTATCACGGGAACTTGGGGCCCAATGTGTTGGGGACAGGGGCT  1858
                |||                |||:::||||
Db    566  AsnProIleHisTrpGlyTyrGlnGlyAsnTrpAla---LeuSerTrpTrpIleAspThr  584

Qy   1859  TCTACG-----ACTGCAACCTTCAACTGACTAAAACTCGCTATATTCCTAATCCC  1909
                |||:::                |||||||
Db    585  AlaThrLysSerLysAlaAlaThrLeuThrPheThrLeuThrTrpThrTyrAsnProAsnPro  604

Qy   1910  GAGCGTATCGCGTTCTTAGTGCCTTATGGATGAATGCATTTATAGATATTAGCTCT  1969
                :::||||||||      |||:::
Db    605  GluArgArgGlyThrLeuPheLeuAlaLeuAsnThrLeuTrpGlySerPheValAspArgSer  624

Qy   1970  CTCCATTATCTTATGTGAGACTGCAAACGAAGGGTGCAGGGAGGACCGTGCTTTTTGGTGT  2029
                :::                |||      :::|||||||
Db    625  IleGlnIleLeuValAlaAlaThrLysValAlaArgGlnSerGlnGluThrArgGlyIleTrpCys  644

Qy   2030  GCTGGATTATCTAAACTCTTCCATTAAGGATAGTACAAAAACACGACGCGGGTTTCGCCAT  2089
                |||||||||                :::|||||
Db    645  GluLysIleLeuSerAsnPheHisLeuSerAspSerThrLysIleAsnLysGlyPheArgHis  664

Qy   2090  TTGAGTGGCGGTTATGTCATAGAGGAGGAAACCTACTACTTGTTCAGATAAGATTCTTAGT  2149
                :::|||      ::.:::
```

```
XX
PF
XX                    01-DEC-1999.      99WO-CA01147.
PR
PR                    01-DEC-1998;      98US-0110339.
PR                    01-DEC-1998;      98US-0110340.
PR                    01-DEC-1998;      98US-0110427.
PR                    01-DEC-1998;      98US-0110428.
PR                    01-DEC-1998;      98US-0110438.
XX
PA    (CONN-) CONNAUGHT LAB LTD.
XX
PI    Murdin AD,   Oomen RP,   Wang J;
XX
DR    WPI; 2000-412339/35.
DR    N-PSDB; AAA30851, AAA30852.
XX
PT    Nucleic acids encoding polypeptide antigens from Chlamydia useful for
PT    preventing, diagnosing and treating diseases such as community acquired
PT    pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
PT    asthma -
XX
PS    Claim 16; Fig 5; 174pp; English.
XX
CC    This sequence is a Chlamydia antigen of the invention, designated
CC    CPN100638. The nucleic acids (and their complementary sequences) may be
CC    used as diagnostic agents for detecting the presence of nucleic acids
CC    encoding Chlamydia antigens in samples according to standard methods,
CC    and therefore, for diagnosing Chlamydia infections. For example, they may
CC    be used as primers and probes for diagnostic polymerase chain reaction
CC    (PCR) assays. Antisense sequences may be used to down regulate
CC    expression of the proteins and may be used to treat infections. The
CC    nucleic acids may also be used to produce the protein antigens they
CC    encode according to standard recombinant DNA methodologies. The
CC    proteins may then be used as antigens for the production of antibodies
CC    (i.e. as vaccines) for preventing infection by Chlamydia. The
CC    antibodies may also be used as diagnostic reagents for detecting
CC    infections. Chlamydia is a pathogen implicated in the development of
CC    (for example) community acquired pneumonia, upper respiratory tract
CC    disease (especially bronchitis and sinusitis, asthmatic bronchitis,
CC    adult-onset asthma and acute exacerbations of asthma in adults.
XX
SQ    Sequence   928 AA;

Alignment Scores:
Pred. No.:                             928
AAY90239                               428
Score:                7.04e-154
Percent Similarity:   1976.00          150
Best Local Similarity: 60.84%          328
Query Match:          45.05%            44
DB:                   36.53%            19
                      21
```

```
US-09-428-122-1 (1-3000) x AAY90239 (1-928)

Qy    101 ATGAAGTCTCTTTCCCCAAGTTGTATTTCTACATTTGCTATTTCCTTTGTCTATG 160
          ||||||||||        ||        |:|:|                 ||:::
Db      1 MetLysSerLeuHisTrpPheLeuIleSerSerSerLeuAlaLeuProLeuSerLeu  20

Qy    161 -----------------------ATTGCTACCGAGACAGTTTTGGATTCAAGTGCCAGTTTCGAT 202
                                  |||    |||     :::  ||||||
Db     21 AsnPheSerAlaPheAlaAlaValAlaValGluIleAsnLeuGlyLeuProThrAsnSerPheSer  40

Qy    203 GGGAATAAAAATGGTAATTTTCAGTTCGTGAGAGTCAGGAAGATGCT---GGAACTACC 259
          ||||   |||||          |||||||||||||||||||||  ||||||
Db     41 Gly------ProGlyThrTyrThrProProAlaGlnThrThrAsnAlaAspGlyThrIle  58

Qy    260 TACCTATTTAAGGAGAAATGTCACTCTAGAAAAATATTCCTGGAACAGGGCACAGCAATCACA 319
          ||        |||:::           |||:::  ||||||||
Db     59 TyrAsnLeuThrGlyAsnValSerIleThrAsn---AlaGlySerProThrAlaLeuThr  77

Qy    320 AAAAGTGTTTTAACACACATCAAGGGCGATTTGACTTTCACAGTTAACGGTAACGGGAACTCTCTA 379
          ||||||        |||:::||:|||||||       ||||:::||:|||
Db     78 AlaSerCysPheLysGluThrThrGlyPheGlnGlyAsnLeuSerPheGlnGlyHisGlyTyrGlnPhe  97
```

```
Db    665 IleSerAlaGlyTyrValValGlyAlaThrThrLeuAlaSerAspAsnLeuIleThr  684

Qy   2150 GCTGCATTTTGTCAGCTTCAGGATAGAGGATAGAGGACTACTTTGTAGCTAAGAATCAAGGT 2209
          ||||||||||||          |||:::|||||||||||||:::|
Db    685 AlaAlaPheCysGlnLeuPheGlyLysAspArgAspHisPheIleLysAsnArgAla  704

Qy   2210 ACAGTCTACGGAGGAACTTCTATTACCAGACAACAACGAAACCTATATCTCTCTCCTTGC 2269
          :::     |||       ::::||:||  |||
Db    705 SerAlaTyrAlaAlaSerLeuGlnHisLeuAlaThrLeuSerSer--------  721

Qy   2270 AAACTACCGGCCTTGTTCGTTGTCTTATGTTCCT--------ACAGAGATTCCTGTTCTC 2320
          |||        |||:::|||||||||||
Db    722 --------ProSerLeuLeuArgTyrLeuProGlySerGluGluSerGlnProValLeu  738

Qy   2321 TTTTCAGGAAAACCTTAGCTACACCCATACGGATAACGATCTGAAAAACCAAGTATACAACA 2380
          :::     ||        |||:::          |||||||||||
Db    739 PheAspAlaGlnIleIleSerTyrIleSerArgLysAsnThrMetLysThrTyrTyrThrGln  758

Qy   2381 TATCCTACTGTTAAAGGAAGCTGGGGAATGAGATAGTTTCGCTTTAGAATTCGGTGGAAGA 2440
          |||        |||||     ||||||
Db    759 AlaProLysGlyGluSerTrpTyrAsnAspGlyCysAlaGluLeuGluAlaSerSer  778

Qy   2441 GCTCCG---ATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTACATGCCCTTCATGAAA 2497
          ||||||        ||  ||||||||||:::||
Db    779 LeuProHisThrAlaLeuSerHisGluGlyLeuPheHisAlaTyrPheProPheIleLys  798

Qy   2498 TTGCAGTTTGTTGTCTATGCACATCAGGAAGGTTTAAAGAACACAGGGAACAGAA--GCTCGT 2554
          :::::::|||        |||     |||||||:::
Db    799 ValGluAlaSerTyrIleHisGlnIleGlnSerPheLysGlnArgAsnThrThrLeuValArg  818

Qy   2555 GAATTTGGAAGTAGCCGTCTTGTGAATCTGCCTTACCTATCCGGATCCGATTTGATAAG 2614
          |||           |||||||  ::||:|||||||||:::
Db    819 SerPheAspSerGlyAspLeuIleAsnValSerValProIleGlyIleThrPheGluArg  838

Qy   2615 GAATCAGACTGCCAAGATGCAACGTACAATCTAACTCCTTGGTTATACTGTGGATCTTGTT 2674
          |||:::||     ||:::|
Db    839 PheSerArgAsnGluArgAlaSerTyrGluAlaThrValIleTyrValAlaAspValTyr  858

Qy   2675 CGTAGTAACCCCGACTGTACGACACACTGCGAATTAGCCGTGATTCTTGGAAAACCTTC 2734
          |||        |||||||||     |||:::
Db    859 ArgLysAsnProAspCysThrThrAlaLeuLeuLeuIleAsnAsnThrSerTrpLysThrThr  878

Qy   2735 GGTACGAATTGGCAAGACAAGCTTAGTCCTTCGTGCAGGGAACCATTTTGCTCTTTAAC 2794
          ||||||:::||||||||        :::  ||||||
Db    879 GlyThrAsnLeuSerArgGlnAlaGlnIleGlyArgAlaGlyIlePheTyrAlaPheSer  898

Qy   2795 TCAAATTTTGAAGCCTTTAGCCAATTTCTTTGAATTGCGTGGGTCATCTCGCAATTAC 2854
          ||        :::  ||||||        |||:::
Db    899 ProAsnLeuGluValThrSerAsnLeuSerMetGluIleLeuArgGlySerSerArgSerTyr  918

Qy   2855 AATGTAGACTTAGGAGCAAAATACCAAATTC 2884
          |||||||||        |||||||
Db    919 AsnAlaAspLeuGlyLeuGlyLysPheGlnPhe  928
```

```
RESULT 14
AAY90239
ID    AAY90239 standard; Protein; 928 AA.
XX
AC    AAY90239;
XX
DT    29-AUG-2000   (first entry)
XX
DE    Chlamydia antigen CPN100638.
XX
KW    Chlamydia antigen; diagnosis; infection; community acquired pneumonia;
KW    therapy; upper respiratory tract disease; bronchitis; sinusitis;
KW    asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma.
XX
OS    Chlamydia pneumoniae.
XX
PN    WO200032794-A2.
XX
PD    08-JUN-2000.
```

```
Qy   380  TTGTTCCAAACGGTGGATGCAGGGACTGTAGCAGGGGCTGCTGTTGTTAACAGCAGCTGGGTA  439
          |||    |||||||     ::|||||||||||      |||
Db    98  LeuLeuGlnAsnIleAspAlaGly------AlaAsnCysThrPheThrAsnThrAlaAla    115

Qy   440  GATAAATCTACCAGTTTATAGGGTTTCTTCGTCATCTTTTAATTGCGTCTCCTGGAAGT     499
          :::||||       :::||       |||       :::       :::
Db   116  AsnLysLeuLeuSerPheSerGlyPheSerTyrLeuSerLeuIleGlnThr------Thr   133

Qy   500  TCGATAACTACCGGCAAAGGAGCCCGTTAGCTGCTCTCACGGGTAGCTTGAGTTGACAAAA   559
          ::   |||||||||     |||||||:::
Db   134  AsnAlaThrThrGlyThrGlyAlaIleLys---SerThrGlyAlaCysSerIleGlnSer   152

Qy   560  AATGTCAGTTTGCTCTTCAGCAAAAACTTTTCAACGGATAATGGGGTGCTATCACCGCA     619
          |||       :::||       |||||||||
Db   153  AsnTyrSerCysTyrPheGlyGlnAsnPheSerAsnAspAsnGlyGlyAlaLeuGlnGly   172

Qy   620  AAAACTCTTTCATTAACAGGAGCTACAAATGCCAGTCTGTTTCTGAAAATACCTCCTCA     679
          :::       ||       :::       ||
Db   173  SerSerIleSerLeuSer--LeuAsnProAsnLeuThrPheAlaLysAsnLysAlaThr   191

Qy   680  AAGAAAGGCGAGCCATTCAGACTTCCGATGCCCTTACCATTACTACTGAAACCAAGGGGAA   739
          ::://||||||     :::       ||||||
Db   192  GlnLysGlyGlyAlaLeuTyrSerThrGlyGlyIleThrIleThrIleAsnAsnThrLeuAsnSer  211

Qy   740  GTCTCTTTTCTGACATATCTTCTCGGATTCTCGGAGCTGCAATTTTTACAGAAGCCTCG     799
          ||||       :::       ||
Db   212  AlaSerPheSerGluAsnThrAlaAlaAsnAsnGlyGlyAlaIleTyrThrGluAlaSer   231

Qy   800  GTGACTATTCTAATAAATGCTAAAGTTCCTTTATTGACAAATAAGGTCACAGGAGCCGAGC   859
          |||       :::       |||
Db   232  SerPheIleSerAsnLysAlaIleAlaAsnSerValThrAlaThrSer   251

Qy   860  TCCTCAACACACGGGGATATGTCAGGAGTGCTATCGTGTCTTATAAAACTAGTACACAGAT  919
          ||||       :::       |||||
Db   252  Ala------ThrGlyGlyAlaIleTyrCysSerSerSerThrSerAlaPro   265

Qy   920  ACTAAGGTC---ACCCTCACTGGAAATCAGATGTTACTCTTCAGCAACAATACATCGACA     976
          |||       |||
Db   266  LysProValLeuThrLeuSerLeuThrLeuIleLeuAsnGlyGluLeuAsnPheIleGlyAsnThrAlaIle  285

Qy   977  ACAGGCGGGGAGGAGTCATCTATGTGAAAAAAGCTCGAACTGCCTTCCGGAGGACTTACCCTA  1036
          |||||||       :::||       ||
Db   286  ThrSerGlyIleGlyAlaIleTyrThrAspAsnLeuValLeuSerAlaLeuGlyGlyProThrLeu   305

Qy  1037  TTCAGTAGAAAATAGTGTCAATGGAGCTACAGTCGAAGGTGGAGCCATTAGCTATCGAA    1096
          :::|||       |||
Db   306  PheLysAsnAsnSerGlyTyrAspThrAlaAlaProLeuGlyLysGlyAlaIleAlaIleAlaAla  325

Qy  1097  GATAGTGGGGAATTGAGTTTATCCGCGATAGTGGTGACATTGTCTTTTAGGGAATACA    1156
          :::       |||:::
Db   326  AspSerGlySerLeuSerGlySerAlaLeuGlyGlyAspIleProThrIleThrProGlyTyrAsnThr   345

Qy  1157  GTC---ACTTCTACTACTCCTGGGACGGAATAGGAAGTAGTAGTATCGACTTAGGA---  1204
          :::|||       |||
Db   346  ValValLysGlyAlaSerSerSerGlnThrThrThrArgGlnAsnSerIleLeuGlyAsn   365

Qy  1205  ACGAGGTCGAAAGATGACAGCTTTGCGTTCTGCGTGGCGTCCGTAGGCAGCCATCTCATGAT  1264
          |||||||       |||
Db   366  ThrAsnAlaAlaLysIleValGlnAsnArgAlaAsnThrIleTyrGlnThrIleLeuTyrrPheTyrAsp  385

Qy  1265  CCCATAACTACAGGATCATCCCACAACAGTTACAGATGTCTTAAAAGTTAATGAACAGCTCCG  1324
          |||||||       :::||
Db   386  ProIleThrThrIleSerIleThrHisAsnSerAspAlaLeuAsnLeuAsnGlyTyrProAsp  405

Qy  1325  GCAGATTCTGCCACTACAATAATACAGGGAACATCATCTTCACAGGAGAAAGTTATCAGAG   1384
          |||||||       :::
Db   406  LeuAlaGlyAsnProAlaTyrGlnGlyThrGlnIleThrValPheSerThrIleGlyLysLeuSerGluGlu  425

Qy  1385  ACAGAGGCCCAGATTCTCTAAAAATCTTACTTCGAAGCTACTACAGCCTGTAACTCTTTCA  1444
          |||||||||
Db   426  AlaGluAlaAlaAlaGluAlaAlaAlaAspAsnLysLeuSerThrIleGlnLeuProLeuThrLeuAla  445

Qy  1445  GGAGGTACTTCTATCTTTAAAACATGAGTGACTCTGCGACTACGGCCATTCACTCCAACAG   1504
          |||||||:::
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```
Qy   446  |||||||||||||||| :::::||::|::|||||||||
          GlyGlyGlnLeuSerLeuLysSerGlyValThrLeuValAlaLeuLysSerPheSerGlnSer  465

Qy  1505  GCAGATTCTGCTCGAAATGACGTAGGAACTACTCTAGAACCTGCTGATACTAGCACC     1564
          |||||||
Db   466  ProGlySerThrLeuLeuMetAspAlaGlyThrThrLeuGluThrAlaAspAlaGlyIleIleThr   485

Qy  1565  ATAAACAATTGGTCATTAACATCAGTTCTATAGACGCGGTGCAAAGAAGGCAAAAATAGAA  1624
          |||       :::||
Db   486  IleAsnAsnLeuValLeuAsnValAspSerLeuLysGlyLysLysThrLysLysLeuLys   505

Qy  1625  ACCAAAGCTACGTCAAAAAAACTGACTTTATCTGGAACCATCACTTTATTGGACCCGACG  1684
          :::       ||       |||||
Db   506  AlaThrGlnAlaSerGlnThrValThrLeuSerGlyLeuSerLeuVallAspProSer   525

Qy  1685  GGCACGTTTTATGAAAATCATAGTTTAAGAAATCCTACGAGTCCTACGACATCTTAGAGCTC  1744
          :::||||||       ||
Db   526  GlyAsnValTyrGluAspValSerTrpAsnAsnProGlnValPheSerCysAsnLysValThrLeu   545

Qy  1745  AAAGTTCT-----GGAACTGTAACAAGCACCGGAGTGACTCCAGATCCTATAAATGGGT   1798
          ||       :::
Db   546  ThrAlaAlaAspAspProAlaAsnIleHisIleThrAspLeuAlaAlaAspProLeuGluLys   565

Qy  1799  GAGAAATTCCATTACGACCTATCAGGGAACTTGGGGCCCCAATTGTTTGGGGACCAGGGGGCT  1858
          |||       :::       |||||
Db   566  AsnProIleHisTrpGlyTyrGlnGlyValAsnTrpAla--LeuSerTrpGlnGluAspThr   584

Qy  1859  TCTACG-------ACTGCAACCTTCAACTGGACTAAAACTGGCTAAAAACTGGCTATATTCCTAATCCC  1909
          ::|||
Db   585  AlaThrLysSerLysAlaAlaAlaThrLeuThrLeuThrProProAsnProAsnPro   604

Qy  1910  GAGGCGTATCGGCTCTTTAGTCCCTAATAGCTTATGGAATGCCATTTATAGATATTAGCTCT  1969
          ||       :::||
Db   605  GluArgArgGlyThrArgGlyLeuValAlaAlaAsnThrLeuTrpGlyTyrSerPheValAspValArgSer   624

Qy  1970  CTCCATTATCTTATGGAGACTTGACTCAAACGAAGGGTTGCAGAGGGACCCGTGCTTTTGGTGT  2029
          :::       ||       :::
Db   625  IleGlnGlnLeuValAlaLeuAlaThrLysValArgGlnLeuSerGlnGluThrGlyGlyIleIleTrpTyrCys  644

Qy  2030  GCTGGATTATCTAACTTCTTCCATAAGGATAGTACAAAAACACGACGCGGGTTCGCCAT     2089
          |||||||       ||
Db   645  GluGlyIleIleSerAsnPhePheHisLysAspSerThrLysIleAsnLysGlyPheArgHis  664

Qy  2090  TTGAGTGGCGGTTATGTCATAGGAGGAGAAACCTACATACTTGTTCAGATAAGAATTCTTAGT   2149
          |||||||       :::
Db   665  IleSerAlaGlyTyrValValGlyAlaThrThrLeuAlaSerAspAsnLeuIleLleThr   684

Qy  2150  GCTGCATTTGTCAGCTCTTTGGAAGGAGATAGAGCTACTTTGTAGCTAAGAATCAAGGT  2209
          :::       ||
Db   685  AlaAlaPheCysGlnLeuPheGlyLysGlyValLeuAspArgAspHisPheIleAsnLysAsnArgAla  704

Qy  2210  ACAGTCTACGGAGGAACTCTCTTATTACCAGACAACAAGAAACCTATATCTCTCCTTCCTGC   2269
          :::       ||||
Db   705  SerAlaTyrAlaAlaSerLeuHisLeuAlaThrLeuSerSer----------------  721

Qy  2270  AAAACTACGGCCTTGTCCTTGTTCGTTGTCTTATGTTCCT-------ACAGAGATTCCTGTTTCTC  2320
          :::||       |||
Db   722  --------ProSerLeuLeuTyrLeuProGlySerGluGlnValLeu   738

Qy  2321  TTTTCAGGAAACCTTAGTACTACACCCATACGGATAACGATCTGAAAACCAAGTATACAACA   2380
          |||       ::||
Db   739  PheAspAlaGlnIleSerTyrIleTyrSerLysAsnThrMetLysThrTyrThrGln   758

Qy  2381  TATCCTACTGTTAAAGAAGGTGGGGAATGAGTAGTTCGCTTAGAATTCGGTGGAAGA     2440
          |||       :::
Db   759  AlaProLysGlyLysSerTrpTyrAsnAlaAspGlyCysAlaLeuGluLeuAlaSerSer  778

Qy  2441  GCTCCG---ATTTGCTTAGATGAAAGTGCTTCATTTGAGCAGTACATGCCCTTCATGAAA  2497
          |||||||       :::
Db   779  LeuProHisThrAlaLeuSerHisGluGlyLeuPheHisAlaTyrPheProPheIleLys   798

Qy  2498  TTGCAGTTTGTCTATGCAATCAGGACATTTTAAAGAACAGGGACCAGAA--GCTCGT   2554
          :::::       |||
```

```
Db     799 ValGluAlaSerTyrIleHisGlnAspSerPheLysGluArgAsnThrThrLeuValArg 818
               |||
Qy    2555 GAATTGGAAGTAGCCGTCTTGAATCTTGCCTTACCTATCCGGATCCATCGGATTGATAAG 2614
               |||||  |||  ||:::::::|||  |||||||  ||||||||  :||||||||
Db     819 SerPheAspSerGlyAspLeuIleAsnValSerValProIleGlyIleLeuThrPheGluArg 838

Qy    2615 GAATTCAGACTGCCAAGATGCAACGACAATCAACTCCTTGGTTATACTGTGGATCTTGTT 2674
               :::   |||   |||   |||||||:  |||  |||  |||  |:::
Db     839 PheSerArgArgAsnGluArgAlaSerTyrGluAlaThrValIleTyrValAlaAspValTyr 858

Qy    2675 CGTAGTAACCCGACTGTACGACAACACTGCGAATTAGCGGTGATTCTTGGAAAACCTTC 2734
               |||  ||||||||  ||:::  ||||||||  ||||||
Db     859 ArgLysAsnProAspCysThrThrAlaLeuLeuIleAsnAsnThrSerTrpLysThrThr 878

Qy    2735 GGTACGGAATTTGGCAAGACCAAGCTTTAGTCCTTCGTGCAGGGAACCATTTTGCTTTAAC 2794
               ||||||  ||||  |||||||||  :::  |||  |||||||||  |||||||
Db     879 GlyThrAsnLeuSerArgGlnAlaGlyIleLeuGlyAlaGlyIlePheTyrAlaPheSer 898

Qy    2795 TCAAATTTGAAGCCTTTAGCAATTTCTTTTGAATTGCGTGGGTCATCTCGCAATTAC 2854
               |||  |||||||||||||||  :::  |||||||:::  :::||||  ||||||||
Db     899 ProAsnLeuGluValThrSerMetGlulleArgGlySerSerArgSerTyr 918

Qy    2855 AATGTAGACTTAGGAGCAAAATACCAATTC 2884
               |||  ||||||  |||::|||||
Db     919 AsnAlaAspLeuGlyLysPheGlnPhe 928
```

RESULT 15

AAY99842

ID   AAY99842 standard; Protein; 936 AA.
XX
AC   AAY99842;
XX
DT   15-SEP-2000 (first entry)
XX
DE   Chlamydia pneumoniae 98 kDa outer membrane protein CPN100640.
XX
KW   Chlamydia; 98 kDa outer membrane protein; antigen; immunogen; infection;
KW   vaccine; antibacterial; community acquired pneumonia; bronchitis;
KW   sinusitis; acute respiratory disease; upper respiratory tract disease;
KW   asthma; atherosclerosis.
XX
OS   Chlamydia pneumoniae.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..11
FT   /label= Signal_peptide
FT   Protein   12..936
FT   /label= 98_kDa_membrane_protein
XX
PN   WO200032784-A1.
XX
PD   08-JUN-2000.
XX
PF   01-DEC-1999; 99WO-CA01148.
XX
PR   01-DEC-1998; 98US-0110439.
PR   03-MAY-1999; 99US-0132272.
XX
PA   (CONN-) CONNAUGHT LAB LTD.
XX
PI   Murdin AD, Oomen RP, Wang J, Dunn P;
XX
DR   WPI; 2000-412330/35.
DR   N-PSDB; AAA48838, AAA48839.
XX
PT   New polynucleotide encoding the Chlamydia 98 kiloDalton outer membrane
PT   protein, useful for preventing or treating Chlamydia infection -
XX
PS   Claim 16; Fig 1; 98pp; English.
XX
CC   The present sequence is CPN100640, the 98 kDa outer membrane protein
CC   from Chlamydia pneumoniae. Chlamydia pneumoniae is a common cause of
CC   community acquired pneumonia and upper respiratory tract symptoms and

CC   diseases, including bronchitis and sinusitis. It also has an association
CC   with atherosclerosis and asthma. The 98 kDa outer membrane protein is a
CC   C. pneumoniae-specific antigen which can confer immune protection against
CC   chlamydial infection. The nucleotide sequence encoding the protein or the
CC   protein itself may be administered as a vaccine to prevent or treat
CC   infection and they may also be used to diagnose infection. The gene
CC   encoding CPN100640 was amplified from Chlamydia pneumoniae genomic DNA
CC   by PCR.
XX
SQ   Sequence 936 AA;

Alignment Scores:
Pred. No.:   5.68e-153   Length: 936
Score: 1965.00   Matches: 411
Percent Similarity: 62.30%   Conservative: 179
Best Local Similarity: 43.40%   Mismatches: 327
Query Match: 36.33%   Indels: 30
DB: 21   Gaps: 16

US-09-428-122-1 (1-3000) x AAY99842 (1-936)

```
Qy     101 ATGAAGTCTCTTCTTCCCCAAGTTGTATTTCTACATTGCTATTTC---CCTTTGTCT 157
               ||||||||||||||||||  :::   ||   |||||   |||
Db       1 MetLysSerSerValSerTrpLeuPhePheSerSerIleProLeuPheSerLeuSer 20

Qy     158 ATGATTGCTACCGACAGCAGTTTTGGATTCAAGT---GCGAGTTTCGATGGGAATAAAAT 214
               :::::|||||||||||||   |||||||  ||||     ||||||  |||||:::
Db      21 IleValAlaAlaGluValThrLeuAspSerSerAsnAsnSerTyrAspGlySerAsnGly 40

Qy     215 GGTAATTTTCAGTTCGTGAGAGTCAGGAA--GATGTGGAACTACCTACCTATTTAAG 271
               |||||||||||||||||||||   :::      ||||||||||||  ||||||||
Db      41 ThrThrPheThrValPheSerThrThrAspAlaAlaAlaGlyThrThrTyrSerLeuLeu 60

Qy     272 GGAAATGTCACTCTAGAAAATATTCCTGAGAACAGCACAGCAATCACAAAAGCTGTTT 331
               :::||||||||   :::|||   ||||||||||  |||   :::
Db      61 SerAspValSerPheGlnAsnAlaAlaGlyAlaLeuGlyIleProLeuAlaSerGlyCysPhe 80

Qy     332 AACACACTAAGGCGATTGACTTTCACAGGTAACGGTAACGGAACTCTCATTGTTCCAAACG 391
               ||||||||||||||  |||||||||||||  ||||||||||  :::::||||
Db      81 LeuGluAlaGlyIleGlyAspLeuThrPheGlnHisAlaLeuHisLysPheAlaPhe 100

Qy     392 GTGGATGCAGGACTGTAGCAGGGGCGTCGTTAACAGCAGCGTGGTAGATAAATCTACC 451
               :::::||||||||||||||||||  ::::||  ||||||  ::::|||||||
Db     101 IleAsnAlaGlySerAlaGlyThrValAlaSerThrSerAlaAlaAspLysAsnLeu 120

Qy     452 ACGTTTATAGGGTTTCTTCGCTATCTTTTATTGGTCTTCCTGGAAGTTCGATAACT-- 508
               ||||||||||||||||  ||||||  :::||||||||||  ::::
Db     121 LeuPheAsnAspPheSerArgLeuSerIleIleSerCysProSerLeuLeuSerPro 140

Qy     509 ACCGGCAAAGGAGGCCGTTAGCTGCTCTCACGGGTAGCTTGACTTTGACAAAAAATGTCAGT 568
               ||||||  |||||||||||  :::  |||   ||||||:::
Db     141 ThrGlyGlnCysAlaLeuLys--SerValGlyAsnLeuSerLeuThrGlyAsnSerGln 159

Qy     569 TTGCTCTTCAGCAAAACTTTCAACGGATAAATGCGGTGCTATCACCGCAAAAACTCTT 628
               |||||||||||||||||||||||::::||||||||||  :::
Db     160 IleIlePheThrGlnAsnPheSerSerAspAsnGlyGlyValIleAspAsnThrLysAsnPhe 179

Qy     629 TCATTAACAGGGACTACAAATGTCAGCTCGTTTTCTGAAAATACC------TCCTCAAAG 682
               |||||||  :::|||   ||||||||||||||||  |||||||
Db     180 LeuLeuSerGlyThrSerGlnAspAlaSerPheSerArgAsnGlnAlaPheThrGlyLys 199

Qy     683 AAAGGCGGAGCCAATTCAGACTTCCGATGCCCTTACCATTACTGAAAACCAAGGGGAAGTC 742
               |||||||||||||||  |||  :::||||||  :::::||||  :::::
Db     200 GlnGlyGlyValValTyrAlaThrGlyThrIleThrIleGluAsnSerProGlyIleVal 219

Qy     743 TCTTTTCTGACAATACTTCCTCCGGATTCGGAGCTGCAATTTTACAGAAGCCTCGGTG 802
               ||||||  |||||  ||||||||||||  |||||||  ::::
Db     220 SerPheSerGlnAsnAlaLeuAlaLysSerGlyAlaValTyrSerThrAspAsnCys 239

Qy     803 ACTATTTCTAATAAATGCTAAAGTTTCCTTTATTGACAATAAGGTCACAGGAGCGAGCTCC 862
               :::::|||||  ||:::  |||||||||||||||  :::::
Db     240 SerIleThrAspAsnPheGlnValIlePheAspGlyAsnSerAlaTrpGluAlaAlaGln 259
```

```
Qy   863  TCAACAACGGGGATATGTCCAGGAGGTGCTATCTGCGTTATAAACTAGTACAGATACT      922
               :::                          ||||||||||
Db   260  Ala------------GlnGlyGlyAlaIleCysCys------ThrThrAspLys          272

Qy   923  AAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAGCAACATTACATCGACAACAGCCG   982
          ||||||||||:::   |||  ||||||||||:::
Db   273  ThrValThrLeuThrGlyAsnLysAsnLeuSerPheThrAsnAspIleThrThrAlaLeuThrTyr  292

Qy   983  GGAGGAGCTATCTATCGTGAAAAAGTTCGAACTGGCTTCCGGAGGACTTACCCTATTCAGT  1042
          ||||||||||:::   :::::::::|||:::||||
Db   293  GlyGlyAlaIleSerGlyLeuLysValSerIleSerAlaGlyLeuGlyProThrLeuPheGln  312

Qy  1043  AGAAATAGTGTCAATGAGGTACAGCTCCTAA------GGTGGAGCCATAGCTATCGAA     1096
                :::::::||:||              :::  |||
Db   313  SerAsn---IleSerGlySerAlaGlyLeuGlyGlyAlaIleAlaIleAsnIleAla      331

Qy  1097  GATAGTGGGAATTGAGTTATCCCCGATAGTGTGACATTGTCTTTTAGGGAATACA        1156
          |||||||||||::::||||||||||:::
Db   332  SerAlaGlyGluLeuAlaLeuAlaSerAlaThrSerGlyAspIleThrPheAsnAsnGln    351

Qy  1157  GTCACTTCTACTCCTGGACGAATAGAGTAGTATCGACTTAGGAACGAGTGCAAAG       1216
          ::::       :::   :::::::::||
Db   352  ValThrThrAsnGlySerThrThr---ArgAsnAlaIleAsnIleIleAspThrAlaLys   370

Qy  1217  ATGACAGCTTTGCGTTCTGCTGGTAGAGCCATCTTCTATGATCCCATAACTACA        1276
          ::::::::::|||:::||::||||||:::
Db   371  ValThrSerIleArgAlaAlaThrGlyGlnSerIleThrTyrPheTyrAspProIleThrAsn  390

Qy  1277  GGATCATCCACAACAGTTACAGATGTCTTAAAAGTAATGAGACTCCGGCAGATTCTGCA    1336
          :::                |||
Db   391  ProGlyThrAlaAlaSerThrAsnThrLeuLysAsnLeuAlaAlaSerProAlaAsnSerGlu  410

Qy  1337  CTACAATATACAGGGACCATCATCTTCACAGGAGAAAAGTTATCAGAGACAGAGGCCGCA  1396
          :::::||   ||:::   ::::||||||       |||:::
Db   411  IleGluTyrGlyGlyValThrAlaIleValPheSerGlyLysLeuSerProGluLysAlaAla  430

Qy  1397  GATTCTAAAAATCTTACTTCAGAAGCTACTACAGCCTGTAACTCTTTCAGGAGGTACTCTA  1456
          |||:::  :::::|||
Db   431  IleAlaAlaAlaAsnValThrSerThrIleArgThrLeuAlaValLeuAlaArgGlyAspLeu  450

Qy  1457  TCTTTAAAAACATGGAGTGACTCTGCAGACTCAGGCCATTCACTCAACAGGCCAGATTCTCGT  1516
          ::::  :::                :::|||
Db   451  ValLeuArgAspSerGlyValThrAlaIleValPheLysAspLeuThrGlnSerProGlySerArg  470

Qy  1517  CTCGAAATGGACTAGGAACTACTCTAGAAACTGCTGATACTAGC---ACCATAAACAAT    1573
          :::::     |||:::        :::     :::
Db   471  IleLeuMetAspGlyThrArgThrThrLeuSerLeuSerAlaAlaAsnLeuLeuAsnGly    490

Qy  1574  TTGGTCATTAACTACCAGTTCTATAGACGGTGCAAAGAGGTGCAAAAATAGAAACCAAAGCT  1633
          :::     ||||||||::::        ::::::   :::
Db   491  LeuAlaValAsnLeuSerSerLeuAspGlyThrArgAsnLysAlaLeuLysThrGluValAla  510

Qy  1634  ACGTCAAAAAAATCTGACTTTATCTGAACCATCACTTATTGGACCCGACCGGCACGTTT     1693
          :::::   :::|||            :::|||
Db   511  AlaAspLysAsnIleSerGlyThrIleThrIleAlaLeuIleLeuSerGlyGlySerPhe    530

Qy  1694  TATGAAAATCATAGTTAAGAAATCCTCAGTCCTACGACATCTTAGAGCTCAAA------  1747
          |||||||||::::   :::
Db   531  TyrGluAsnHisAsnLeuLysSerAlaSerThrTyrProLeuGluLeuThrThrAla    550

Qy  1748  ---GCTTCTGGAAACTGTAACAGCACCGACGACCCCAGATCCTATAATGGTGAGAAA     1804
             :::::   :::
Db   551  GlyAlaAsnGlyThrArgIleThrLeuThrLeuGlyAlaLeuSerThrLeuGluProGlu  570

Qy  1805  TTCCATTACGGCTATCAGGGAACTTGGGGCCCAATTGTTGGGGGGACCAGGGGCCTTCTACG  1864
          |||||:::                |||
Db   571  ThrHisTyrGlyTyrArgGlnTyrAsnTrp---GlnLeuSerTrpAlaAsnArgGlyLysSer  589

Qy  1865  ---ACTGCAACCTTCAACTGGACTAAAACTGGCTATATTCCTAATCCCGAGCGTATCGGC   1921
          :::                     |||||||||||
Db   590  LysIleGlySerIleLeuAsnTrpThrArgTrpArgTyrArgIleTyrIleProSerProGluArgLysSer  609

Qy  1922  TCTTTAGTCCCCTAATAGTCTTATGGAATGCATTATAGATATTAGCTCTCTCCATTATCTT  1981
```

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Db   610  :::   |||                            ||||||||||
          AsnLeuProLeuAsnSerLeuTrpGlyAsnPheIleAspIleArgSerIleAsnGlnLeu    629

Qy  1982  ATGGAGACTGCAAACGACAGAGGGTGCAGGAGGACCGTGCTTTTGGTGTCGTCGATTATCT  2041
          :::                             :::::::::|||
Db   630  IleGluThrLysSerGlyValProPheGluLeuProPheLeuArgGlyLeuSerGlyIleIleAla  649

Qy  2042  AACTTCTTCCATAAGATAGTACAAAAACACGACAGCGCGGGGTTCGCCATTGAGTGCGCGGT  2101
          :::::::||||||::::::::||
Db   650  AsnPhePheTyrArgAspSerMetProThrArgHisGlyPheArgHisIleSerGlyGlyGly  669

Qy  2102  TATGTCATAGGAGGAAACCTACATACTTGTTCAGATAAGATCTTAGTGCTGCCATTTTGT  2161
          ||||   :::::||||            |||
Db   670  TyrAlaLeuGlyIleThrAlaThrProAlaGluAspGlnLeuThrPheAlaPheCys       689

Qy  2162  CAGCTCCTTTGGAAGAGATAGAACTACTTCTGAGCTAGAAATCAAGGTACAGTCTACGGA  2221
          ||||||||||:::   :::
Db   690  GlnLeuPheAlaArgAspArgAsnHisIleThrGlyLysAsnHisGlyAspThrTyrGly   709

Qy  2222  GGAACTTCTATTACCAGCACAACGAAACCTATATCCTCTTCCCTTGCAAACTA-------  2275
          :::||||||
Db   710  AlaSerLeuTyrPheHisHisThrGlyLeuPheAspIleAlaAsnPheLeuTrpGlyTyr   729

Qy  2276  ------CGGCCTTGTTCGTTGCTTATGTTCCTACAGAGATTCCTACGTTCTCTTT       2323
                         :::
Db   730  LysAlaThrArgAlaProTrpValLeuSerGlnIleIleSerGlnIleIleProLeuSerPhe  749

Qy  2324  TCAGGAAACCTTAGTACTACACCCATACGGATAACGATCTGAAAACCAAGTATACAACATAT  2383
          ||||||||::::   :::||||
Db   750  AspAlaAlaLysPheSerTyrLeuHisThrAspAsnHisMetLysThrTyrTyrThrAspAsn  769

Qy  2384  CCTACTGTTAAAGGAAGCTGGGGAGATGATAGTTTCGGTCGGTCGGTGGAAGAGCT      2443
          :::::                ||||||||||
Db   770  SerIleIleLysGlySerTrpArgAsnAspAlaPheCysAsnAspLeuGlyArgAlaSerLeu  789

Qy  2444  CCGATTTGCTTAGATGAAAGTGCTCTCATTGAGCAGGAAGTGCATCCCCTTCATGAAATTGCAG  2503
          :::||||||||||:::
Db   790  ProPheValIleSerValProTyrLeuLeuLysGluValGluProPheValLysValGln    809

Qy  2504  TTTGTCTATGCACATCAGGAACGTTTTAAAGACAGGGAACAGAGGCTCGTGAATTTGGA   2563
          :::::::::|||||||::::
Db   810  TyrIleTyrAlaHisGlnGlnAspPheTyrGluArgHisAlaGluGlyArgAlaPheAsn  829

Qy  2564  AGTAGCCGTCTTGTGGATTCTGCCTTACCTATCCGGATCCGATTTGATAAGGAATCAGAC  2623
          :::::   ||||||:::
Db   830  LysSerGlyValLeuLeuIleAsnValGluProIleGlyValThrPhePheGluLysSerIleLys  849

Qy  2624  TGCCAAGATGCAACGTACAATCTAACTCTTGGTTATACTGTGGATCTTGTTCCTAGTAAC  2683
          :::                |||
Db   850  SerGluLysGlyGlyThrTyrAspLeuMetTyrIleLeuAspMetTyrIleLeuLeuAspAlaTyrArgArgAsn  869

Qy  2684  CCCGACTGTACGACAACACTGCCAACTAGCGGTGATTCTTGGAAAAACCTTCCGTACGAAT  2743
          |||::::|||:::
Db   870  ProLysCysGlnThrThrLeuLeuIleLeuAlaSerSerAspAlaAsnTrpMetAlaTyrGlyThrTyrAsn  889

Qy  2744  TTGGCAAGACAAGCTTTAGTCCTTCGGTGCAGGGGAACCATTTTGCTTTAACTCAAATTT   2803
          |||||||:::
Db   890  LeuAlaArgGlnGlyPheSerValArgAlaAlaAsnHisPheGlyValAsnProHisMet  909

Qy  2804  GAAGCCCTTAGCCAATTTCTTTGAATTGCGTGGGCATCCTGCAATTACAATGTAGAC     2863
          ::::::           ||||||||||
Db   910  GluIlePheGlyGlnPheAlaPheGluValAlaArgSerSerArgAsnTyrAsnThrAsn  929

Qy  2864  TTAGGAGCAAAATACCAATTC  2884
          ||||||:::|||
Db   930  LeuGlySerLysPheCysPhe  936
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Search completed: December 16, 2003, 10:31:21
Job time : 168.5 secs

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                GenCore version 5.1.6
        Copyright (c) 1993 - 2003  Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on:      December 16, 2003, 10:21:34 ; Search time 27 Seconds
                              (without alignments)
                              9402.413 Million cell updates/sec

Title:          US-09-428-122-1
Perfect score:  5409
Sequence:       1 cgctcttacctagtagaggt.........tgtttgctaaaacactttc 3000

Scoring table:  BLOSUM62
     Xgapop  10.0 , Xgapext  0.5
     Ygapop  10.0 , Ygapext  0.5
     Fgapop   6.0 , Fgapext  7.0
     Delop    6.0 , Delext   7.0

Searched:       328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters:    657434

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09428122/runat 16122003_102129_10818/app query.fasta_1.3143
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USR=US09428122 @CGN 1_1 33 @runat 16122003_102129_10818 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  Issued_Patents_AA:*
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     3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
     4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
     5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep:*
     6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2997	55.4	597	4	US-09-198-452A-29	Sequence 29, Appl
2	1940	35.9	930	4	US-09-198-452A-470	Sequence 470, App
3	1917.5	35.5	927	4	US-09-198-452A-472	Sequence 472, App
4	1871	34.6	949	4	US-09-198-452A-478	Sequence 478, App
5	1572.5	29.1	643	4	US-09-198-452A-474	Sequence 474, App
6	1417.5	26.2	922	4	US-09-198-452A-15	Sequence 15, Appl
7	1264	23.4	671	4	US-09-198-452A-468	Sequence 468, App
8	1214	22.4	230	4	US-09-198-452A-30	Sequence 30, Appl
9	1204	22.3	507	4	US-09-198-452A-32	Sequence 32, Appl
10	1130	20.9	1132	4	US-09-198-452A-466	Sequence 466, App
11	1126.5	20.8	1006	4	US-09-556-877-190	Sequence 190, App
12	1126.5	20.8	1006	4	US-09-620-412C-190	Sequence 190, App
13	1126.5	20.8	1006	4	US-09-598-419-190	Sequence 190, App
14	1124.5	20.8	982	4	US-09-556-877-176	Sequence 176, App
15	1124.5	20.8	982	4	US-09-620-412C-176	Sequence 176, App
16	1124.5	20.8	982	4	US-09-598-419-176	Sequence 176, App
17	1015.5	18.8	450	4	US-09-198-452A-35	Sequence 35, Appl
18	888	16.4	530	4	US-09-198-452A-482	Sequence 482, App
19	874	16.2	177	4	US-09-198-452A-28	Sequence 28, Appl
20	865	16.0	880	4	US-09-556-877-175	Sequence 175, App
21	865	16.0	880	4	US-09-620-412C-175	Sequence 175, App
22	865	16.0	880	4	US-09-598-419-175	Sequence 175, App
23	856	15.8	866	4	US-09-556-877-189	Sequence 189, App
24	856	15.8	866	4	US-09-620-412C-189	Sequence 189, App
25	856	15.8	866	4	US-09-598-419-189	Sequence 189, App
26	842	15.6	483	4	US-09-198-452A-27	Sequence 27, Appl
27	821	15.2	494	4	US-09-198-452A-33	Sequence 33, Appl
28	792	14.6	427	4	US-09-198-452A-31	Sequence 31, Appl
29	708	13.1	294	4	US-09-198-452A-469	Sequence 469, App
30	680.5	12.6	1617	4	US-09-198-452A-1035	Sequence 1035, Ap
31	667	12.3	1146	4	US-09-198-452A-580	Sequence 580, App
32	650.5	12.0	969	4	US-09-198-452A-501	Sequence 501, App
33	604.5	11.2	940	4	US-09-198-452A-500	Sequence 500, App
34	582	10.8	1530	4	US-09-556-877-178	Sequence 178, App
35	582	10.8	1530	4	US-09-620-412C-178	Sequence 178, App
36	582	10.8	1530	4	US-09-598-419-178	Sequence 178, App
37	559	10.3	1752	4	US-09-556-877-180	Sequence 180, App
38	559	10.3	1752	4	US-09-620-412C-180	Sequence 180, App
39	559	10.3	1752	4	US-09-598-419-180	Sequence 180, App
40	546.5	10.1	964	4	US-09-556-877-177	Sequence 177, App
41	546.5	10.1	964	4	US-09-620-412C-177	Sequence 177, App
42	546.5	10.1	964	4	US-09-598-419-177	Sequence 177, App
43	546.5	10.1	977	4	US-09-556-877-191	Sequence 191, App
44	546.5	10.1	977	4	US-09-620-412C-191	Sequence 191, App
45	546.5	10.1	977	4	US-09-598-419-191	Sequence 191, App

ALIGNMENTS

```
RESULT 1
US-09-198-452A-29
; Sequence 29, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmen
;  TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pre
;  TITLE OF INVENTION: and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/09/198,452A
;  CURRENT FILING DATE: 1998-11-24
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 29
;  LENGTH: 597
;  TYPE: PRT
;  ORGANISM: Chlamydia pneumoniae
US-09-198-452A-29

Alignment Scores:
Pred. No.:                                   3.44e-256
Score:                                       2997.00
Percent Similarity:        99.67%            Length:              597
Best Local Similarity:     99.67%            Matches:             596
Query Match:               55.41%            Conservative:          0
DB:                                          Mismatches:            1
                                             Indels:                2
                                             Gaps:                  0

US-09-428-122-1 (1-3000) x US-09-198-452A-29 (1-597)

Qy    544 CTTGAGTTGACAAAAAATGTCAGTTTGCTCTTCAGCAGAAAAACTTTTCAACGGATAATGG 603
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 LeuGluPheAsp-LysAsnValSerLeuLeuPheSerLysLysAsnPheSerThrAspAsnGl 20

Qy    604 CGGTGCTATCACCGCAAAAAACTCTTCATTAACAGGGACTACAAATGTCAGCTCTGTTTTC 663
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     20 yGlyAlaIleThrAlaLysThrLeuSerLeuThrGlyThrThrMetSerAlaLeuPheSe 40
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Qy   1744  CAAAGCTTCTGGAACTGTAACAGCACCGCAGTGACTTCCAGATCCTATAATGGTGAGAA  1803
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    400  uLysAlaSerGlyThrValThrSerThrAlaValThrProAspProIleMetGlyGluLy   420

Qy   1804  AATTCCATTACGGCTATCCAGGAACTTGGGGCCCAATTGTTGGGGGACAGGGGCTTCTAC  1863
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420  sPheHisTyrGlyTyrGlnGlyThrTrpGlyProIleValTrpGlyThrGlyAlaSerTh   440

Qy   1864  GACTGCAACCTCAACTGGACTAAAACTGGCTATATCCTAATCCCAGGCGTATCGGCTC  1923
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    440  rThrAlaThrPheAsnTrpThrLysThrGlyTyrIleProAsnProArgIleGlySe   460

Qy   1924  TTTAGTCCTAATAGCTTATGGAATGCATTATAGATATTAGCTCTCCATATCTTAT  1983
                 |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    460  rLeuValProAsnSerLeuThrAsnAlaPheIleAspIleSerSerLeuHisTyrLeuMe   480

Qy   1984  GGAGACTGCAAACGAACGAAGGGTTGCAGGGAGACCGTGCTTTTTGGTGTGCTGGATTATCTAA  2043
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480  tGluThrAlaAsnGluGlyLeuGlnGlyAspArgAlaPheTrpCysAlaGlyLeuSerAs   500

Qy   2044  CTTCTTCCATAAGGATAGTACAAAAAACGACGCGGGTTTCGCCATTGAGTGGCGGTTA  2103
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    500  nPhePheHisLysAspSerThrLysThrArgArgGlyPheArgHisLeuSerGlyGlyTy   520

Qy   2104  TGTCATAGAGGAGAAACCTACATACTTGTTCAGATAAGATTCTAGTGTGCTGCATTTTGTCA  2163
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    520  rValIleGlyGlyAsnLeuHisThrCysSerAspLysIleLeuSerAlaAlaPheCysGl   540

Qy   2164  GCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAATCA-AGGTACAGTCTTACGGAG  2222
                 |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    540  nLeuPheGlyArgAspArgAspTyrPheValAlaLysAsnGlnArgTyrSerLeuArgAr   560

Qy   2223  GAACTCTATTACCAGCACAACGAAACCTATATCTCTTCCTTGCAAACTACACGGCCTT  2282
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    560  gAsnSerLeuLeuProAlaGlnArgAsnLeuTyrLeuSerSerLeuGlnThrThrAlaLe   580

Qy   2283  GTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCTCTTTTCAGGAAACCT  2334
                 ||||||||||||||||||||||||||||||||||||||||||
Db    580  uPheValValLeuCysSerTyrArgAspSerCysSerLeuPheArgGlysPro  597
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RESULT 2

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Alignment Scores:
Pred. No.:                                          Length:          930
Score:               9.18e-163                      Matches:         416
Percent Similarity:  60.97%                         Conservative:    165
Best Local Similarity: 43.65%                       Mismatches:      324
Query Match:         35.87%                          Indels:           48
DB:                  4                               Gaps:             17

US-09-428-122-1 (1-3000) x US-09-198-452A-470 (1-930)

Qy    101  ATGAGAGTCTCTTTCCCCAAGTTGTATTTTCTACATTTGCTATTTCCCTTTGTCTATG  160
                 |||||||                     ||       |||  :::
Db      1  MetLysIleProLeuHisLysLeuLeuIleSerSerThrLeuValThrProLeuLeuLeu   20
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Qy    664  TGAAAATACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTACCATTAC  723
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     40  rGluAsnThrSerSerLysLysGlyGlyAlaIleGlnThrSerAspAlaLeuThrIleTh   60

Qy    724  TGGAAACCAAGGGAAGTCTCTTTTTCTGACAATACTTCTCGGATTCTGGAGCTGCAAT  783
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60  rGlyAsnGlnGlyGlyValSerPheSerAspAsnThrSerSerGlyAlaAlaIl   80

Qy    784  TTTTACGAAGCCTCGGTGACATTCTAATATGCTAAAGTTCCTTTATTGACAATAA  843
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     80  ePheThrGluAlaSerValThrIleSerAsnAlaLysValSerPheIleAspAsnLy  100

Qy    844  GGTCACAGGAGGCGAGCTCCTCAACAACGGGGATAATGTCAGGAGTGCTATCGTGCTTA  903
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    100  sValThrGlyAlaSerSerSerThrThrGlyAspMetSerGlyGlyAlaIleCysAlaTy  120

Qy    904  TAAAACTAGTACAGATACTAAGGTCACCCTACTCATGTGAAAAAGCTCGACTGGCTTCCGG  963
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120  rLysThrSerThrAspThrLysValThrLeuThrGlyAsnGlnMetLeuLeuPheSerAsGl  140

Qy    964  CAATACATCGACACAGCGGGAGGAGCTATCATGTGAAAGCTCGAACTGGCTTCCCGG  1023
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    140  nAsnThrSerThrThrAlaGlyValGlyAlaIleTyrValValLysLysLeuAlaSerGl  160

Qy   1024  AGGACTTATCGAAGATAGTGTGGGAATTGAGTTTATCCGCCGATAGTAGTGGTGACATTGTCTT  1083
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    160  yGlyLeuThrLeuPheSerArgArgAsnSerValAlaGlyIleGlyThrAlaProLysGlyGlyAl  180

Qy   1084  CATAGCTATCGAAGATAGTGGGAATTGAGTTTATCCGCCGATAGTAGTGGTGACATTGTCTT  1143
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180  alIleAlaIleGluGluAspSerGlyGluLeuSerGluLeuSerAlaAlaSerGlyAspIleValPh  200

Qy   1144  TTTAGGGAATACAGTCACTTCTACTCCTGGACGAGATAGAAGTAGTCATCGACTTAGG  1203
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    200  eLeuGlyAsnThrValThrSerThrProGlyThrArgSerSerIleAspLeuGlyIl  220

Qy   1204  AACGAGTGCAAAGATGACAGCTTTGGCGTTCTGCTGGTGAGCCATCTACTTCTATGA  1263
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    220  yThrSerAlaLysMetThrAlaLeuAlaPheCysTrpTrpSerHisLeuLeuTyrPheTyrAs  240

Qy   1264  TCCCATAACTAACTACAGGATCATCCACAACAGTACAGATGTCTAAAAGTTAATGAGACTCC  1323
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    240  pProIleThrThrGlySerThrThrValThrAspValThrAspValLysLysValAsnGluThrPr  260

Qy   1324  GGCAGATTCTGCACTACATATCAGGGACATATCATCTTCACAGGAGAAAAGTTATCAGA  1383
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    260  oAlaAspSerAlaLeuGlnTyrThrGlyAsnIleIlePheThrGlyGluLysuSerGl  280

Qy   1384  GACAGAGGCCGCAGATTCTAAAAATCTTACTTCGAAGCTACTACAGCCTGTAACTCTTTC  1443
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    280  uThrGluAlaAlaAspSerLysAsnLeuThrSerLysLeuLeuGlnProValThrLeuSe  300

Qy   1444  AGGAGGTACTCTATCTTTAAAACATGGAGTGACTCCTGACGATTCCAGGCATTCACTCAACA  1503
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    300  rGlyGlyThrLeuSerLeuLysHisGlyValThrLeuGlnAsnThrGlnAlaPheThrGlnGl  320

Qy   1504  GGCAGATTCTCGTCTGCTGAAATGACGTGTAGGGAACGACTACTCTCGATACTACGAC  1563
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    320  nAlaAspSerArgLeuLeuGluMetAspValGlyThrThrLeuGluProAlaAspThrSerTh  340

Qy   1564  CATAAAACAATTTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGAAGGCAAAAATAGA  1623
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    340  rIleAsnAsnLeuValIleAsnIleSerIleSerGlyAlaAlaLysLysAlaLysIleGl  360

Qy   1624  AACCAAAGCTACGTCAAAAAATCTGACTTTTATCTGAACCATCACTTTATTGACCCGAC  1683
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    360  uThrLysAlaThrSerLysAsnLeuThrLeuSerGlyThrIleThrLeuLeuAspProTh  380

Qy   1684  GGGCACGTTTTATGAAAATCATAGTTAAGAAAATCCTCAGTCCTACGACATCTTAGAGCT  1743
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    380  rGlyThrPheTyrGluAsnHisSerLeuArgAsnProGlnSerTyrAspIleLeuGluGlu  400
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Qy   161  ---ATTGCTACC--------GAGACAGTTTGATTCAAGTGCGAGTTTCGATGGGAAT  208
             |||||              ::       ||||||||||||||||||
Db    21  SerIleAlaThrGlyAlaAspAlaSerLeuSerProThrAspSerPheAspGlyAla   40

Qy   209  AAAAATGGTAATTTTCAGTTCGTCGAGAGATGCTCAGGAGAGTCGGAACTACCTATTT  268
             |||::    ::    :::      |||||    |||||
Db    41  GlyGlySerThrPheThrProLysSerThrAlaAspAlaAsnGlyThrAsnTyrValLeu 60

Qy   269  AAGGGAAATGTCACTCTAGAAAAATATTCCTGGAACAGGACAGCAATCACAAAAAGCTGT 328
             :::                ::        |||
Db    61  SerGlyAsnValTyrIle---AsnAspAlaGlyIleLysGlyThrAlaLeuThrGlyCysCys 79

Qy   329  TTTAACAACATCAAGGGCGGATTTGACTTTGCACAGGTAACGGGAACTCTCTATTGTTCCAA 388
             |||               |||      |||
Db    80  PheThrGluThrThrGlyAspLeuThrPheThrGlyTyrLysGlyTyrSerPheSerPheAsn 99

Qy   389  ACGGTGGATGCAGGGACTGTAGCAGGGGCTGCTGTTAACAGCAGCGTGGTAGATAAATCT 448
             ||||||:::    ||::      ||:::        :::
Db   100  ThrValAspAlaGlySerAsnAlaGlyValAlaAlaAla---SerThrThrAlaAspLysAla 118

Qy   449  ACCACGTTTATAGGGTTTTTCTGCTATCTTTATTGCGTCTCCTGGAAGTTCGATAACT 508
             ||||||||||||      ||||::    ::    ||
Db   119  LeuThrPheThrGlyPheSerAsnLeuSerPheIleAlaAlaProGlyThrThrValAla 138

Qy   509  ACCGGCAAAGAGCCGTTAGCTGCTCCTACGGGTAGCTTGAGTTTGACAAAAAATGTCAGT 568
             :::|||      :::||||      |||      ||
Db   139  SerGlyLysSerThrLeuSer---SerAlaGlyValAlaLeuAsnLeuThrAspAsnGlyThr 157

Qy   569  TTGCTCTTCAGCAAAAACTTTTCAACGGAT--------AATGGCGGTGCTATCACCGGCA 619
             :::||      |||::    ||||||      ||||||
Db   158  IleLeuPheSerGlnAsnValSerArgAsnGluAlaAsnAsnAsnGlyAlaIleThrAla 177

Qy   620  AAAACTCTTTCATTAACAGGGACTACAATGTCAGTCTGTTTTCTGAAAATACCTCCTCA 679
             :::||||||      ||||      ||||||      :::
Db   178  LysThrLeuSerIleSerGlyAsnThrSerSerIleThrPheThrSerAsnSerAlaLys 197

Qy   680  AAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCCTACCATTACTGGAAACCAAGGGGAA 739
             ||||||      ||||||      :::            :::
Db   198  LysLeuGlyGlyAlaIleGlnThrSerSerAlaAlaAlaSerIleSerGlyAsnThrGlyGln 217

Qy   740  GTCTCTTTTTCTGACAATACTTCTTCGGATTCTGGAGCTGCCAATTTTACAGAAGCCTCG 799
             :::      |||||      ||||||            |||
Db   218  LeuValPheMetAsnAsnLysGlyGluThrGlyValGlyAlaAlaLeuGlyPheGluAlaSer 237

Qy   800  GTGACTATTTCTAATAATGCTAAAGTTTCCTTTATTGACAATAAGGTCACAGGAGCGAGC 859
             |||      ||:::    ::    |||:::
Db   238  SerSerIleThrGlnAsnAsnSerLeuProPheSerGlyAsnThrAlaThrPheAlaGlnAla 257

Qy   860  TCCTCAACACGGGGGATATGTCAGGAGGTGCTATCTGTGCTTATAAACTAGTACAGAT 919
             ||||||      |||::      |||||
Db   257  ProThrLeuThrIleSerGlyAsnThrPheAlaGlyAsnSerSerValThr 271

Qy   920  ACTAAGGTCACCCTCACTGGAAATCAGATGTTTACTCTTCAGCAACAATACATCGACAACA 979
             :::|||      ::    |||||:::
Db   272  SerSerIleThrGlnAsnSerLeuThrPheAlaGlyAsnThrSerValGlyAla 291

Qy   980  GCGGGAGGAGCTATCTATGTGGAAAAAGCTGCCGAGGACTTACCCTATTC 1039
             |||||||||||      :::    |||||
Db   292  GlnIleGlyAlaIleCysAlaHisAspSerLeuAspLeuGlySerAlaAlaIleAlaIleAlaAsp 311

Qy  1040  AGTAGAAATAGTGTCAATGAGGTACAGCTCCTAAAGGTGAGCCATAGCTATCGAAGAT 1099
             ||||||||||      |||      ::    |||::
Db   312  SerAsnAsnArgCysGlyAsnThrAlaAlaLysGlyGlyLysGlyAlaIleAlaIleAlaAsp 331

Qy  1100  AGTGGGGAATTGAGTTTATCCCGCCGATAGTGGTGACATTGTCTTTTTAGGGGAATACAGTC 1159
             |||||||||||:::      ::    |||      |||::
Db   332  SerGlySerLeuSerLeuAsnGlnGlyAspIleThrPheLeuGlyLeuAsnThrLeu 351

Qy  1160  ACTTCTACTACT---CCTGGGACGAATAGAAGTAGTATCGAATCAGAAGGTGCAAAG 1216
             ::            ||||||      ::    ||||||
Db   352  ThrSerThrSerAlaProThrSerThrArgAsnAlaIleTyrLeuGlyLysSerAlaLys 371

Qy  1217  ATGACACAGCTTTGCGTTGCGTTCTGCTCTGCGTGAGAGCCATCTCTATGATCCATA------ 1270
             |||||||||||
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Qy   372  IleThrAsnLeuArgAlaAlaLeuGlnGlyGlnSerIleTyrPheTyrAspProIleAlaSer  391
            :::|||    |||||||||||||||||||
Db  1271  ---ACTACAGGATCATCCACAACAGTTACAGATGTCTTAAAAGTTAATGAGACTCCGGCA   1327

Qy   392  AsnThrThrGlyAlaSer------                    AspValLeuThrIleAsnGlnProAspSer  407
            |||::::                                     :::
Db  1328  GATTCTGCACTACAATATACAGGGAACACATCATCTTCACAGGAGAAAGTTATCAGAGACA   1387

Qy   408  AsnSerProLeuAspTyrSerGlyTyrIleValPheSerArgGlyGluLysSerAlaAsp   427
            :::|||    :::      :::
Db  1388  GAGGCCGCCAGATTCTAAAAATCTTACTCGAAGCTACTACAGCCTGTAACTCTTCAGGA   1447

Qy   428  GluAlaLysAlaLeuAlaAspAsnPheThrSerIleLeuLysGlnProLeuAlaLeuAlaSer  447
            :::|||      |||
Db  1448  GGTACTCTATCTTAAACATGGAGTGACTCTGCGACTCAGGCATTCACTCAACAGGCA   1507

Qy   448  GlyThrLeuAlaLeuLysGlyAsnValGluLeuAspValAsnGlyPheThrGlnThrGlu   467
            |||||||||::      :::    ||
Db  1508  GATTCCGTCTCGAAATGGACGTAGGGAACTACTCTAGACCTGCTGATACTAGCACCATA   1567

Qy   468  GlySerThrLeuLeuMetGlnProGlyThrLysLeuLys---AlaAspThrGluAlaIle   486
            ::
Db  1568  AAC------AATTGGTCATTAACATCAGTTCTATGAGACGTGCAAGAAGCAAAAATA   1621

Qy   487  SerLeuThrLysLeuValValAspLeuSerAlaLeuGluGlyLysAsnLysSerValSerIle  506
            :::||||||      ::      |||
Db  1622  GAAACCAAAGCTACGTCAAAAAAATCTGACTTTATCCAGTTAATGGAACCATCACTCTTATTGGACCCG   1681

Qy   507  GluThrAlaGlyAlaLysAsnLysSerThrIleThrLeuThrSerProLeuValPheGlnAsnAspSer  526
            :::                    ::
Db  1682  ACGGGCACGTTTTATGAAAATCATAGTTTAAGAAATCATCCAGTCCTACGACCATCTTAGAG   1741

Qy   527  SerGlyAsnPheTyrGlySerHisThrIleAsnGlnAlaPheThrGlnProLeuValVal   546
            :::                    ::::::
Db  1742  CTCAAAGCTTCT----------                    GAACCTGTAACAAGCACCGCA   1774

Qy   547  PheThrAlaAlaThrAlaAlaSerAspIleTyrIleAspAlaLeuLeuThrSerProVal   566
            |||:::
Db  1775  GTGACTCCAGATCCTATAATGGTGAGAAATCCATTACGGCTATCAGGGAACTTGGGGC   1834

Qy   567  HisTyrGlyTyrGlnGlyHisHisTrpGluVal   580
            |||:::                    :::
Db  1835  CCAATTGTTGGGGACAGGGCCTTCTACGACGTTCCAACTTCAACTGGACTAAAACTGGC   1894

Qy   581  AlaThrTrpAlaAspThrArgAlaLysSerGlyIleThrMetThrTrpValThrThrGly   600
            :::    :::
Db  1895  TATATTCCTAATCCCGAGCGTATCGGCTCTTAGTCCCTAATAGCTTATGGAATGCATTT   1954

Qy   601  TyrAsnProAsnProGluArgArgAlaSerValValProAspSerLeuTrpAlaSerPhe   620
            |||    :::                    :::||||||
Db  1955  ATAGATATTAGCTCTCCATTATCTTTATGGAGACTGCAAACGAGGGTTGCAGGGGAGAC   2014

Qy   621  ThrAspIleArgThrLeuGlnIleAsnIleMetThrSerGlnAlaAsnSerIleTyrGlnGln  640
            |||||||||::
Db  2015  CGTGCTTTTGGTGTGCTGGATTATCTAACTCTTCCATAAGGATAGTACAAAAACACGA   2074

Qy   641  ArgGlyLeuTrpAlaSerGlyThrAlaAsnPheHisLysAspHisLysSerAspLeuPheIle  660
            |||      :::                    :::||
Db  2075  CGCGGGGTTTCGCCATTGAGTGGTGCCGGTTATGTCATAGGAGGAAACCTACATACTTGTTCA   2134

Qy   661  GlnAlaPheArgHisLysSerTyrGlyTyrIleValGlyValGlySerAlaGluAspPheSer   680
            :::                    ::                    |||||
Db  2135  GATAAGATTCTTAGTGCTGCCATTTGTCAGTTCGCAGCTCTTTTGGAAGAAGATAGACTACTTGTA   2194

Qy   681  GluAsnIlePheSerValAlaPheCysGlnLeuPheGlyLysLysAspLeuLysAspLeuPheIle  700
            |||||||      |||::      :::
Db  2195  GCTAAGAATCAAGGTACAGGTCCAGAGGAACTCTCATTACCAGCACAACGAACAAACCTAT   2254

Qy   701  ValGluAsnThrSerHisAsnTyrLeuAlaSerLeuTyrLeuGlnHisArgAlaPheLeu   720
            :::|||      ::    ||
Db  2255  AACTCTCCTTCCTTGCAAACTACGGGCCCTTGT--------                    -TCGTTGCTTATGTTCCTACAGAG   2308
            ||::::::    ||:::::    :::
```

```
Db    721  GlyGlyLeuPro-------MetProSerPheGlySerIleThrAspMetLeuHisLysAsp  737

Qy   2309  ATTCCGTTCTCTTTTCAGGAAACCTTAGCTACACCCATACGGATAACGATCTGAAAACC  2368
           ||||||||||  :::  : ||        :::                        ||
Db    738  IleProLeuIleLeuAsnAlaGlnLeuSerThrTyrSerTyrThrLysAsnAspMetAspThr  757

Qy   2369  AAGTATACAACATATCCTACTGTTAAAGGAAGCTGGGGAATGATAGTTTCGCTTTAGAA  2428
           :::||| |:||::||||                 |||||||||||||||
Db    758  ArgTyrThrSerTyrProGluAlaGlnGlySerTrpThrAsnSerGlyAlaLeuGlu  777

Qy   2429  TTCGGTGGAGAGCTCCGATTGCTTA---GATGAAAGTGCTCTATTTGAGCAGTACATG  2485
           ||||||            |||  :::    |||||||      |||:||
Db    778  LeuGlyGlySerLeuAlaLeuTyrLeuProLysGluAlaProPheGlnGlyTyrPhe  797

Qy   2486  CCCTTCATGAAATTGCAGTTTGTCTATGCACATCAGGAAGGTTTTAAAGAACAGGGAACA  2545
           :::||     ||::||||||||        |||    ||||||||||    :||
Db    798  ProPheLeuLysPheGlnIleAlaValTyrSerArgGlnGlnAsnPheLysGluSerGlyAla  817

Qy   2546  GAAGCTCGTGAATTGGAAGTAGCCGGTTCTGCCTAACCTACCTATCGGGATCCGA  2605
           ||||||            :::|||| ||||:    :::|||:|||||||||
Db    818  GluAlaArgAlaPheAspGlyAspGlyAsnCysSerIleProValGlyIleArg  837

Qy   2606  TTTGATAAGGAATCAGACTGCCAAGATGCAACACTACAATCTAACTCTTGGTTATACTGTG  2665
           |||          :::  ||||||:::                |||:::|||||
Db    838  LeuGluLysIleSerGluAspGluLysAsnAsnPheGluIleSerLeuAlaTyrIleGly  857

Qy   2666  GATCTCGTTCGTAGTACACCCGACTGTACGACAACATGCGGAATTACGCGGTGATTCTTGG  2725
           :::||   :::|||| :::||          ||||||||||||||||||
Db    858  AspValTyrArgLysAsnProArgSerArgThrSerLeuMetValSerGlyAlaSerTrp  877

Qy   2726  AAAACCTTCGGTACGAATTGGCAAGACAAGCTTAGTCCCTTCGTGCAGGAACCATTT  2785
           :::        |||||||||||||||||:::||
Db    878  ThrSerLeuCysLysAsnLeuAlaArgGlnAlaPheLeuAlaSerAlaGlySerHisLeu  897

Qy   2786  TGCTTTAACTCAAATTTGAAGCCTTTAGCCAATTTCTTTTGAATTGCGTGGGTCATCT  2845
           :::  :::|||||||||||||:::      :::||||||||||:::
Db    898  ThrLeuSerProHisValGluLeuSerGlyLeuAlaAlaTyrGluArgGluArgGlySerAla  917

Qy   2846  CGCAATTACAATGTAGACTTAGGAGCAAAATACCAATTC  2884
           ||||||        :::    |:::||||||
Db    918  HisIleTyrAsnValAspCysGlyLeuArgTyrSerPhe  930
```

RESULT 3
US-09-198-452A-472
; Sequence 472, Application US/09198452A
; Patent No. 6559294
GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 472
; LENGTH: 927
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1...927
; OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-472

Alignment Scores:
Pred. No.:
Score: 1917.50
Percent Similarity: 60.23%
Best Local Similarity: 44.81%
Query Match: 35.45%

Length: 927
Matches: 427
Conservative: 147
Mismatches: 328
Indels: 51
Gaps: 4

8.89e-161

```
US-09-198-452A-472 (1-3000) x US-09-198-452A-472 (1-927)

Qy    101  ATGAAGTCTTCTTTCCCCAAGTTGTATTTCTACATTGCTATTTTCCCTTGTCTATG  160
           ||||||||||||||  :::  : ||
Db      1  MetLysSerSerLeuHisTrpPheLeuIleSerSerLeuAlaLeuProLeuSerLeu  20

Qy    161  ----------ATTGCTACCGACAGCAGTTTGGATTCAAGTGCGAGTTTCGAT  202
                    :::||| |:||::||||
Db     21  AsnPheSerAlaPheAlaAlaValValGluIleAsnGlyProThrAsnSerPheSer  40

Qy    203  GGGAATAAAAATGGTAATTTTCAGTTCGTGAGAGTCAGGAAGATGCT---GGAACTACC  259
           ||||||            |||  :::
Db     41  Gly------ProGlyThrTyrProProAlaGlnThrThrAsnAlaAspGlyThrIle  58

Qy    260  TACCTATTTAAGGGAAAATGTCACTCAGGAAGGTTTTAAAGAACAGGCACAGCAATACA  319
           :::||     ||::||||||||
Db     59  TyrAsnLeuThrGlyAspValSerIleThrAsn---AlaGlySerProThrAlaLeuThr  77

Qy    320  AAAAGCTGTTTTAACACACTAGGGGCCGATTTGACTTTCACAGGTAACGGAACTCCTCTA  379
           :::||     ||::||||||||
Db     78  AlaSerCysPheLysGluThrThrGlyAsnLeuSerPheGlnGlyHisGlyTyrGlnPhe  97

Qy    380  TTGTTCCAAACGGTGGATGCAGGAGACTGTAGCAGGGGCTGCTGTTAACAGCAGCGGTGGTA  439
           |||          :::  ||||||:::
Db     98  LeuLeuGlnAsnIleAspAlaGly------AlaAsnCysThrPheThrAsnThrAlaAla  115

Qy    440  GATAAAATCTACCACGTTTATAGGGTTTCTTCGTCATCTTTATTGGCGTCTCCTGGAAGT  499
           :::||   :::||||
Db    116  AsnLysLeuSerPheSerGlyThrPheTyrLeuLeuIleGlnThr------Thr  133

Qy    500  TCGATAACTACCGGCAAAGGAGCCGTTAGCTGCTGCTCACGGGTAGTCTTGAGTTTGACAAAA  559
           :::        |||||
Db    134  AsnAlaThrThrGlyThrGlyAlaIleLeuLys---SerThrGlyAlaCysSerIleGlnSer  152

Qy    560  AATGTCAGTTGCTCTTCAGCAAAAACTTTCAACGGCGATAATGGCGGTGCTATCACCGCCA  619
           |||  :::|||||||||||||
Db    153  AsnTyrSerCysTyrPheGlyGlnAsnPheSerAsnAspAsnGlyAlaLeuGlnGlyGly  172

Qy    620  AAACTCTTTCATTAACAGGGACTTAGGAGCATGTCAACAATGGGAAAATACCTCCTCA  679
           ||||||        :::
Db    173  SerSerIleSerLeuSer---LeuAsnProAsnLeuThrPheAlaLysAsnLysAlaThr  191

Qy    680  AAGAAGGCGGAGCCATTCAACGATGCCCTGATGCCCATACCATTACTGGAAACCAAGGGGAA  739
           :::||||||  ::::::
Db    192  GlnLysGlyGlyAlaLeuTyrSerThrGlyLyIleThrPheGlyLyIleAsnThrLeuAsnSer  211

Qy    740  GTCTCTTTTCTGACAATACTCTTCGGATTCTGGAGCTGCAATTTTTACAGAGAGCCTCG  799
           :::||   :::||||
Db    212  AlaSerPheSerGluAsnThrAlaAlaAsnAsnGlyGlyAlaIleTyrThrGluAlaSer  231

Qy    800  GTGACTATTTCTAATAATGCTAAAGTTCCTTTATTGACAATAAAGGCTCAGGAGGCGAGC  859
           :::||||||  ::|||
Db    232  SerPheIleSerSerAsnLysAlaIleSerPheIleAsnSerValThrAlaThrSer  251

Qy    860  TCCTCAACAGCGGGGATATGTCAGGAGGTGCTATCTGTGCTTATAAAACTAGTACAGAT  919
           :::||
Db    252  Ala------ThrGlyGlyAlaIleTyrCysSerSerThrSerAlaPro  265

Qy    920  ACTAAGGTC---ACCCTCACTGGAAATCAGATGTTACTCTTCAGCACAACAATACGACA  976
           :::|||||:::
Db    266  LysProValLeuThrLeuSerAspAsnGlyLeuLeuAsnPheIleGlyIleAsnThrAlaIle  285

Qy    977  ACAGCGGAGGAGCTTATCTATGTGAAAAAGCTCGAACTGGCTTCCGGAGGACTTACCCTA  1036
           :::||||||||||||||:::||
Db    286  ThrSerGlyGlyAlaIleTyrThrAspAsnLeuValLeuSerGlyGlyProThrLeu  305

Qy   1037  TTCAGTAGAAATAGTGTCAATGGAGGTACAGCTCCTAAAGGTGGAGCCATAGCTATCGAA  1096
           :::||||||||||||
Db    306  PheLysAsnSerAlaAsnSerAlaIleAs</AspThrAlaAlaProLeuGlyGlyAlaIleAlaAla  325

Qy   1097  GATAGTGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGGTGACTTTTTAGGGAATACA  1156
           :::||||||||||||:::
Db    326  AspSerGlySerLeuSerLeuAlaLeuGlyGlyAspIleThrPheGluThrGlyAsnThr  345
```

```
Qy  2201 AATCAAGGTACAGTCTACGGAGGAACTCTCTATTACCAGGACAACGAAACCTATATCTCT 2260
              ::::::   :::      ||||||        ::::|||||  |||||||
Db   701 AsnArgAlaSerAlaTyrAlaAlaSerLeuHisLeuGlnHisLeuGlnThrLeuSerSer 720

Qy  2261 CTTCCTTGCAAACTACGGCCTTGTTCGTTCGTTCTTATGTTCCT--------ACAGAGATT 2311
                             ::::|||                          ::|||
Db   721 -----------------ProSerLeuLeuArgTyrLeuProGlySerGluSerGluGln 734

Qy  2312 CCTGTTTCTCTTTTCAGGAAACCTTAGCTACCACCCATACACGGATAACGATCTGAAACCCAAG 2371
              |||||||||       ::::::     ::|||    |||||||   :::||||
Db   735 ProValLeuPheAspAlaGlnIleSerTyrIleTyrSerLysAsnThrMetLysThrTyr 754

Qy  2372 TATACAACATATCCTACTGTTAAAGGAAGAGCTGGGGGAATGATAGTTTCGCTTTAGAATTC 2431
              ||||||||        :::       |||||||||||         |||
Db   755 TyrThrThrGlnAlaProLysGluSerTrpTyrTyrAsnAspGlyCysAlaLeuGluLeu 774

Qy  2432 GGTGGAAGAGCTCCG--ATTTGCTTAGATGAAAGTGCTCTATTTGAGCAGTACATGCCC 2488
              |||||       ::                |||||||  |||||:::|||||||||
Db   775 AlaSerSerLeuProHisThrAlaLeuSerHisGluGlyLeuPheHisAlaTyrPhePro 794

Qy  2489 TTCATGAAATTGCAGTTGTCTATGCAACATCAGGAAGGTTTAAAGAACAGGAGAACAGAA 2548
              |||:::||:::||||||||     ::::||||||||||||||||||
Db   795 PheIleLysValGluAlaSerTyrIleHisGlnAspSerPheLysGluArgArgAsnThrThr 814

Qy  2549 ---GCTCGTGAATTGGAAGTAGCCGTCTGTGAATCTTGCTTACCTATCGGGATCCGA 2605
                 |||   |||||||||||||        :::::::::::|||||||
Db   815 LeuValArgSerPheSerGlyAspSerGlyLeuIleAsnValSerValProIleGlyIleThr 834

Qy  2606 TTTGATAAGGAAATCAGACTGCCAGAATGCAACGTACAACATCTAACTCTTGGTTATACTGTG 2665
              |||            :::     |||||||||:::||||||:::|||
Db   835 PheGluLysArgPheSerArgAsnGluArgAlaSerTyrGluAlaThrValIleTyrValAla 854

Qy  2666 GATCTTGTTCGTAGTAACCCGACTGTACAACAACCACTGCGAATTAGCGGTGAATTCTGG 2725
              :::|||  |||        :::|||||||||:::|||||||||||||||
Db   855 AspValTyrArgLysAsnProAspCysThrThrAlaLeuLeuIleAsnAsnThrSerTrp 874

Qy  2726 AAAACCTTCGGTACGAATTTGGCAAGACAAGCTTTAGTCCTTCGTGCAGGGAACCATTTT 2785
              |||||||||:::                 :::      |||||||
Db   875 LysThrThrThrGlyThrAsnLeuSerArgGlnAlaGlyIleGlyArgAlaGlyIlePheTyr 894

Qy  2786 TGCTTTAACTCAAATTTGAAGCCTTTAGCCAATTTCTTTTGAATTGCCGTGGGTCATCT 2845
              :::|||       |||||||||        |||||||
Db   895 AlaPheSerProAsnLeuGluValThrSerAsnLeuSerMetGluValGlySerSer 914

Qy  2846 CGCAATTACAATGTAGACTTAGGAGCAAAATACCAATTC 2884
              |||||||||||||        |||||||||||||
Db   915 ArgSerTyrAsnAlaAspLeuGlyLyLysPheGlnPhe 927
```

RESULT 4
US-09-198-452A-478
; Sequence 478, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
;   APPLICANT: Griffais, R.
;   TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmen
;   TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pre
;   TITLE OF INVENTION: and treatment of infection
;   FILE REFERENCE: 9710-003-999
;   CURRENT APPLICATION NUMBER: US/09/198,452A
;   CURRENT FILING DATE: 1998-11-24
;   NUMBER OF SEQ ID NOS: 6849
;   SEQ ID NO 478
;   LENGTH: 949
;   TYPE: PRT
;   ORGANISM: Chlamydia pneumoniae
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: 1..949
;   OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-478

Alignment Scores:
Pred. No.:   1.15e-156   Length: 949

us-09-428-122-1.rai

```
Score:                1871.00      Matches:         413
Percent Similarity:   60.49%       Conservative:    175
Best Local Similarity: 42.49%      Mismatches:      334
Query Match:          34.59%       Indels:           50
DB:                     4          Gaps:             22

US-09-428-122-1 (1-3000) x US-09-198-452A-478 (1-949)
```

```
Qy     50  TTGGTGTATCCTTAAAATATTAAATT----------------CAAAATCAAAGTATA   91
               ||||||||||            :::       :::||||||
Db      1  LeuIleTyrLeuPheCysPheTyrIleAspAlaAsnSerSerLeuLysAsnLysSerIle   20

Qy     92  TATTTTACAATGAAGTCTTCTTCCCCAAGTTGTATTTCTACATTTGCTATTTTCCCT  151
               |||||:::||      ::::||||||           :::  |||||
Db     21  ----ThrMetLysThrSerIleProTrpValSerSerValLeuValAlaPheSer   38

Qy    152  ----TTGTCTATGATTGCTACCGAGACAGTTTTGATTCAAGTGGAGTTCGATGGG  205
               ::::|||           ::::|||
Db     39  CysHisLeuGlnSerLeuAlaAsnGluGluLeuLeuSerProAspSerPheAsnGly   58

Qy    206  AAT--------AAAAATGGTAATTTTCAGTTCGTGAGAGTCAGGAAGAGATGCTGAACTACCTAC  262
               :::|||     :::||||:::  ::: |||
Db     59  AsnIleAspSerGlyThrPheThrProLysThrSer--------AlaThrThrTyr   74

Qy    263  CTATTTAAGGAAAATGCACTCTAGAAAAATATTCCTGAACAGCCACAGCAATCACAAAA  322
               ||||||         ::::::
Db     75  SerLeuThrGlyAspValPhePheTyrGlu---ProGlyLysGlyThrProLeuSerAsp   93

Qy    323  AGCTGTTTTAACACACTCAAGGGCGATTGACTTTCACAGTTCAGAGGTAACGGGAACTCTATTG  382
               ||||||         ::  |||||||   ||:::  |||||
Db     94  SerCysPheLysGlnThrThrAspAsnLeuThrPheLeuGlyAsnGlyAsnGlyHisSerLeuThr  113

Qy    383  TTCCAAACGGTGCGGATGCGAGGGAGACTCTGTAGCAGGGGCTGCTGTTAACACGAGCGGTGGTAGAT  442
               |||           ::::|||||
Db    114  PheGlyIlePheIleAspAlaGlyThrArgHisAlaGlyIleThrAlaAlaAla---SerThrAlaAsn  132

Qy    443  AAATCTACCACCGTTTATAGGGTTTCTTCCGTATCTATCTTTATTGCGTCCTCCGAAGTCG  502
               |||||||:::  ||||         :::|||
Db    133  LysAsnLeuThrPheSerGlyPheSerLeuLeuSerLeuSerLeuSerPheAspSerProSerThrThr  152

Qy    503  ATAACTACCGGCCAAAGGAGCCGTTAGCTCGTTACGGGTAGCTTGAGTTGACAAAAAAT  562
               ||||||||         :::|||
Db    153  ValThrThrGlyGlnGlyThrLeuSer---SerAlaGlyGlyValAsnLeuGluAsnIle  171

Qy    563  GTCAGTTTGCTCTTCAGCAAAAAACTTTTCAACCGGATAATGGCCGGTGCTATCACCGCAAAA  622
               :::|||||||:::           |||||
Db    172  ArgLysLeuValValAlaGlyValAlaAsnPheSerThrAlaAspGlyValGlyAlaIleLeuLysGlyAla  191

Qy    623  ACTCTTTTCATTAACAGGACTACAATGTCAGCGTGTTTCTGAAAATACCTCTCAAAG  682
               :::           |||||||||||
Db    192  SerPheLeuLeuThrGlyThrSerGlyAlaAspPheSerAlaLeuPheSerAsnAsnSerSerThr  211

Qy    683  AAAGGCGGAGCCATTCAGATCTTCCGTATGCCCTTACCATTACTGGAAACCAAGGGGAAGTC  742
               |||         ::::||||||
Db    212  LysGlyGlyAlaIleIleAlaThrThrAlaGlyIleAlaArgIleAlaAlaAsnAsnThrGly  231

Qy    743  TCTTTTTTTCTGACAATACTTCTTCCGATTCGGAGCTGCAATTTTTTACAGAAGCCTCGGTG  802
               :::  ||||||
Db    232  ArgPheLeuSerAsnIleLeuThrThrSerGlyThrSerGlyIleValAlaIleLeuAspAspSerPro  251

Qy    803  ACTATTCTAATAATGCTAAAGTTCCTTTATTGACAATAAGGTCACAGGAGGCCTCC  862
               :::           ::::::
Db    252  IleLeuSerAsnAsnLysPheLeuTyrPhe----------GluGlyAlaAsnAlaAla  266

Qy    863  TCAACAACGGGGGATATGTCAGGAGTGCTATCGGCAATTGTTATAAACTAGTACAGATACT  922
               ||||||         ||||||
Db    267  LysThrThr--------GlyGlyAlaIleAlaIleGly------  282

Qy    923  AAGGTCACCCTCACTGGAATAGTTACTCTTCACGAACATCATCGACAACAGCG  982
               ||||||:::  |||
Db    283  GluLeuIleSerAsnAsnLysThrLeuIlePheAlaSerAsnValAlaGluThrSer  302

Qy    983  GGAGGAGCTATCTATGTGAAAAAGTCGAACTAGCTGCTTCCGGAGGACGGACTTACCCTATTCAGT 1042
               :::  |||||||||
```

```
Db    303  GlyGlyAlaIleHisAlaLysLeuAlaLeuSerGlyPheThrGluPheLeu  322

Qy   1043  AGAAATAGTGTCAATGAGGTACAGCTCCTAAAGGTGGAGCCATAGCTATCGAAGAGATAGT 1102
               :::||            ||
Db    323  ArgAsnAsnValSerSerAlaThr---ProLysGlyGlyAlaIleSerIleAspAlaSer  341

Qy   1103  GGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGTCTTTTTAGGGATTACAGTCACT 1162
               ||||||            :::||||||
Db    342  GlyGluLeuSerLeuSerAlaAlaGluThrGlyAsnIleThrPheValArgAsnThrLeuThr  361

Qy   1163  TCTACT--------ACTCCTGGGACGAATAGAGTAGTATCGACTTAGGAACGAGTGCAAAG 1216
               :::           ||
Db    362  ThrThrGlyThrPheThrProLysThrProLysGlyGlyAlaIleSerAsnGlyLys  381

Qy   1217  ATGACAGCTTTGGCTTCTGCTGGTCGCTGGTAGAGCCATCTCACTTCTATGATCCCATAACTACA 1276
               |||||||||
Db    382  PheThrGluLeuArgAlaAlaLysAsnHisThrIlePheProThrTyrAspProIleThr---  400

Qy   1277  GGATCATCCACAACAGTTACAGATGTCTTAAAAGTTAATGACTCCGGCAGATTCTGCA 1336
               :::  ||||||
Db    401  ---SerGluGlyThrSerSerAspValLeuLysIleAsnAsnGlySerAlaGlyAlaLeu  419

Qy   1337  CTACAAATATACAGGGAACATCATCTTCACAGGAGAAAAGTTATCAGAACAGAGGCCCCA 1396
               ||||||:::||||||
Db    420  AsnProTyrGlnGlyThrIleLeuProSerGlyValGluThrLeuThrAlaAspGluLeuLys  439

Qy   1397  GATTCTAAAAATCTTACTTCGAAGCTACTACAGCCCTGTAACTCTTTCAGGAGTACTCTA 1456
               :::           ||
Db    440  ValAlaAspAsnLeuLysSerSerPheThrGlnIleProValSerLeuSerGlyGlyLysLeu  459

Qy   1457  TCTTTAAAACATGGAGTGACTCTGCAGACTCAGGCATTCACTCAACAGGCAGATTCTCGT 1516
               :::||||||
Db    460  LeuLeuGlnLysGlyValThrLeuGluSerThrSerPheSerGlnLeuAlaGlySerLeu  479

Qy   1517  CTCGAAATGGACGTAGGAACTACTCTAGAA-----CCTGCTGATACTAGCACCATAAACAAT 1573
               ||||||||
Db    480  LeuGlyMetAspSerGlyThrThrLeuSerThrThrAlaGlySerIleThrIleThrAsn  499

Qy   1574  TTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGAAGCCAAAAATAGAAACCAAAGCT 1633
               ||||||
Db    500  LeuGlyIleLeuAsnValAspSerLeuGlyLeuLysGlnProValSerLeuThrAlaLysGly  519

Qy   1634  ACGTCAAAAAATCTGACTTTATCTGAACCATCACTTTATTGGACCCGACGGGCACGTTT 1693
               :::
Db    520  AlaSerAsnLysValIleLeuValSerLeuLeuSerLeuLeuAspIleGluGluAsnIle  539

Qy   1694  TATGAAAATCATAGTTAAGAAATCCTCAGTCCAGCATCTTACGAGCTCAAAGCTTCT 1753
               :::    ::
Db    540  TyrGluSerHisMetPheSerHisAspGlnLeuPheSerLeuLeuLysIleThrValAsp  559

Qy   1754  GGAACTGTAACAAGC--------ACCGCAGTGACTGACTCCAGATCCTATAAATGGGTGAG 1801
               :::  :::::::
Db    560  AlaAspValAspThrAsnValAspIleSerSerLeuIleProValProAlaGluAspPro  579

Qy   1802  AAAATTCCATTACGACGGCTATCCAGGGAACTTGGGGCCCAATTGTTGGGGGACCAGGGGCTTCT 1861
               :::           ||
Db    580  AsnSerGluThrTyrGlyPheGlnGlynTrpAsn---ValAsnTrpThrThrAspThrAla  598

Qy   1862  ACGACT--------GCAACCTTCAACTGACTAAAAACTGGCTAATAATTCCTAATCCCGAG 1912
               :::           :::::::
Db    599  ThrAsnThrLysGluAlaThrArgThrTrpThrLysGlyMetGluHisLysGlnLyPheVal  618

Qy   1913  CGTATCGGCTCTTAGTCCCTAAGTGCTTATAAACTAGCATTATGGAATGCATTTATAGATATTAGTCTCTC 1972
               :::  ||||||
Db    619  ArgLysSerAlaLeuValCysAsnThrLeuValPheThrAspIleArgSerLeu  638

Qy   1973  CATTATCTTTATGGAGACTGCAAAACGAAAGGGTGCAGGGGGAGACCCGTGCTTTTTGGTGTGCT 2032
               |||||||||
Db    639  GlnIleLeuGluIleGlyMetGlyMetGluHisLysGlnLyPheTrpValSer  658

Qy   2033  GGATTATCTAACTTCTTCCATAAGAGTAGTACAAAAACACGACGCGCGGGTTCGCCATTTG 2092
               :::::::||||||||
```

```
;   TYPE: PRT
;   ORGANISM: Chlamydia pneumoniae
US-09-198-452A-474

Alignment Scores:
Pred. No.:                  2.2e-130      Length:            643
Score:                      1572.50       Matches:           314
Percent Similarity:         64.50%        Conservative:      93
Best Local Similarity:      49.76%        Mismatches:        209
Query Match:                29.07%        Indels:            15
DB:                         4             Gaps:              6

US-09-428-122-1 (1-3000) x US-09-198-452A-474 (1-643)
```

```
Qy   1022  GGAGGACTTACCCGTTCCATTCAGTAGAAATAGTGTCAATGAGGTACAGCTCCTAAAGGTGGA  1081
           ||||||                   :: ::||||||||   :: ::||     ||||||
Db     18  GGIYGlyGlyIleSerPheSerAsnAsnIleValGlnGlyThrThrAlaGlyAsnGlyGly    37

Qy   1082  GCCATAGCTATCGAAGATAGTGGGGAATGAGTTTATCCGCCGATAGTGTGACATTGTC      1141
           ||||         :: :: ::||||         ::||||||||::|||||
Db     38  AlaIleSerIleLeuAlaAlaGlyGluCysSerSerAlaGluAlaGlyAspIleThr      57

Qy   1142  TTTTTAGGGAATACAGTCACTTCTACTACTCCT---GGGACGAATAGAGTAGTATCGAC    1198
           ||:: :||         ||| ::||||||||||||
Db     58  PheAsnGlyAsnAlaAlaIleValAlaIleValThrProGlnThrThrLysArgAsnSerIleAsp  77

Qy   1199  TTAGGAACGAGTGCAAAGATGCAAAGATGCAGTCGTTTGCGTTCTGCGTCGTGAGAGCCATCTACTTC  1258
           ::|||||||||               :: ::||         :: :||||     ||||||
Db     78  IleGlySerThrAlaLysIleThrAsnLeuArgAlaAlaIleSerGlyHisSerIlePhePhe    97

Qy   1259  TATGATCCCATAACTACAGAGATCATCCACAACAGTTACAGATGTCTTAAAGTTAATGAG   1318
           ||||||||||         :: :: :||
Db     98  TyrAspProIleThrAlaAsnThrAlaAlaAspSerThrAlaAspSerThrLeuAsnLeuAsnLys  117

Qy   1319  ACTCCGGCAGATTCTGCACTACATATACAGGAGAACATCATCTTCACAGGAGAAAAGTTA    1378
           ::|||||         :: ::||::|||||     ::|||||
Db    118  AlaAspAlaAlaGlyAsnSerThrAspTyrSerGlySerIlePheSerGlyGluLysLeu    137

Qy   1379  TCAGAGAGGAGGCCGACGATTCTAAAAATCTTACTTCGAAGCTACTACAGCCTGTAACT    1438
           ||||||                :: :: :||         :: :: :||     |||
Db    138  SerGluAspGluAlaLysValAlaAlaAspAsnLeuThrSerThrLeuLysGlnProValThr  157

Qy   1439  CTTTCAGGAGGTACTCTATCTTTAAAACATGGAGGTGACTCTGCAGACTCAGGCATTCACT  1498
           ||||::|||         :: :: ::||||||||||||
Db    158  LeuThrAlaGlyAsnLeuValLeuLysValArgGlyValValValAspThrThrLysGlyPheThr  177

Qy   1499  CAACAGGCAGATTCTCGTCTCGAAATGGACGTAGGAAGAACTACTCTAGAAACCTGCT---GAT  1555
           ||::|||||         :: :: :: ||||||||         :: :||
Db    178  GlnThrAlaGlySerValIleMetAspAlaGlyThrThrLeuLysAlaSerThrGlu    197

Qy   1556  ACTACGACCATAAAACAATTGGTCATTAACATCAGTTCATAGAGACGTGCAAGAAGGCA    1615
           :: :||         :: :||         ||||||
Db    198  GluValThrLeuThrGlyLeuSerIleProValAspSerLeuGlyGluGlyLysLysVal  217

Qy   1616  AAAATAGAAACCAAAGCTACGTCAAAAAATCGACTTATCTGGAACCATCACTTATTG    1675
           ||||||         :: ::
Db    218  ValIleAlaAlaSerAlaAlaSerLysAsnValAlaLeuSerGlyProIleLeuLeuLeu  237

Qy   1676  GACCCGACGGCACGTTTATGAAAATCATAGTTTAAGAAATCCTCAGTCCTACGACACATC  1735
           ||||||||         :: :
Db    238  AspAsnGlnAlaGlyAsnAlaTyrGluAsnHisAspLeuGlyLysThrGlnAspPheSerPhe  257

Qy   1736  TTAGAGCTCAAAGCTTCTGGAACTGTAACAAGCACCGAGTGACTCCAGATCCTATAAATG  1795
           ||::|::|::|||         :: :||||||
Db    258  ValGlnLeuSerAlaLeuGlyThrAlaThrThrAspValProAlaValProThrVal    277

Qy   1796  GGTGAGAAATTCCATTACGGCTATCAGGGAGACTTGGGCCCCAATTGTTTGG--------  1846
           ||||||::|||         ||| ::|||
Db    278  AlaThrProThrHisTyrArgGlyTyrGlnGlyThrArgGly---MetThrTrpValAspAsp  296

Qy   1847  ------GGGACAGGGGCTTCTACGACTGACAACCTTCAACTGGACTAAAAACTGGCTATATT  1900
           ::     |||
Db    297  ThrAlaSerThrProLysThrLysThrAlaThrLeuAlaThrTrpThrAsnThrGlyTyrLeu  316
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Db    659  SerMetThrAsnPheLeuHisLysThrGlyAlaAspGluAsnArgLysGlyPheArgHisThr  678

Qy   2093  AGTGGCGGTTATGTCATAGGAGGAGAAACCTACATACTGTTCAGATAAGATTCTTAGTGCT  2152
           |||||||                 ||| ::: |||
Db    679  SerGlyGlyTyrValIleGlyGlyGluThrTyrIleThrProLysAspLysPheThrPhe    698

Qy   2153  GCATTTTGTCAGCTCTTGGAAGAGAGATAGAGAGACTACTTTGTAGCTAAGAATCAAGGTACA  2212
           ||||||||         :: ||||||
Db    699  AlaPheCysHisLysPheAlaArgAspLysAspCysPheIleAlaHisAsnAsnSerArg    718

Qy   2213  GTCTACGGAGGAACTCTCTATTACCAGCACAACGAAACC----------TATATC       2257
           |||||||||::: |||          ||
Db    719  ThrTyrGlyGlyThrLeuPheLysPheHisSerHisThrLeuGlnProGlnAsnTyrLeu    738

Qy   2258  TCTCTT---CCTTGCAAACTACGGCCTTGTGTCTTGTGTCTTATGTTCCTACCAGAGATTCCT  2314
           ||:: |||         :: ::||||||
Db    739  ArgLeuGlyAlaArgLysPheGluSerGluSerAlaIleGluLysPheProArgGluIlePro  758

Qy   2315  GTTCTCTTTTCAGGAAACCTTAGCTACACACCCATGACGATCTGAAACCAAGTAT       2374
           ::: |||::: :: ||||||
Db    759  LeuAlaLeuAspValGlnValSerPheSerHisSerAspLysAsnArgMetGluThrHisTyr  778

Qy   2375  ACAACATATCCTACTGTTAAAGGAAGGAATGATGATAGTTTCGCTTTAGAATTCGGT     2434
           |||||::: ::: ||||||
Db    779  ThrSerLeuProGluSerGluValGlySerTrpSerAsnGluCysIleAlaGlyGlyIleGly  798

Qy   2435  GGAAGAGCTCCGATTGCTTA---GATGAAAGTGCTCTATTGACAGCAGTACATGCCCTTC   2491
           ||||||          ::: :: :||
Db    799  LeuAspLeuProPheValLeuSerAsnProHisProLeuPheLysPheLeuThrPheProGln  818

Qy   2492  ATGAAAATTGCAGTTGTCATGCACAATCAGGAGAGGTTTAAAGAACAGGAACAGAAGCT    2551
           |||||||         :: ::||         :: ::||
Db    819  MetLysValGluMetValTyrValSerGlnAsnSerPhePheGluSerSerSerAspGly  838

Qy   2552  CGTGAATTGGAAGTAGCCGTCTTGTGAATCTTGCCTTACCTATCGGGATCCGATTTGAT   2611
           ||| |||          :: ::||::: ||||||
Db    839  ArgGlyPheSerIleGlyArgLeuLeuAsnLeuSerIleProValGlyValAlaLysPhe--  857

Qy   2612  AAGGAAATCAGACTGCCAAGATGCA---ACGTACAATCTAACTCTTGGTTATACTGTGGAT  2668
           |||||          :: :: :||::: ||||||
Db    858  ValGlnIleGlyAspIleGlyAspSerTyrThrTyrAspLeuSerGlyPhePheValSerAsp  877

Qy   2669  CTTGTTCCGAGTAACCCCGACTGTACGACAACACTGCCAAACTAGCGGTGATTCTTGGAAA  2728
           :: :: :||||          :: :||||||
Db    878  ValTyrArgAsnAsnProGlnSerThrAlaThrLeuValLeuValArgGlyValArgTrpLys  897

Qy   2729  ACCTTCGGTACGAATTGGCAAGACAAGCTTAGTCCTTCGTCAGGAGAACCATTTTTGC    2788
           ||||||||::: ::: |||          ::||
Db    898  IleArgGlyLysAsnLeuSerArgGlnAlaPheLeuLeuArgGlySerAsnAsnTyrVal  917

Qy   2789  TTTAACTCAAATTTTGAAGCCTTTAGCCAATTTTCTTTTGAATTGCGTGGGTCATCTCGC  2848
           ::: :: :||         ::: :: :||||||
Db    918  TyrAsnSerAsnCysSerGluLeuPheGlyHisTyrAlaMetGluLeuArgGlySerSerArg  937

Qy   2849  AATTACAAATGAGACTTAGGAGGACAAAATACCAATTC  2884
           |||||||          :: ::||||||
Db    938  AsnTyrAsnValAspValGlyThrGlyValGlyPhe  949
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RESULT 5
US-09-198-452A-474
; Sequence 474, Application US/0919845A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION:     thereof and uses thereof, in particular for the diagnosis, preve
; TITLE OF INVENTION:     and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 474
; LENGTH: 643
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; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pre
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 15
; LENGTH: 922
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1...922
; OTHER INFORMATION: Xaa=unknown or other
US-09-198-452A-15

Alignment Scores:
Pred. No.:   Length: 922
Score: 1417.50   Matches: 347
Percent Similarity: 52.89%   Conservative: 156
Best Local Similarity: 36.49%   Mismatches: 385
Query Match: 26.21%   Indels: 63
DB: Gaps: 26

US-09-428-122-1 (1-3000) x US-09-198-452A-15 (1-922)

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Qy    113  TTCCCC---AAGTTGTATTTCTACATTTGCTATTTCCCTTTGCTATGATTGCTACC  169
                ||||       :::||||||||:: :::||:|
Db      8  PheProLeuValPheSerPheThrLeuLeuSerValPheAspThrSerLeuSerAlaThr   27

Qy    170  GAGACAGTTTGATTCAAGTGCGAGTTCGATGGGAATGGAATAAAAATGTAATTTTCAGTT  229
                |||:|                                    :::
Db     28  ThrIleSerLeuThrProGluAspSerPheHisGlyAspSerGlnAsn-----AlaGlu   45

Qy    230  CGTGAGAGTCAGGAAGATGCTCGGAACTACCTATTTAAGGGAAATGTCACTCTAGAA  289
                |||||                                      :::||||||
Db     46  ArgSerTyrAsnValGlnAlaGlyValTyrSerLeuThrGlyAspValSerIleSer   65

Qy    290  AATATTCCTGGAACAGGAGGTTTAACAACTGTGTTTAACACTACCTAGGGCGAT  349
                |||:                          :::|||:  ||||
Db     66  AsnVal------AspAsnSerAlaLeuAsnLysAlaCysPhe***ValThrSerGlySer   83

Qy    350  TTGACTTTCACAGGTAACGGAACTCTCTATTGTTCCAAACGGTGGATGCAGGGACTGTA  409
                :::||||||                         |||    :::|||||
Db     84  ValThrPheAlaGlyAsnHisHisGly***TyrPheAsnIleSerSerGlyThrThr   103

Qy    410  GCAGGGGCTGCTGTTAACAGCAGCCGTGGTAGAATAAATCTACCACG---TTTATAGGGTTT  466
                :::|||||||                           ||| :::|||||
Db    104  LysGluGlyAlaValValCysCysGlnAspProGlnAlaThrAlaArgPheSerGlyPhe  123

Qy    467  TCTTCGCTATCTTTTATTGGTCGTCCCTGGAAGTTCGATAACTACCGGCAAAGAGAGCCGTT  526
                ||||:|||||                                    :::---------
Db    124  SerThrLeuSerPheAsnGlnSerProGlyAlaAspIleLysGluGlnGly-----  139

Qy    527  AGCTGC------TCTACGGGTAGCTTGAGTTGACAAAAAATGTCAGTTTGCTTCTTCAGC  580
                |||:|                               :::|||:
Db    140  ---CysLeuTyrSerLysAsnAlaLeuMetLeuLeuAsnAlaAsnTyrValValArgPheGlu  158

Qy    581  AAAAACTTTTCAACGGATAATGGCGTGCTATCCACCGGCAAACTCTTTCATTAACAGGG  640
                :::|||||||                                  :::
Db    159  GlnAsnGlnSerLysProHeLysGlyAlaAlaAsnValThrLeuValGly  178

Qy    641  ACTACAGTGACAGTTAGGACGCAAAATACCAATTC  700
                :::|||||                      :::
Db    179  AsnTyrAspSerValSerPheTyrGlnAsnAlaAlaThr---PheGlyGlyAlaIleHis  197

Qy    701  ACTTCGACATGCCTACCATTACTGGAAACTGAAGTCTCTTTTCTGACAATACT  760
                :::|||||              :::|||
Db    198  SerSerGlyLeuProLeuIleAlaValAsnGlnIleLeuArgPheAlaGlnAsnThr  217
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Qy   1901  CCTAATCCCGAGCGTATCGGCTCTTTAGTCCTAATAGCTTATGAATGCATTTATAGAT  1960
                ||||||||                              :::|||
Db    317  ProAsnProGluArgGlnHisGlyProLeuProLeuAsnSerLeuTrpGlySerPheAsp  336

Qy   1961  ATTAGCTCTCCATTATCTTATGAGACTTGCAAACGAGGGTTGCAGGAGACCGTGCT  2020
                :::||||||                              :::
Db    337  IleGlnAlaIleGlyValIleGluArgSerAlaLeuThrLeuCysSerAspArgGly  356

Qy   2021  TTTTGGTGTGCTGGATTATCTTTCCTCCATAAGGATAGTACAAAAAACACGACGCGGG  2080
                |||||                                :::|||
Db    357  PheTrpProAlaAlaGlyValAlaAlaAsnPheLeuAspLysLysGlyGluValArgLys  376

Qy   2081  TTTTGGCCATTTGAGTGCGCGGTTATGTCATAGGAGGAAACCTACATACTTGTTCAGATAAG  2140
                :::|||||||                          :::|||
Db    377  TyrArgHisLysSerGlyGlyTyrAlaAlaIleGlyGlyAlaAlaGlnThrCysSerGluAsn  396

Qy   2141  ATTCTTAGTGCTGCATTTGTGCAGCTCTTGGAAGAGATAGAGACTACTTTGTAGCTAAG  2200
                :::||||||                                :::
Db    397  LeuIleSerPheAlaPheCysGlnLeuPheGlySerAspLysAspLysPheLeuValAlaLys  416

Qy   2201  AATCAAGGTACAGTCTCACGGAGGAACTCTATTACCAGCACAACGAAACCTATATCTCT  2260
                ||||||                                :::
Db    417  AsnHisThrAspThrTyrAlaGlyAlaPheTyrIleGlnHis------IleThr  432

Qy   2261  CTTCCCTGCAAACTACGGCCCTTGTTCCGTTCGTTATGTTCCT--------ACAGAGATT  2311
                :::|||                                        :::
Db    433  GluCysSerGlyPheIleGlyCysLeuLeuAspLysLeuProGlySerTrpSerHisLys  452

Qy   2312  CCTGTTCTCTTTCAGGAAAACCTTAGCTACACCCATACGGATTAACGATCTGAAAAACCAAG  2371
                |||:|:||                                    :::|||
Db    453  ProLeuLeuLeuGlyGlnLeuAlaTyrSerHisValSerAsnAspLeuLysThrLys  472

Qy   2372  TATACACACATATCCTACTGTGTTGAAAGAAGCTCGGGGAATGATAGTTTCGCTTTAGAATTC  2431
                ||||||                                    :::|||
Db    473  TyrThrAlaTyrProGluValLysGlySerTrpProGlyAsnAsnAlaPheAsnAlaMetMetLeu  492

Qy   2432  GGTGGAGAGCTCCGATTTGCTTAGATGAAAGTGTCTCTATTGGAGCAGTACATGCCCTTC  2491
                :::|||                                    :::
Db    493  GlyAlaSerSerHisSerTyrProGluTyrLeuHisCysPheAspThrTyrAlaProTyr  512

Qy   2492  ATGAAAATGCAGTTTGTCTATCGCACATCAGGAGAGGTTTAAAGAACAGGAGGACAGAGCT  2551
                :::|||                                      :::
Db    513  IleLysLeuAsnLeuThrTyrIleArgGlnAsnLeuThrTyrIleArgGlnLysPheGluGlyIly  532

Qy   2552  CGTGAATTTGGAAGTAGCCGTCTTGGAATCTCTGCCTACCATCGGGAATCCGATTTGAT  2611
                |||                                      :::|||
Db    533  ArgSerPheAspAspSerAsnLeuPheAsnLeuSerLeuProIleGlyValAsnLysPheGlu  552

Qy   2612  AAGGAATCAGACTGCCAAGATGCCAAGATGCACGTACAATCTAACTCTTGGTTATACTGTGGGATCTT  2671
                ||||||                                    :::|||
Db    553  LysPheSerAspCysAsnAspSerTyrAspLeuPheLeuSerTyrValProAspLeu  572

Qy   2672  GTTCGTAGTAACCCCGACTGTACGACACAACACTGCGAATTAGCCGTGATTCTTGGAAAACC  2731
                |||:|:|||                              :::|||
Db    573  IleLeuArgAspProLysCysThrThrAlaLeuLeuValIleSerGlyAlaSerTrpGluThr  592

Qy   2732  TTCGGTACCGAATTTGCAAGACAGCTTAGTGCTCCGTGCAGGGAACCATTTTTGCTTTT  2791
                |||||                                    :::
Db    593  TyrAlaAsnAsnLeuAlaArgGlnAlaLeuArgAlaGlySerHisTyrAlaPhe  612

Qy   2792  AACTCAAATTTTGAAGCCTTTAGCCAATTTCTTTTGAATTGCCTGGGTCATCTGCAAT  2851
                :::|||||                                    :::
Db    613  SerProMetPheGluValLeuGlyGlnPheValPheGluValArgGlySerSerArgIle  632

Qy   2852  TACAAATGTAGACTTAGGAGCAAAATACCAATTC  2884
                |||||                    :::
Db    633  TyrAsnValAspLeuGlyLysLysPheGlnPhe  643
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RESULT 6
US-09-198-452A-15
; Sequence 15, Application US/09198452A
; Patent No. 6559294

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Qy   557  --------HisTyrGlyPheGlnGlyAsnTrp-----LysLeuAlaTrpThrGlyThrGly  572
               |||          |||:::||||              :::        ||||||||||||
Db  1856  GCTTCACGACTGCAACCTTCAACTGGCTAAAACTGGCTATATCCTAATCCGAGGCGT    1915

Qy   573  ---AsnLysValGlyGluPhePheTrpAspIlePheLysProArgProGluLys       591
                :::||||||||   ||||||||||||       ||||:::
Db  1916  ATCGGCTCTTAGTCCCTAATAGCTTATGGAATGCATTATGAAGATATTAGCTCTCCAAT  1975

Qy   592  GluGlyAsnLeuValProAsnIleLeuTrpGlyAsnAlaValAspValArgSerLeuMet  611
               ||||:::||||          ::: ||      |||:::
Db  1976  TATCTTATGGAGACTGCAAACGAGAGGTTGCAGGGAGACCGTGCTTTTGGTGTGCTGGA  2035

Qy   612  GlnValGlnGluThrHisAlaSerSerLeuGlnThrAspArgGlyLeuTrpIleAspGly  631
               ::: |||               ||||||||
Db  2036  TTATCTAACTTCTTCCATAGGATGATGACTAAAAACGACGGGGGTTCGGCCATTGAGT   2095

Qy   632  IleGlyAsnLeuPheHisValSerValSerAlaSerGluAspAsnAsnIleArgTyrArgHisAsnSer  651
               :::||||||         |||         |||:::
Db  2096  GGCGGTTATGTCATAGGAGGAGAAACCTACATACTTGTTCAGATAAGAATTCTAGTGCTGCA  2155

Qy   652  GlyGlyTyrValLeuSerValAsnAsnGluIleThrProLysHisTyrThrSerMetAla  671
                ::: |||               |||
Db  2156  TTTTGTCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAATCAAGGTACAGTC  2215

Qy   672  PheSerGlnLeuPheSerGluArgAspLysSerTyrAlaValSerAsnAsnGluTyrArgMet  691
               |||         :::          ||||
Db  2216  TACGAGGAACTCTCATTACCAGCACAACGAAACC-------------TATATC        2257

Qy   692  TyrLeuGlySerTyrLeuTyrGlnThrTyrThrSerLeuGlyAsnIlePheArgTyrAla  711
               |||:::          |||
Db  2258  TCTCTTCCTGCAAACTACGGCCTTGTCTTATGTTCGTTGTCTTATGTGCTTATGTCT----  2314

Qy   712  SerArgAsnProAsnValAsnValGlyIleLeuLeuSerArgArgPheLeuGlnAsnProLeu  731
               |||         ::: |||
Db  2315  GTTTCTTTTCAGGAAACCTTAGCTACCACCCATACGATCGAAAACCAAGTAT          2374

Qy   732  MetIlePheHisIlePheLeuCysAlaTyrGlyHisAlaThrAsnAspMetLysThrAspTyr  751
               :::||||||              |||
Db  2375  ACAACATATCCACTGTTAAAGGAGGAGTGGGGGAATGATAGTTTCGCTTTAGAATTCGGT  2434

Qy   752  AlaAsnPheProMetValLysAsnSerTrpArgAsnAsnCysTyrTrpAlaIleGluCysGly  771
               :::          ||||
Db  2435  GGAAGAGCTCCCATTTGCTTGACAGTACATGCCCTTC---CTATTTGAGCAGTACATGCCCTTC  2491

Qy   772  GlySerMetProLeuLeuValPheGluAsnGlyArgLeuPheGluGlyAlaIleProPhe  791
               ||| ::: |||
Db  2492  ATGAAATTGCAGTTTGTCTATGCACATCAGGAAGGTTTAAAGAACAGGGAACAGAGAGCT  2551

Qy   792  MetLysLeuGlnLeuValTyrAlaTyrArgGlnGlyAspPheGluThrThrAlaAspGly  811
               |||          |||
Db  2552  CGTGAATTGGAAGTAGCCGTCTTGTGAATCTTCCTTACCTATCGGATCCGATTTGAT    2611

Qy   812  ArgArgPheSerAsnGlySerLeuThrSerIleSerValProLeuGlyIleArgPheGlu  831
               ||| :::          |||
Db  2612  AAGGAATCAGATCTGCCAAGATGCAACGTACAATCTAACTCTTGGTTATACTGTGGATCTT  2671

Qy   832  LysLeuAlaLeuSerGlnAspValLeuTyrAspPheSerPheSerTyrIleProAspIle  851
               |||          :::
Db  2672  GTTCGTAGTAACCCCGACTGTACGACAACACTGCGAATTAGCGGTGATTCTTGGAAAACC  2731

Qy   852  PheArgGlyAspProSerCysGluValAlaLeuAlaLeuIleSerGlyAspSerTrpLeuVal  871
               ||| :::          |||
Db  2732  TTCGGTACGAATTGGCAAGACAAGCTTTAGTCCTTCGTCGCAGGGAACCCATTTTGCTTT  2791

Qy   872  ProAlaAlaHisValSerArgArgHisAlaPheValGlySerGlyThrGlyArgTyrHisPhe  891
               |||:::          |||
Db  2792  AACTCAAATTTGAAGCCTTTAGCCAATTTCTTTTGAATTGCGTGGGTCATCTCGCAAT  2851

Qy   892  AsnAspTyrThrGluLeuLeuCysArgGlySerIleGluCysArgProHisAlaArgAsn  911
               |||:::
Db  2852  TACAATGTAGACTTAGGAGCAAAATACCAATTC         2884
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(continued left/bottom block)

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Qy   761  TCTTCGGAT---TCTGGAGCTGCAATTTTACAGAAGCCTCGGTGACTATTCTAATAAT  817
               :::||||||      :::         :::::::||
Db   218  AlaLysAsnGlySerGlyAlaValTyrSerArgGlyAlaLeuTyrSerAspIleAspGlnGlnAsn  237

Qy   818  GCTAAAGTTCCTTATTGACAATAAGGTCACAGGAGCGAGCTCCTCAACAACGGGGGAT  877
               |||         :::              |||
Db   238  AlaTyrValLeuPheArgGluAsnGlu-----AlaLeuThrThrAlaIle      252

Qy   878  ATGTCAGGAGGTGCTATCTGTCTTATAAAACTAGTACAGATACTAAG-----    925
               |||:::         |||
Db   253  GlyLysGlyGlyAlaValCysCysLeuProThrSerSerProValProIle   272

Qy   926  GTCACCCTACTGGAAATCAGATGTTACTCCTCAGCAACAATACATCGACAACGCGGGA  985
               |||:::         |||
Db   273  ValThrPheSerAspAsnLysGlnLeuValPheGluArgAsnHisSerIleMetGlyGly  292

Qy   986  GGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTCCGGAGGACTTACCCTATTCAGTAGA  1045
               ||| :::         |||
Db   293  GlyAlaAlaIleTyrArgAlaArgLysLeuSerIleSerSerGlyGlyTyrProThrLeuPheIleAsn  312

Qy  1046  AATAGTGTCAATGGAGGTACAGCTCCTAAAGGTGGAGCCATAGCTATCGAAGATAGTGGG  1105
               ::: |||         |||
Db   313  AsnIleSerTyrAlaAsnSerGlnAsnLeuGlyLyGlyLyAlaIleAlaIleAspThrGlyGly  332

Qy  1106  GAATTGAGTTTTATCCGCCGATAGTGGTGACATTGTCTTTTTTAGGGAATACAGTCACTTCT  1165
               |||:::         |||
Db   333  GluIleLeuSerLeuSerAlaGluLysGlyThrIleThrPheGlnGlyLysAsn------ArgThr  350

Qy  1166  ACTACTCCTGGGACGAATAGAAGTAGTATCCGACTTAGGAACGAGTGCAAAGATGACAGCT  1225
               ::: |||
Db   351  SerLeuProPheLeuAsn-----GlyIleHisLeuGlnAsnAlaLysPheLeuLys     368

Qy  1226  TTGCCTTCTGCTGCTGGTAGAGCCATCTACTTCTATGATCCCATAACTACAGGATCATCC  1285
               :::::||||||         |||
Db   369  LeuGlnIleAlaArgAsnGlyTyrSerIleGluPheTyrArgAspProIleThr-----SerGlu  386

Qy  1286  ACAACAGTTACAGATGTCTTAAAAGTAATGACAGACTCCGGCAGATTCTGCACTACACATAT  1345
               ||| :::
Db   387  AlaAspGlySerThrGlnLeuAsnIleAsnGlyAspProLysAsnLys------GluTyr  404

Qy  1346  ACAGGGAACATCATCTTCACAGGAGAAAAGTTATCAGAGACAGAGGCCGCAGATTCTAAA  1405
               ||| ::: :::
Db   405  ThrGlyThrIleIlePheSerGlyGlyLys--------SerLeuAlaAsnAspProArg  421

Qy  1406  AATCTTACTTCGAAGCTACTACAGCCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAA  1465
               ::: |||:::         |||
Db   422  AspPheLysSerThrIleProGlnAsnValAsnLeuSerAlaGlyTyrArgLeuValIleLeuLys  441

Qy  1466  CATGGAGTGACTCTGCAGACTCAGGCATTCACTCAACAGGACGAGATTCTCGTCTCGAAATG  1525
               ::: |||
Db   442  GluGlyAlaGlyAlaThrValSerIleLysPheThrGlnSerProGlySerHisLeuValLeu  461

Qy  1526  GACGTAGGAACTACTCTA---GAACCTGCTGATACTAGCACCATAAAACAATTTGGTCATT  1582
               :::          |||
Db   462  AspLeuGlyThrThrLeuLysGluIleIleAlaSerLysLysProThrIleAlaIleThrGlyLeuAlaIle  481

Qy  1583  AACATCAGTTCTTATAGACGGTCAAAGAAGGCAAA--ATAGAAACCAAAGCTACGTCA   1639
               |||:::         ||:::
Db   482  AspIleSerSerLeuSerSerSerThrAlaAlaValIleLeuLysAlaAlaAsnThrAlaAsn  501

Qy  1640  AAAAATCTGACTTTATCTGGAACCATCACTTTATTGGACCCGACGGGCACGTTTTTATGAA  1699
               |||:::         :::
Db   502  LysGlnIleSerValThrAspSerIleGluLeuIleLeuSerProThrGlyAlaAlaTyrGlu  521

Qy  1700  AATCATATGTTTAAGAAATCCTACGACATCTTAGAGCTCAAA------GCTTCT  1753
               :::          |||
Db   522  AspLeuArgAlaMetArgAsnSerGlnThrPheProLeuLeuSerLeuGluProGlyAlaGly  541

Qy  1754  GGAACTGTAACAAGCACCGCA-------GTGACTCCAGATCCTATAATGGGT  1798
               :::
Db   542  GlySerValThrValThrAlaGlyAlaAspPheLeuProValSerPro------  556

Qy  1799  GAGAAATTCCATTACGGCTATCAGGAGAACTTGGGGCCCAATTGTTGG---GGGACAGGG  1855
```

```
Db      912 TyrAsnIleAsnCysGlySerLysPheArgPhe 922

RESULT 7
US-09-198-452A-468
; Sequence 468, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
;   APPLICANT: Griffais, R.
;   TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;   TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
;   TITLE OF INVENTION: and treatment of infection
;   FILE REFERENCE: 9710-003-999
;   CURRENT APPLICATION NUMBER: US/09/198,452A
;   CURRENT FILING DATE: 1998-11-24
;   NUMBER OF SEQ ID NOS: 6849
;   SEQ ID NO 468
;   LENGTH: 671
;   TYPE: PRT
;   ORGANISM: Chlamydia pneumoniae
US-09-198-452A-468

Alignment Scores:
Pred. No.:              3.92e-103      Length:        671
Score:                  1264.00        Matches:       285
Percent Similarity:     62.43%         Conservative:  132
Best Local Similarity:  42.66%         Mismatches:    226
Query Match:            23.37%         Indels:        25
DB:                     4              Gaps:          15

US-09-428-122-1 (1-3000) x US-09-198-452A-468 (1-671)

Qy   101 ATGAAGTCTTCTTTCCCCAAGTTGTATTTTGTACATTGCTATTTTC---CCTTTGTCT 157
             ||||||||               :|:||||||| ||:||||
Db     1 MetLysSerValSerTrpLeuPhePheSerIleProLeuPheSerLeuSer 20

Qy   158 ATGATTGCTACCGAGACAGTTTGGATTCAAGT--GCGAGTTTCGATGGGAATAAAAAT 214
            :::|||||          :||||| ||||           |||||||:::
Db    21 IleValAlaAlaGluValThrLeuAspSerSerAsnAsnSerTyrArgAspGlySerAsnGly 40

Qy   215 GGTAATTTTTCAGTTCGTGAGAGTCAGGAA---GATGCTGGAACTACCTACCTATTTAAG 271
            ||:||||         ::     :||||||||||
Db    41 ThrThrPheThrValPheSerThrArgAspAlaAlaAlaGlyThrThrThrTyrSerLeuLeu 60

Qy   272 GGAAATGTCACTCTAGAAAATATTCCTGGAACAGGCACAGCAATCCACAAAAAGCTGTTTT 331
            :::||||         ::|||
Db    61 SerAspValSerPheGlnAsnAlaGlyValAlaLeuGlyIleIleProLeuAlaSerGlyCysPhe 80

Qy   332 AACAACACTAAGGGCCGATTGACTTCACAGGTAACGGGAACTCCTATTGTTCCAAACG 391
            |||||||||||||||||          ::|||
Db    81 LeuGluValGlyGlyAspPheThrPheGlnHisAlaLeuLysPheAlaPhe 100

Qy   392 GTGGATGCAGGGACTGTAGCAGGGGCTGCTGTTAACAGCAGCGTGGTAGATAAATCTACC 451
            :::::||||||          ||||||              ||||||:::
Db   101 IleAsnAlaGlySerAlaGlyThrValAlaSerThrSerAlaAlaAspLysAsnLeu 120

Qy   452 ACGTTTATAGGGTTTTCTTCGCTATCTTTATTCGCTCCTGGAAGTTCGATAACT--- 508
            :::||||||||||             :::::::|||
Db   121 LeuPheAsnAspPheArgLeuSerIleSerCysProSerLeuLeuSerPro 140

Qy   509 ACCGGCAAAGGACGTCCGTTAGCTGCTCTCACGGTAGCTTGAGTTGCACAAAAATGTCAGT 568
            ||||||:::        ||:|:    :::|||||||:::
Db   141 ThrGlyGlnCysAlaLeuLys--SerValGlyAsnLeuSerLeuThrGlyAsnSerGln 159

Qy   569 TTGCTCTTCAGCAAAAACTTTTCAACGGATAATGGGGTGCTATCACCGCAAAAACTCTT 628
            :::::||||||:|:|||||||          ||
Db   160 IleIlePheThrGlnAsnPheSerSerAspAsnGlyGlyValIleAlaAsnThrLysAsnPhe 179

Qy   629 TCATTAACAGGGACTACAATGTCAGCTCGTTTTTCTGAAAATACC------TCCTCAAAG 682
            |||                  ::         ::
Db   180 LeuLeuSerGlyThrSerGlnPheAlaSerPheSerArgAsnGlnAlaPheThrGlyLys 199

Qy   683 AAAGGCGGGAGCCATTCAGACTTCCGATGCCCTTACCAGAACCAAGGGGAAGTC 742
            :::||||||          |||     :::        :::
Db   199 GlyAlaAlaAsnGlyThrIleThrLeuGlyAlaLeuSerThrLeuThrGlnProGlu 570
```

```
Db   200 GlnGlyGlyValValTyrAlaValThrAlaThrGlyThrIleThrIleGluAsnSerProGlyIleVal 219

Qy   743 TCTTTTCTGACAATACTTCTTCGGATTCGAGCTGCAATTTTACGAAGGCTCGGTG 802
            ||||||||    :::      ||||||     :::
Db   220 SerPheSerGlnAsnLeuAlaLysGlySerGlyValAlaLeuTyrSerThrAspAsnCys 239

Qy   803 ACTATTTCTAATAATGCTAAAGTTCCTTATTGACAATAAAGTCACAGGAGCGAGCTCC 862
            :::::||||||       ||:|||||||||
Db   240 SerIleThrAspAsnPheGlnValIlePheAspGlyAsnSerAlaTrpGluAlaAlaGln 259

Qy   863 TCAACAACGGGGATATGTCAGGAGGTGCTATCTGTGCTTATAAAACTAGTACAGATACT 922
            :::         ||||||||||||
Db   260 Ala------------GlnGlyGlyAlaIleCysCys------ThrThrThrAspLys 272

Qy   923 AAGGTCACCCTCACTGGAACCAGATGTACTCTTCAGCAACAATAACATCGACAACAGCG 982
            |||||||||||||||||:::||||:||||||||||||
Db   273 ThrValThrLeuThrGlyAsnLysAsnLeuSerPheThrAsnAThrAlaLeuThrTyr 292

Qy   983 GGAGGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTCCGAGGACTTACCCTATTCAGT 1042
            |||||||||||               :::::          :::
Db   293 GlyGlyAlaIleSerGlyValLeuLysValSerIleSerArgAlaGlyGlyProThrLeuPheGln 312

Qy  1043 AGAAATAGTGTCAATGGAGGTACAGCTCCTAAA-----GGTGAGCCATAGTCATCGAA 1096
            ||||||        :::||||||||||:::
Db   313 SerAsn---IleSerGlySerAlaGlyGlnGlyGlyGlyGlyAlaIleAsnIleAla 331

Qy  1097 GATAGTGGGGAATTGAGTTTATCCGCCGATAGTGGTGCATTGGTTCTTTTTAGGGAATACA 1156
            |||||||||||||||||          |||||||
Db   332 SerAlaGlyGluLeuAlaLeuSerAlaThrSerGlyAspIleThrPheAsnAsnAsnGln 351

Qy  1157 GTCACTTCTACTACTCCTGGGACGAAGAGTAGTATCGACTAGGAACGAGTGCAAAG 1216
            ||||||||          :::|||||||
Db   352 ValThrAsnGlySerThrSerThr---ArgAsnAlaIleIleAspThrAlaLys 370

Qy  1217 ATGACAGCTTTGCGTTCTGCTGCTGGTAGAGCCATCTCATGATCCCATAACTACA 1276
            ||||||||          ||:|||||||
Db   371 ValThrSerIleArgAlaAlaThrGlyGlnSerIleTyrPheTyrAspProIleThrAsn 390

Qy  1277 GGATCATCCACAACGTACAGATGTCTTAAAAGTAATGAGACTCCGGACGAGATTCTGCA 1336
            ||||||||          |||||||          :|:|||
Db   391 ProGlyThrAlaAlaSerThrAspThrLeuAsnLeuAsnLeuAlaAspAlaAsnSerGlu 410

Qy  1337 CTACAATATCAGGGAACATCATCTTCACAGGAGAAAGTTATCAGAGACAGAGGCCGCA 1396
            :::::|||          ::|||||||
Db   411 IleGluTyrGlyValGlyAlaIleValPheSerGlyGluLysLeuSerProThrGluLysAla 430

Qy  1397 GATTCTAAAAATCTTACTCTCGAAGCTACTACAGCCCTGTAACCTTCAGGAGGTACTCTA 1456
            |||||||||||          :::||||
Db   431 IleAlaAlaAsnValThrSerThrIleArgGlnProAlaValLeuAlaIleArgGlyAspLeu 450

Qy  1457 TCTTTAAAACATGGAGTGACTCTCGAGACTCAGGCCATTCACTCACACAGGCAGAATTCTCGT 1516
            ||||||||          |||          ||||||
Db   451 ValLeuArgAspGlyValThrValThrPheLysAspLeuThrGlnSerProGlySerArg 470

Qy  1517 CTCGAAATGGACGTAGGAACTACTCTAGAACCTGCTGATACTAGC--ACCATAAACAAT 1573
            :::          :::||||||          ||||||:::
Db   471 IleLeuMetAspGlyLeuGlyThrThrLeuSerAlaLysGluLeuAsnLeuAsnGly 490

Qy  1574 TTGGTCATTAACATCAGTTCTATAGACGGTGCAAAGAAGGCAAAATAGAAACCAAAGCT 1633
            ||||||||||||          :::||||||          :::
Db   491 LeuAlaValAsnLeuSerLeuSerAspGlyThrAsnLysAlaAlaLeuLysThrGluAla 510

Qy  1634 ACGTCAAAAAATCTGACTTTATCTGAACCATCACTTATTGGACCCGACGCGGCACGTTT 1693
            ||||||||||||          ||:||
Db   511 AlaAspLysAsnIleSerGlyLeuSerGlyThrIleAlaLeuIleAspThrGlySerPhe 530

Qy  1694 TATGAAAATCATAGTTTAAGAAAATCCCAGTCCTACGACATCTTAGAGCTTCAAA------ 1747
            ||||||||||||          :::|||
Db   531 TyrGluAsnHisAsnLeuLysSerAlaSerThrTyrProLeuLeuGluLeuThrAla 550

Qy  1748 ---GCTTCTGGAACTGTAACAAGCACCGCAGTGACTCCAGATCCTATAATGGGTGAGAAA 1804
            :::|||          :::          :::
Db   551 GlyAlaAlaAsnGlyThrIleThrLeuGlyAlaLeuSerThrLeuThrGlnProGlu 570
```

RESULT 8
US-09-198-452A-30
; Sequence 30, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
;   APPLICANT: Griffais, R.
;   TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;   TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
;   TITLE OF INVENTION: and treatment of infection
;   FILE REFERENCE: 9710-003-999
;   CURRENT APPLICATION NUMBER: US/09/198,452A
;   CURRENT FILING DATE: 1998-11-24
;   NUMBER OF SEQ ID NOS: 6849
;   SEQ ID NO 30
;   LENGTH: 230
;   TYPE: PRT
;   ORGANISM: Chlamydia pneumoniae
US-09-198-452A-30

Alignment Scores:
Pred. No.:
Score: 6.26e-99
                          1214.00
Percent Similarity: 100.00%
Best Local Similarity: 99.56%
Query Match: 22.44%
DB: 4

Length: 230
Matches: 226
Conservative: 1
Mismatches: 0
Indels: 0
Gaps: 0

US-09-428-122-1 (1-3000) x US-09-198-452A-30 (1-230)

```
Qy  1805 TTCCATTACGGCTATCAGGGAACTTGGGGCCCAATTGTTTGGGGACACGGGGCTTCTACG 1864
              |||||||                    |||||
Db   571 ThrHisTyrGlyThrGlnGlyAsnTrp--GlnLeuSerTrpAlaAsnAlaThrSerSer 589

Qy  1865 --ACTGGACTAAAACTGGCTATATTCCTAATCCCGAGCGTATCGGC 1921
              :::        |||||||||              :::|:||:
Db   590 LysIleGlySerIleAsnTrpThrArgThrGlyThrIleProSerProGluArgLysSer 609

Qy  1922 TCTTAGTCCCTATAGCTAATGCATTATAGAGTATATATTATAGATAGTAGCTCTCCATTATCTT 1981
              :::|||              |||||||||:::|:|:||     |||
Db   610 AsnLeuProLeuAsnSerLeuTrpGlyAsnPheIleAspIleArgSerIleAsnGlnLeu 629

Qy  1982 ATGGACAACTGCAAACGAAGGGTTGCAGGGAGACCGTGCTTTTTGGTGTGCTGGATTATCT 2041
              :::|||||   |||                 :::|       :::
Db   630 IleGluThrLysSerGlyTyrGlyProPheGluArgGlu-TyrGlyPheGlnGlyLeuAr 649

Qy  2042 AACTTCTTCCATAAGGATAGTA 2063
              ||:||||
Db   649 gIleSerSerIleGluIleLeu 656
```

RESULT 9
US-09-198-452A-32
; Sequence 32, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
;   APPLICANT: Griffais, R.
;   TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
;   TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pre
;   TITLE OF INVENTION: and treatment of infection
;   FILE REFERENCE: 9710-003-999
;   CURRENT APPLICATION NUMBER: US/09/198,452A
;   CURRENT FILING DATE: 1998-11-24
;   NUMBER OF SEQ ID NOS: 6849
;   SEQ ID NO 32
;   LENGTH: 507
;   TYPE: PRT
;   ORGANISM: Chlamydia pneumoniae
US-09-198-452A-32

Alignment Scores:
Pred. No.:
Score: 6.85e-98
                          1204.00
Percent Similarity: 62.88%
Best Local Similarity: 46.35%
Query Match: 22.26%
DB: 4

Length: 507
Matches: 241
Conservative: 86
Mismatches: 168
Indels: 25
Gaps: 9

US-09-428-122-1 (1-3000) x US-09-198-452A-32 (1-507)

```
Qy  1360 CTTCACAGG--------AGAAAAGTTATCAGAGACAGAGGCCGGAGAGCCGAGATTCTAAAAAATCT 1410
              ||||||     ||:::  :::|||:::SerLysLysProAsp-----AsnLe
Db     2 LeuHisArgPheLeuTrpArgGluThrLeuArg-SerLysLysProAsp-----AsnLe 19

Qy  1411 TACTTCGAAGTACTACCAGCCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAACATGG 1470
              |||||||||                 :::|||
Db    19 uLysSerThrPheThrArgAlaValGluAlaAlaGlyAlaLeuValLeuValLeuLysAspGl 39

Qy  1471 AGTGACTTCGCAGTACGCCATTCACTCAACAGACAGATTCTCGTCTCCGAAATGGCACGT 1530
              |||||
Db    39 yValThrValAlaAlaAsnThrIleThrGlnValGluGluValValMetAspGl 59

Qy  1531 AGGAACTACTCTAGAA---CCTGCTGATACTAGCAGCACCATAAACAATTTGGTTCATTAACAT 1587
              |||||              :::|||   |||   |||
Db    59 yGlyThrThrPheGluAlaSer---AlaGluGlyValThrLeuAsnGlyLeuAlaIleAsnIl 79

Qy  1588 CAGTTCTATAGACGTGCAAAGAAGGCAAAAAATAGAAACCAAAGTACGTCAAAAAATCT 1647
              :::|||||                 :::|||
Db    79 eAspSerLeuAspGlyThrAsnLysAlaLysIleLeuIleLysAlaThrAlaAlaSerLysAspVa 99
```

```
Qy  2204 CAAGGTACAGTCTACGGACGGAGGAACTTCTATTACCAGCACAACGAAACCTATATCTCTCTT 2263
              :::|||             |||||||          |||
Db     4 LysGlyThrValTyrGlyGlyThrLeuTyrTyrGlnHisSerGluThrTyrIleSerLeu 23

Qy  2264 CCTTGCAAACTACGGCCCTTGTTCGTTCCTTATGTTCCTACAGAGATTCCTGTTCTCTTT 2323
              |||||||                 |||||||
Db    24 ProCysLysLeuArgProCysSerLeuSerTyrValProThrGluIleProValLeuPhe 43

Qy  2324 TCAGGAAAACCTTAGCTACACCCCATAACGATACGAATAACAGATCTGAAAAACCAAGTATACAACACATAT 2383
              |||||||||
Db    44 SerGlyAsnLeuSerTyrThrHisThrAspAsnAspSerGlyAsnLeuSerThrLysThrThrTyr 63

Qy  2384 CCTACTGTGTAAAGGAAGCTGGGGAATGGATAGTTCGCTTAGAATTCGGTGGAAGAGCT 2443
              |||||||||
Db    64 ProThrValLysGlyGluAlaGlySerTrpProGlyAsnAspSerPheAlaLeuGluGlyArgAla 83

Qy  2444 CCGATTGCTTAGCTAGATGAAAGTGCTCTATTGAGCAGTACATGCCCTTCATGAAATTGCAG 2503
              |||||||||
Db    84 ProIleCysLeuAspGluSerAlaLeuGluPheLysGlnTyrMetProPheMetLysSerGln 103

Qy  2504 TTTGTCTATCGCATCAGGAAGGTTTAAAGAACACAGGAACAGAAGCAGAAGCTTCGTGAATTTGGA 2563
              |||||||||
Db   104 PheValTyrAlaHisGlnAsnGlyThrGlnGlyValThrGluAlaAspArgGluPheGly 123
```

```
Qy  2564 AGTAGCCGTTCTTCTGTGAATCTTGCTTACCTATCGGGATCCGATTGATAAGGAATCAGAC 2623
              :::                |||||||
Db   124 SerSerArgLeuValAsnLeuAlaLeuProIleGlyIleArgPheAspLysGluSerAsp 143

Qy  2624 TGCCAAGATGCAACGTACAATCTAACTGGTTATACTGGTATACTGTGGATCTTGTTCGTAGTAAC 2683
Db   144 CysGlnAspAlaThrTyrAsnLeuThrGlyLeuTyrTrpValAspLeuValArgSerAsn 163

Qy  2684 CCCGACTGTACGACAACACTGCGGTGATTCTTGGAAAACCTTCGGTACGAAT 2743
              |||||||||
Db   164 ProAspCysThrThrThrLeuArgIleLeuGlyAspSerTrpLysThrPheGlyThrAsn 183

Qy  2744 TTGGCAAGACAACTTTAGTCCTTCGTGCGCAGGGAACCATTTTTGCTTTAACTCAAATTTT 2803
Db   184 LeuAlaArgGlnAlaLeuValLeuAlaArgGlyAlaAlaGlyAsnHisPheCysPheAsnSerAsnPhe 203

Qy  2804 GAAGCCTTTAGCCAATTTCTTTGAATTGCGTGGGTCATCTCCCAATTACAATGTAGAC 2863
Db   204 GluAlaPheSerGlnPheSerPheGluLeuArgGlyLeuArgGlySerSerArgAsnTyrAsnValAsp 223

Qy  2864 TTAGGAGCAAAATACCAATTC 2884
              |||:::
Db   224 LeuGlyAlaLysTyrGlnPhe 230
```

```
Qy  2707  AATTAGGCGGTGATTCTTGGAAAACCTTCGGTACGAATTGGCAAGACAAGCTTAGTCCT  2766
               :::|||:|||||:||||||||||||| ||:|||:||||||::|||||:::::||
Db   448  tValSerGlyAspSerTrpSerThrCysGlyThrSerLeuSerArgGlnAlaLeuLeuVa  468

Qy  2767  TCGTGCAGGGAACCATTTTGCTTAACTCAAATTTGGAGCCTTTAGCCAATTTCTTT  2826
               |||||||:|||||||||||||||||:||||||||||||||||||||:|
Db   468  lArgAlaGlyAsnHisHisAlaPheAlaSerAsnPheGluValPheSerGlnGluVa  488

Qy  2827  TGAATTGCGTGGTCATCTCGCAATTACAATGTAGACTTAGGAGCAAAATACCAATTC  2884
               :::|||||||||||||
Db   488  lGluLeuArgGlySerArgSerTyrAlaIleAspLeuGlyArgPheGlyPhe  507
```

```
Alignment Scores:
Pred. No.:                                Length:          1132
Score: 3.38e-91                           Matches:          316
Percent Similarity: 1130.00               Conservative:     133
Best Local Similarity: 39.28%             Mismatches:       310
Query Match: 27.65%                       Indels:           384
DB: 20.89%                                Gaps:              24
                                                              4
```

```
US-09-428-122-1 (1-3000) x US-09-198-452A-466  (1-1132)

Qy  101  ATGAAGTCTCTTCTTTCCCCAAGTTGTGTATTTCTCACATTTGCTATTTCCCTTTG---TCT  157
              ||||| ||| :: ::|| |||||||| ||
Db    1  MetLysTyrSerLeuProTrpLeuThrSerSerAlaLeuValPheSerLeuHisPro  20

Qy  158  ATGATTGCTACCGAGACAGTTTTGGATTCAAGTGCGAGTTTCGATGGGAATAAAATGGT  217
              ::::|||||||| ||||| |||||||||||:
Db   21  LeuMetAlaAlaAsnThrAspLeuSerSerSerAspAsnTyrGluAsnGlySerSerGly  40

Qy  218  AAT------TTTTCAGTTCGTGAGAGTCAGGAAGATGCTGGAACTACCTACCTATTTAAG  271
              ::        :|||| ||||:
Db   41  SerAlaAlaPheThrAlaLysGluThrSerAspAlaSerGlyThrThrTyrThrLeuThr  60

Qy  272  GGAAATGCTACTCAGAAAATATTCCTGGAACAGCAGCACAGCAATCACA-------AAA  322
              |||||||
Db   61  SerAspValSerIleThrAsnVal----------SerAlaIleThrProAlaAspLys  76

Qy  323  AGCTGTTTTAACAACACTAAGGGCGATTTGACTTTCACAGGTAACGGGAACTCCTATTG  382
              ||||| :::|||:
Db   77  SerCysPheThrAsnThrGlyLysGlyAlaLeuSerPheValGlyAlaAspHisSerLeuVal  96

Qy  383  TTCCAAACCGTGGATGCAGGAGTCGTAAAGGAAGTGTGGGGCTGCGTGTTAACAGCAGCCGTGGTAGAT  442
              :::||||||
Db   97  LeuGlnThrIle---AlaLeuThrHisAlaAspGlyAlaAlaIleAsnAsnThr------Asn  113

Qy  443  AAATCTACCACCGTTTATAGGTTTTCTTCGCTATCTTTTATTGCGTCTCCTGGAAGTTCG  502
              :::||
Db  114  ThrAlaLeuSerPheSerGlyPheSerSerLeuLeuLeuIleAspSerAlaProAlaThrGly  133

Qy  503  ATAACTACCGGCAAAGGAGGAGCCGTTAGCTGCTCTACG----------GGTAGCTTGAGT  550
              :::||||
Db  134  ThrSerGlyGlyLysGlyAlaIle---CysValThrAsnThrGluGlyThrAlaThr  152
```
```
Qy  1648  GACTTTATCTGAACCATCACTTATTGGAACGACGGGCACGTTTATGAAAATCATAG  1707
               : ||||||| |||:||| |||  :::|||:::|||
Db    99  lAlaLeuSerGlyProIleMetLeuValAspAlaGlnGlyAsnGlyAsnTyrTyrGluHisHisAs  119

Qy  1708  TTTAGAAAATCCTCACGACATCTTAGAGCTCAAAGCTTCTGGACTGTAACAAG  1767
               |||| :: :|||||||
Db   119  nLeuSerGlnInGlnValPheAlaLeuIleGluLeuSerAlaGlnGlyThrMetThrTh  139

Qy  1768  CACCCAGTGACTCCAGATCCTATATAGGGTGAGAAATTCCATTACGGCTATCAGGGAAC  1827
               |||:|| :::|||||||
Db   139  rThrAspIleProAspThrProIleLeuAsnAsnHisThrAsnHisTyrGlyIleLysGlyTh  159

Qy  1828  TTGGGGCCCAATTGTTTGG--------GGGACAGGGGGCTTCCTACGACTCCAACCTTCAA  1878
               ||||
Db   159  r---GlyIleIleIleValIleAspValAspAspAlaThrAlaLysThrLysAsnAlaThrLeuTh  178

Qy  1879  CTGGACTAAAACTGGCTATATTCCTAATCCCGAGCCGCTCTTTAGTCCCTAATAG  1938
               :: ::|||||||
Db   178  rTrpThrGlyThrGlyTyrLysProAsnProGluArgGlnGlyProLeuValProLeuAsnSe  198

Qy  1939  CTTATGGAATGCATTTATAGATATTAGCTCTCCATTATCTTATGAGACTGCAAACGA  1998
               ||||||||| :: ::
Db   198  rLeuTrpTlySerPheValAspValArgSerIleGlnSerLeuMetAspArgSerThrSe  218

Qy  1999  AGGGTTGCAGGGGAGACCGTGCTTTTTGGTGTGCTGATTATCTAACTTCTTCCATAAGGA  2058
               |||
Db   218  rSerLeuSerSerSerThrAsnLeuTrpValSerGlyIleIleAlaAspPheLeuHisGluAs  238

Qy  2059  TAGTACAAAAACACGACGCGGGTTCCCATTGAGTGGCCGGTTATGTCATAGGAGGAAA  2118
               :: ::| |||||| ||
Db   238  pGlnLysGlyAsnGlnArgSerTyrArgHisSerSerAlaGlyTyrTyrAlaLeuGlyGlyGl  258

Qy  2119  CCTACATACTGTTCAGATAAGATTCTTAGTGTGCATTTGTCAGCTCTTTGGAAGAGA  2178
               :::  ||| |||
Db   258  yPhePheAlaSerGluAsnPhePheAsnPheAlaPheCysGlnGlnLeuPheGlyTyrArgTyrAs  278

Qy  2179  TAGAGACTACTTTGTAGCTAAGAATCAAGGTACAGTCTACGGAGGAACTCTCTATTACCA  2238
               |||||:||
Db   278  pLysAspHisLeuValAlaLysAsnHisThrHisValThrTyrAlaLeuGlyAlaMetSerTyrAr  298

Qy  2239  GCAC------AACGAAACCTATATCTCTCTTCCTTGCAAACTACGGCCTTGTTCCTT  2289
               |||
Db   298  gHisLeuGlyLeuSerLysThrLeuAlaLysIle----------Le  310

Qy  2290  GTCTTATGTTCCTACAGAGATTCCGTCTTTCAGGAGAAACTTAGTCACACCCATAC  2349
               :: ||| |||||:|||
Db   310  uSerGlyAsnSerAspSerLeuProPheValPheAsnAlaArgPheAlaTyrGlyHisTh  330

Qy  2350  GGATAACGATCTGAAAACCAAGTATACAACAATATCCTACTGTTAAAGGAAGTGGGGGAA  2409
               ||||||||| :::||| |||||||
Db   330  rAspAsnAspMetThrLysTyrThrGlyTyrThrGlyTyrTyrSerProValLysGlySerTrpGlyAs  350

Qy  2410  TGATAGTTTCGCTTAGAATTCGGTGGAGAAGCTCGATTGCTTAGAT--GAAAGTGC  2466
               ||||| :
Db   350  nAspAlaPheGlyIleGluCysGlyGlyIleAlaIleProValValAlaSerGlyArgArgSe  370

Qy  2467  TCTATTTGAGCAGTACATGCCCTTCATGAAATTGCAGTTTGTTCATGCACATCAGGAAGG  2526
               ||||||||||| :::|||
Db   370  rTrpValAspThrHisThrProPheLeuAsnLeuGluMetIleTyrAlaHisGlnAsnAsnAs  390

Qy  2527  TTTTAAAGAAACAGGGAACAGGGAAAGCTCGGTGAATTGGAAGTGTAAAGGAAGTGTGTGAATCTTGC  2586
               ||||||||||||||
Db   390  pPheLysGluAsnGlyThrGlyGlyTyrSerPheGlnSerGluAspLeuPheAsnLeuAsnLeuAl  410

Qy  2587  CTTACCTATCGGGATCCGATTCGGTTAGAATTCGGTGGAGAAATCAGACTGCCAAGATGCAACGTACAAATC  2646
               :::||||:
Db  410   aValProValGlyIleLeuLysPheGluLysPhePheSerAsp-----LysSerThrTyrAspLe  428

Qy  2647  AACTCTTGGTTATACTGTGATCTTGTTCGTAGTAACCCGACTGTACGACAACACTGCG  2706
               :::|||||::|:||
Db  428   uSerIleAlaTyrProAspValIleArgAspValIleArgAsnAspArgProGlyCysThrThrThrLeuMe  448
```

```
Qy   551  TTGACAAAAAATGTCAGTTGCTCTTCAGCAAAAACTTTTCAACGGATAATGGCGGTGCT  610
          |||       ||| ||||||:|     |||||||||    :::|||||
Db   153  PheThrAspAsnAlaSerValThrLeuGlnLysAsnThrSerGluLysAspGlyAlaAla  172

Qy   611  ATCACCCGCAAAAACTCTTTCATTAACAGGGACTACAATGTCAGCTCAGTCTTTCTGAAAAT  670
          :::::::||    ||||       |||   ||||:|||         :::|||
Db   173  ValSerAlaTyrSerIleAspLeuAlaLysThrThrAlaAlaLeuLeuAspGlnAsn  192

Qy   671  ACCTCCTCAAAGAAGAAGGCCGGAGCCATTCAGACTTCCGATGCCCTTACCATTACTGGAAAC  730
          |||||:::|||||||||       :::::    |||||||    |||||
Db   193  ThrSerThrLysAsnGlyGlyAlaLeuCysSerThrAlaAsnThrThrValGlnGlyAsn  212

Qy   731  CAAGGGGAAGCTCTCTTTTTCTGACAATACTTCTTCGGATTCGGAGCTGCAATTTTT---  787
          |||    ||:::|||||||||         |||   |||||
Db   213  SerGlyThrValThrPheSerSerAsnThrAlaThrAspLysGlyGlyGlyIleTyrSer  232

Qy   788  ---------------ACAGAGCCTCGGTGACTATTTCTAATAATGCTAAA  823
                         :::::  ::::::   |||||
Db   253  AlaLysThrGlyGlyAlaTrpSerSerAspAspAsnLeuAlaLeuThrGlyAsnThrGln  272

Qy   824  GTTTCCTTTATTGACAATAGGTCACAGGA--GGCAGCTCCTCAACAACGGGGGATATG  880
          |||  ::|||||  |||||||       :::
Db   273  ValLeuPheGlnGluAsnLysThrThrGlySerAlaAlaGlnAlaAsnAsnProGluGly  292

Qy   881  TCAGGAGGTGCTATCTGTGCTTAT--AAAACTAGTACAGAT----------  919
          ||||    ||||:::|| |||        |||:::|||||
Db   293  CysGlyGlyAlaIleCysCysTyrLeuAlaThrAspThrAlaThrAspLysThrLeuAlaIle  312

Qy   920  --ACTAAGGTCACCCTCACTGAAAATCAGATGTTACTCTTCAGCAACAACATCATG  973
             ||||||  |||||      ||||  |||   ||||      |||||:::
Db   333  TyrAlaThrLysCysGlyGlyAlaLeuAspGlyAsnThrLeuThrPheAspAsnThrAla  352

Qy   974  ACA--------------------  976
          |||
Db   353  ThrAlaGlyCysGlyGlyAlaIleTyrThrGluThrGlyAspPheSerLeuLysGlySer  372

Qy   976  ------------------------  976
Db   373  ThrGlyThrValThrPheSerThrAsnThrAlaLysThrGlyGlyAlaLeuTyrSerLys  392

Qy   976  ------------------------  976
Db   393  GluAsnSerSerLeuThrGlyAsnThrAsnLeuPheSerGlyAsnLysAlaThrGly  412

Qy   976  ------------------------  976
Db   413  ProSerAsnSerSerAlaAsnGlnGlyCysGlyGlyAlaIleLeuSerPheLeuGlu  432

Qy   976  ------------------------  976
Db   433  SerAlaSerValSerThrLysLysGlyLeuTrpIleGluAspAsnGluAsnValSerLeu  452

Qy   976  ------------------------  976
Db   453  SerGlyAsnThrAlaThrValSerGlyGlyGlyAlaIleTyrAlaThrLysCysAlaLeuHis  472

Qy   976  ------------------------  976
Db   473  GlyAsnThrThrLeuThrPheAspGlyAsnThrAlaGluThrAlaGlyGlyAlaIleTyr  492

Qy   976  ------------------------  976
Db   493  ThrGluThrAspPheThrLeuThrGlySerThrValThrPheSerThrAsn  512

Qy   976  ------------------------  976
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Qy   513  ThrAlaLysThrAlaGlyAlaLeuHisThrGlyAsnThrSerPheThrLysAsnLys  532
Db   976  ------------------------------------  976

Qy   533  AlaLeuValPheSerGlyAsnSerAlaThrAlaThrThrThrThrAspGlnGlu  552
Db   976  ------------------------------------  976

Qy   553  GlyCysCysGlyAlaIleLeuCysAsnIleSerGluSerAspIleAlaThrLysSerLeu  572
Db   976  ------------------------------------  976

Qy   573  ThrLeuThrGluAsnGluSerLeuSerPheIleAsnAsnThrAlaLysArgSerGlyGly  592
Db   976  ------------------------------------  976

Qy   593  GlyIleTyrAlaProLysCysValIleSerGluSerGluSerIleAsnPheAspGlyAsn  612
Db   977  ------ACAGCGGAGAGAGCTATCTATGTGAAAAAGTTCGAACTGGCTTCCCGGAGGA  1027
                  :::|||||:||    |:::|||||||||   :::|||
Db   613  ThrAlaGluThrSerGlyGlyAlaIleTyrSerLysAsnLeuSerIleThrAlaAsnGly  632

Qy   1028 CTTACCCTATTCAGTAGAAAATAGTGTCAATGAGTACAGCTCCAAAAGGTGGAGCCATA  1087
          ||||||          |||||        ||::::::   ---LysGlyGlyAlaIle  647
Db   633  ProValSerPheThrAsnAsnSer-------GlyGly

Qy   1088 GCTATCGAAGATAGTGGGAATTGAGTTATCCGCCATAGTGGTGACATTGTCTTTTTA  1147
          |||||      |||   |||||||||  ||||||||
Db   648  TyrIleAlaAspSerGlyGluLeuGluLeuAlaIleAspGlyAspIleThrPheSer  667

Qy   1148 GGGAATACAGTCACTTCTACTACCTCCTGGACACGAAATAGAAGTAGTATCGACTAGGAACG  1207
          |||            |||      :::::   ||||||      SerIleHisLeuGlyAla  685
Db   668  GlyAsnArgGlyAlaThrGluGlyThrSerThrProAsn-----

Qy   1208 AGTGCAAAGATGACAGCTTTGCGTTCGCTGCTGGTGAGAGCCCATCACTTCCTATGATCCC  1267
          |||||||||       ||:::||| ||||||  ||||||||||:|||
Db   686  GlyAlaLysIleThrLysLeuAlaIleAlaIleAlaProGlyHisThrIleTyrPheTyrAspPro  705

Qy   1268 ATAACT---ACAGGATCATCCACAACAGTTACACAGAT  1300
          |||||       |||  |||:::
Db   706  IleThrMetGluAlaProAlaSerGlyGlyThrIleGluGluLeuValIleAsnProVal  725

Qy   1301 -----------------------GTCTTAAAAGTTAATGAG  1318
                                  :::
Db   726  ValLysAlaIleValProProGlnProLysAsnGlyProIleAlaSerValProVal  745

Qy   1319 ACTCCGGCAGATTCTGCACTACAATATACAGGGAACATCATCTTCACAGGAGAAAAGTTA  1378
          ||||||||||       |||||||||||||||||||||||||
Db   746  ValProValAlaProAlaAsnProAsnThrGlyThrIleValPheSerSerGlyLysLeu  765

Qy   1379 TCAGAGACAGAGGCCGGAGATTCTAAAAATCTTAACTCTGAAGCTACTACAGCCTGTAACT  1438
          :::|||||||       ||| |||||||||   ||:::::   |||||||
Db   766  ProSerGlnAspAlaSerIleProAlaAsnThrThrThrLeuLeuAsnGlnLysIleAsn  785

Qy   1439 CTTTCAGGAGGTACTCTATCTTTAAAAACATGAGTGACTCTGCAGATCTCAGCCATTCACT  1498
          |||||:::||| |||||:::|||||        |||||||||||:::|||
Db   786  LeuAlaGlyLysAsnValValLeuLysGluValTyrGluGlnValTyrSerPheThr  805

Qy   1499 CAACAGGCAGATTCTGCTCGCACAAATGGAAGAACTACTTCTAGAAACCTGCTGATACT  1558
          |||||:::||| |||||||||:::|||||||||||||||
Db   806  GlnGlnProAspSerThrValPheMetAspAlaGlyThrThrLeuGluThrThrThr  825

Qy   1559 AGCACC----------------ATAAACAATTGGTCATTAACATCAGTTCAT ATAGAC  1600
          |||:::                :::
Db   826  AsnAsnThrAspGlySerIleAspLeuLysAsnLeuSerValAlaAsnLeuAspAlaLeuAsp  845

Qy   1601 GGTGCAAAGAAGGCAAAAATGAAACCAAAGCTACGTCAAAAAATCTGACTTTATCTGGA  1660
          :::      ||||||||||||||:::|||||||||:::|||||:::
Db   846  GlyLysArgMetIleThrIleAlaValAsnSerThrSerGlyValLeuLysIleSerGly  865

Qy   1661 ACCATCACTTTATTGGACCCGACGGGCACGTTTATGAAGAAATCATAGTTAAGAAATCCT  1720
          |||:::||||||||:::|||:::||
Db   976  ------------------------------------  976
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;       TYPE: PRT
;       ORGANISM: Chlamydia
US-09-556-877-190

Alignment Scores:
Pred. No.:
Score:                  6.53e-91          Length:               1006
                        1126.50           Matches:               303
Percent Similarity:     46.02%            Conservative:          160
Best Local Similarity:  30.12%            Mismatches:            372
Query Match:            20.83%            Indels:                171
DB:                     4                 Gaps:                   30

US-09-428-122-1 (1-3000)  x  US-09-556-877-190 (1-1006)
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Qy   242 GAAGATGCTGGAACTACCTACCTATTTAAGGAGAAATGTCACTCTGAAAATATTCCTGGA 301
             :::  ||||||||||        |||||||::::||||||||
Db    47 AspProSerGlyThrThrValPheSerAlaGlyLeuThrLeuLeuAsnLeuAspAsn     66

Qy   302 ACAGGCACAGCAATCACAAAAAGCTGTTTAACACACTAAGGGCGATTTGACTTTCACA    361
             :::  |||  ||||||||        |||  ||||||
Db    67 SerIleAlaALaLeuProLeuGlySerCysPheGlyAsnLeuGlySerPheThrValLeu  86

Qy   362 GGTAACGGGAACTCCTATTGTTCCAAACGGTGGATGCAGGGACTGAGCAGGGGTGCT    421
             |||  |||         ||||||||          ||||||
Db    87 GlyArgGlyHisSerLeuThrPheGluAsnIleArgThrSerThr---AsnGlyAlaAla 105

Qy   422 GTTAACAGCAGCGTGGTAGATAAATCCACCGTTATAGGGTTTCTTCGCTATCTTT     481
             :::::||||||  ||||||||
Db   106 LeuSerAsnSerAlaAlaAspGlyLeuPheThrIleGluGlyPheLysGlnLeuSerPhe 125

Qy   482 ----------------------ATTGCGTCTCCTGGAGTTCGATAACTACGGCAAAGGAGCCGTT 526
                                    :::  ::: |||        ::: |||
Db   126 SerAsnCysAsnSerLeuLeuAlaValLeuProAlaAlaThrThrAsnLysGlySerGln 145

Qy   527 AGCTGCTCTACGGGTAGC----------------------------------TTGAGT 550
             :::  |||                                          ||||
Db   146 ThrProThrThrSerThrProSerAsnGlyThrIleTyrSerLysThrAspLeuLeu    165

Qy   551 TTGACAAAAAATGTCAGTTGCTTCTTCAGCAAAAACTTTCACGGCGATAATGCGGTGCT  610
             |||                    ::: |||
Db   166 LeuLeuAsnAsnGluLysPheSerPheTyrSerAsnLeuValSerGlyAspGlyGlyAla 185

Qy   611 ATCACCGCAAAAACTCTTTCATTAACAGGACTACAATGTCAGCTCGTTTTCTGAAAAT    670
             |||  |||||||        :::::||||::::
Db   186 IleAspAlaLysSerLeuThrValGlnGlyIleSerLysLeuCysValPheGlnLeuAsn 205

Qy   671 ACCTCCTCAAAGAAGAGGCGGAGCCATTCAGACTTCCGAATGCCCTTACCATTACTGGAAAC 730
             ||||          :::::||
Db   206 ThrAlaGlnAlaAspGlyGlyAlaCysGlnValValThrSerPheSerAlaMetAlaAsn 225

Qy   731 CAAGGGGAAGTCTCTTTT-----------------------------------748
             :::  ::::::||
Db   226 GluAlaProIleAlaPheValAlaAsnValAlaGlyValAlaArgGlyGlyIleAlaAla 245

Qy   749 ------------------------TCTGACAATACTTCTTCGGATTCT----------772
                                      :::::||||||::::::
Db   246 ValGlnAsnGlyGlnGlnGlnValSerSerSerThrSerThrGluAspProValValSer 265

Qy   773 -----------------------------------GGAGCTGCAATT 784
                                                 ||||||||
Db   266 PheSerArgAsnThrAlaValGluPheAspGlyAsnValAlaAlaArgValGlyGlyIle 285

Qy   785 TTTACAGAAGCCTCCGTGACTATTCTAATAATGCTAAAGTTTCCTTTATTGACAT---  841
             :::::||||||        ||||||
Db   286 TyrSerTyrGlyAsnValAlaPheLeuAsnAsnGlyLysThrLeuPheLeuAsnAsnVal 305

Qy   842 -----------------------------AAGGTCACAGGACGGAGCGCCTCAACAACG 871
                                           ||        :::::||
Db   306 AlaSerProValTyrIleAlaAlaAlaLysGlnProThrSerGlyIleAlaSerAsnThrSer 325

Qy   872 GGGGATATG----TCAGGAGGTGCTATCTGTGCTTATAAA--------------------ACTAGT 913
             :::                    :::::||
Db   326 AsnAsnTyrGlyAspGlyGlyGlyAlaIlePheCysLysLysAsnGlyAlaGlnAlaGlySerAsn 345
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Db   866 AspLeuLysPheHisAsnAsnGlyGlySerPheTyrAspAsnProGlyLeuLysAlaAsn 885
             :::        |||                    ::: |||
Qy  1721 CAGTCCTACGACACATTTAGAGCTCAAAGCT---TCTGAACTGTAACAAGCACCGCAGTG 1777

Db   886 LeuAsnLeuProPheLeuAspLeuProSerSerThrSerGlyThrValAsnLeuAspAspPhe 905
             |||  |||         |||||||||::::|||
Qy  1778 ACTCCAGATCCTATAATGGGTGAGAAATTCCATTACGGCTATCAGGGAACTTGGGGC---  1834

Db   906 AsnProIleProSerSerMetAlaAlaProAspTyrGlyTyrGlnGlySerTrpThrLeu 925
             ||                    |||||||
Qy  1835 ---CCAATTGTTGGGGACGAGGGGGTTCTTACGACTGCAACCTTCAACTGGACTAAAACT 1891

Db   926 ValProLysVal---GlyAlaGlyGlyValThrLeuValAlaGluThrGlnAlaLeu     944
             |||||                    ||::: |||
Qy  1892 GGCTATATTCCTAATCCCGAGCCGTATCGGCTCTTAGTCCCTAATAGCTTATGGAATGCA 1951

Db   945 GlyTyrThrProLysProGluGluArgAlaThrLeuValProAsnSerLeuTrpAsnAla 964
             |||  |||         ||||||
Qy  1952 TTTATAGATATTAGCTCTCCATTATTGATGGAGACTGCAAAACGGGGGTTGCAGGGA    2011

Db   965 TyrValAsnIleHisSerIleGlnGlnGluIleAlaThrAlaMetSerAspAlaProSer 984
             :::::||||||:::        |||||||
Qy  2012 GACCGTGCTTTTGGTGTCGTGATTATCTAACTTCTTCCATAAGGATAGTACAAAAACA 2071

Db   985 HisProGlyLeuIleTrpIleGlyLeuGlyAsnAlaPheHisGlnAsnProLysGlnLysGlu 1004
             |||        ||:::                    |||||||
Qy  2072 CGACGCGGGTTCGCCATTTGAGTGCGGTTATGTCAAGGTAATGTATGATAGGAGAAACCTACATACTGT 2131

Db  1005 AsnAlaGlyPheArgLeuIleSerArgGlyThrTyrIleValGlyIleGlySerMetThrThrPro 1024
             ||||||        |||
Qy  2132 TCAGATAAGATTCTTAGTGCTGCATTTGTCAGCTCTTGGAAGAGATAGAGACTACTTT 2191

Db  1025 GlnGluThrThrPheAlaValAlaIleAlaPheSerGlnLeuPheGlyLysSerLysAspTyrVal 1044
             :::::||        |||::: |||
Qy  2192 GTAGCTAAGAATCAAGGTACAGTCTACGGAGGAACTCTCTATTACCAGCACAACGAAACC 2251

Db  1045 ValSerAspIleLysSerSerLeuValTyrAlaGlyValTyrAlaGlnGln--SerSerTyr 1063
             ||||||                    :::        ::: |||
Qy  2252 TATATCTCTTCCTTCCAAACTACACGGCCCTTGTTCGTTCGTTGTCTTATGTT---------- 2299

Db  1064 ValIleProLeuHisSerSerLeuArgArgHisValLeuSerIleValLeuProGluLeu 1083
             |||||||        :::::||
Qy  2300 CCTACACAGAGATCCTGTTCTGTTTCTCAGGAAAAACTTAGCTACACCACCGGATAACGAT 2359

Db  1084 ProGlyGluThrProLeuValLeuHisGlyGlnValSerTyrGlyArgAsnHisHisAsn 1103
             |||||        :::::||
Qy  2360 CTGAAAACCAAGATAACACACATATCCTACTGTTAAAGGAAGCTGGGGGAATGATAGTTTC 2419

Db  1104 MetThrThrLysLeuAlaAsnAsnThrGlnLeuGlyLysSerAspTrpAspSerHisSerSer 1123
             :::        |||
Qy  2420 GCTTTAGAA 2428
             ||||:::
Db  1124 LeuLeuLys 1126
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RESULT 11
US-09-556-877-190
; Sequence 190, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT:   Probst, Peter
; APPLICANT:   Bhatia, Ajay
; APPLICANT:   Skeiky, Yasir
; APPLICANT:   Fling, Steve
; APPLICANT:   Maisonneuve, Jeff
; TITLE OF INVENTION:   COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION:   DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE:   2101121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE:  2000-04-19
; NUMBER OF SEQ ID NOS:  305
; SOFTWARE:  FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 190
; LENGTH: 1006
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Qy   1871  ACCTTC--------AACTGGACTAAAAACTGGCTATATCCTAATCCGAGCGTATC  1918
                 :::                  ||||||||||| ||||||  |||||||||| |||
Db    679  ProTyrThrLeuLysAlaThrTrpThrLysThrGlyTyrAsnProGlyProGlnArgVal  698

Qy   1919  GGCTCTTAGTCCCTAATAGCTTATGGAATGCATTGGAATGCATTATAGATATTAGCTCTCCATTAT  1978
                 |||||||||||||||||     ::::||||||||| |||
Db    699  AlaSerLeuValProAsnSerLeuTrpGlySerIleLeuAspIleArgSerAlaHisSer  718

Qy   1979  CTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGACCGTGCTTTTGGTGTGTGCTGATTA  2038
                 ||||||||||||||||||||||||||||||||||||||||  :::
Db    719  AlaIleGlnAlaSerValAspGlyArgSerTyrCysArgGlyLeuTrpValSerGlyVal  738

Qy   2039  TCTAACTTCTTCCATAAGGACTAGTACAAAAAACACGACGCGGGTTTCGCCATTGAGTGGC  2098
                 |||||||||||||||                   :::||:::|||||:::|||||||
Db    739  SerAsnPhePheTyrHisAspArgAspAlaLeuGlyGlnGlyTyrArgTyrIleSerGly  758

Qy   2099  GGTTATGTCATAGGAGGAGAAACCTACATACTTGTTCAGATAAGAATTCTTAGTGCTGCATTT  2158
                 |||||||||                      ::: |||
Db    759  GlyTyrSerLeuGlyAlaAsnSerTyrPheGlySer---SerMetPheGlyLeuAlaPhe  777

Qy   2159  TGTCAGCTCTTTGGAAGAGATAGAGACTACTTTGTAGCTAAGAATCAAGGTACAGTCTAC  2218
                 ::::|||| |||   |||  :::  :::
Db    778  ThrGluValPheGlyArgSerLysAspTyrValCysArgSerAsnHisHisAlaCys  797

Qy   2219  GGAGGAACTCTCTATTACCAGCACACGAAACCTATATCCTCCTTCCTTGCAAACTACGG  2278
                 :: ::::||||||
Db    798  IleGlySerValTyrLeuSerThrGlnGlnAlaLeu--------  809

Qy   2279  CCTTGTTCGTTGTCTTATGTTCCTACAGAGATTCCTGTTCCTTTTCAGGA  2329
                 ||:|| ||||||||||
Db    810  ---CysGly---SerTyr--------LeuPheGlyAspAlaPheIle  820

Qy   2330  AACCTTAGCTACACCCATACGGATAACGATCGAAAACCAAGTACACAATATCCTACT  2389
                 :::      ::::|||||||
Db    821  ArgAlaSerTyrGlyPheGlyAsnGlnHisMetLysThrSerTyrPheAlaGluGlu  840

Qy   2390  GTTAAAGGAAGCTGGGGAATGATAGTTCGCTTTAGAAATTCGGTGGAAGAGCTCCGATT  2449
                 ::: |||  ::::||||
Db    841  SerAspValArgTrpAsnAsnCysLeuLeuAlaGlyLeuGluLleuGlyAlaGlyLeuProIle  860

Qy   2450  TGCTTAGATGAAAGTGCTCATTT---GAGCAGTACATGCCCTTCATGAAATTTCAGTTT  2506
                 ::: :::                   ||:||||
Db    861  ValIleThrProSerLysLeuTyrLeuAsnGluLeuArgProPheValGlnAlaGluPhe  880

Qy   2507  GTCTATGCACATCAGGAAGGTTTAAAGAACAGGACAGAAGCTCGTGAATTGGAAGT  2566
                 |||||||||||||||                     :::
Db    881  SerTyrAlaAspHisGluSerPhePheMetAlaAlaTyrIleCysAspAlaTyrArgIleSer  900

Qy   2567  AGCCGTCGTTGTGAATCTTGCCTTACCTATCCGGATCCGATTTGATAGGAATCAGACTGC  2626
                 |||||||||                      :::
Db    901  GlyHisGluThrLeuSerHisGlnGluThrTrpPheAspArgCysSerSerThr  920

Qy   2627  CAAGATGCAACGTACAAATCTAACTCTTGGTATACTGTGATACTGTTCGTAGTAACCCCC  2686
                 ::::
Db    921  HisProAsnLysTyrSerPheMetAlaAlaTyrIleCysAspAlaTyrArgThrIleSer  940

Qy   2687  GACTGTACGACAACACTGCGAATTAGCGGTGATTCTTGGAAAACCTTCGGTACGAATTTG  2746
                 |||||||||||
Db    941  GlyThrGluThrLeuSerHisGlnGluThrTrpThrAspAlaPheHisLeu  960

Qy   2747  GCAAGACAAGCTTTAGTCCTTCGTCGCAGGGAACCCATTTTGTCTTTAACTCAAATTTTGAA  2806
                 ||||||||                                :::
Db    961  AlaArgHisGlyValValValArgGlySerMetTyrAlaSerLeuThrSerAsnIleGlu  980

Qy   2807  GCCTTTAGCAAATTTCTTTTGAATTGCGTGGGTCATCTCCCAATTACAATGTAGACTTA  2866
                 :::                 ||:::|||
Db    981  ValTyrGlyHisGlyArgTyrGluTyrArgAspAlaSerArgGlyTyrGlyLeuSerAla  1000

Qy   2867  GGAGCAAAATACCAATTC  2884
                 |||||||:::|||
Db   1001  GlySerLysValArgPhe  1006
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RESULT 12

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Qy    914  ACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAGCAACAATACATCG  973
                 |||         ::: ||||||:::|||
Db    346  AsnSerGlySerPheAspPheGlyGlyLysGlyValPheAsnPheSerSerAsnValAla  365

Qy    974  ACAACAGCGGGAGCTATCTATGTGAAAAAGCTCGAACTGGCTTCCGGAGGACTTACC  1033
                 ||||||||||||||||||||||:::|||
Db    366  AlaGlyLysGlyGlyAlaIleTyrAlaLysLysLeuSerValAlaAlaAsnCysGlyProVal  385

Qy   1034  CTATTCAGTAGAAATAGTGTCAATGAGGTACAGCTCCTAAAGGTGGAGCCATAGCTATC  1093
                 ||||||         |||||
Db    386  GlnPheLeuArgAsnIleAlaAsn----------AspGlyGlyAlaIleTyrLeu  400

Qy   1094  GAAGATAGTGGGGAATTGAGTTATCCGCCGATAGTGGTGACATTGTCTTTTTAGGGAAT  1153
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Db    401  GlyGluSerGlyGlyLeuLeuSerLeuLeuSerAlaAspTyrGlyAspIleIlePheAspGlyAsn  420

Qy   1154  ------ACAGTCACTTCACTTCCTGGGACGAAT---------AGAAGT  1189
                 ::: ||||| |||
Db    421  LeuLysArgThrAlaLysGluAsnAlaAlaAspValAsnGlyValThrValSerSerGln  440

Qy   1190  AGTATCGACTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTGGTAGAGCC  1249
                 :::::: ||:::  |||||:::|||
Db    441  AlaIleSerMetGlySerGlyGlyLysIleGlyIleThrArgLeuArgAlaLysArgAlaLysGlyAlaGlyHisGln  460

Qy   1250  ATCTACTTCTATGATCCCATAACTACAGGATCATCCACAACA------GTTACA  1297
                 ||| :::                                  :::
Db    461  IleLeuPheAsnAspProIleGluMetAlaAsnGlyAsnGlnProAlaGlnSerSer  480

Qy   1298  GATGTCTTAAAAGTTAATGAGACTCCGGCAGATTCTGCACTACAATATACAGGGAACATC  1357
                 ||:||:::|||||                             ||||||||
Db    481  LysLeuLeuLeuLysIleAsnAspGlyGluGly---------TyrThrGlyAspIle  495

Qy   1358  ATCTTCACAGAGAGAAAGTTATCAGAGACAGAGGCCCGAGATTCTAAAAATCTTACTTCG  1417
                 :::||||                :::|||
Db    496  ValPheAla-----------------AsnGlySerSer  502

Qy   1418  AAGCTACTACACCTGTAACTCTTTCAGGAGGTACTCATCTTTTAAAACATGGAGCTGGGACT  1477
                 |||:::|||              :::|||
Db    503  ThrLeuTyrGlnAsnValThrHisLeuGlnGlyIleGlyArgIleValIleGlyValAlaLys  522

Qy   1478  CTGCAGACTCAGGCATTCATCCAACAGGCCAGATTCCGTCTGCGAAATGGACGTAGGAACT  1537
                 |||                    :::|||||||||
Db    523  LeuSerValAlaAsnSerLeuserGlnThrGlyGlySer---LeuTyrMetGluAlaGlySer  541

Qy   1538  ACTCTAGAA-----------------------------CCTGCTGATACTAGC------  1561
                 |||||:::                          |||||
Db    542  ThrLeuAspPheValThrProGlnProProGlnProProAlaValIleGlySer---ThrThr  561

Qy   1562  ACCATAAAACAATTTGGTCATTAACATCAGTTCTATA-------------  1597
                 ::::||||:::||||||
Db    562  ThrLeuSerAsnLeuHisLeuSerLeuSerLeuSerLeuLeuAlaAsnAlaValThrAsn  581

Qy   1598  --------GACGGTGCAAAGAAGAGGCAAAAAATAGAAACCAAAGTACG  1636
                 :::                    ||| :::||
Db    582  ProProThrAsnProProAlaGlnProProAlaValIleGlySer---ThrThr  600

Qy   1637  TCAAAAAATCTGACTTTATCTGGAACCATCACTTTATTGGACCCGACGGGCACGTTTTAT  1696
                 ::: ::::::|||                    |||
Db    601  AlaGlySerValThrIleSerGlyTyrProIlePhePheGluAspLeuAspThrAlaTyr  620

Qy   1697  GAAAATCATAGT---TTAAGAAATCCTCAGTCCTACGACATCTTAGAGCTTCAAAGCTTCT  1753
                 ::: :::                      :::::||:::
Db    621  AspArgTyrArgAspTyrLeuGlySerAsnGlnLysIleAsnValLeuLysLeuGlnLeu--  639

Qy   1754  GGAACTGTAACAAGCACCGCAGTGACACCGACTCCAGATCCTATAATGGTGAGAAATTC---CAT  1810
                 |||||||:::|||                       :::||:::
Db    640  GlyThrLysProProAlaAsnAlaProSerAspLeuThrLeuGlyAsnGluMetProLys  659

Qy   1811  TACGGCTATCAGGGAACTTGGGGCCCCAATTGTTTGGGGACAGGGGCTTCTACGACTGCA  1870
                 ||||||:::|||       :::
Db    660  TyrGlyTyrGlnGlySerTrp---LysLeuAlaTrpAspAspThrAlaAsnThrAlaAsnGly  678
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US-09-620-412C-190
; Sequence 190, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SEQ ID NO 190
; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-620-412C-190

Alignment Scores:
Pred. No.:
Score: 6.53e-91   Length: 1006
Percent Similarity: 1126.50   Matches: 303
Best Local Similarity: 46.02%   Conservative: 160
Query Match: 30.12%   Mismatches: 372
DB: 20.83%   Indels: 171
                          4   Gaps: 30

SOFTWARE: FastSEQ for Windows Version 3.0/4.0

US-09-428-122-1 (1-3000) x US-09-620-412C-190 (1-1006)

Qy   242 GAAGATGCTGGAACTACCTATTTAAGGGAAATGTCACTCTAGAAAATATTCCTGA   301
                ::: |||||||||||||| :::|||||||: :::|||:::
Db   47 AspProSerGlyThrThrValPheSerAlaGlyLeuThrLeuLysAsnLeuAspAsn 66

Qy   302 ACAGGCACAGCAATCACAAAAGCTGTTTAACACACTAAGGGCGATTTGACTTTCACA   361
                 :||| |||||||||| ||||| |||||||||||||||
Db   67 SerIleAlaIleLeuProLeuSerCysPheGlyLeuLeuGlySerPheThrValLeu   86

Qy   362 GGTAACGGGAACCTCCATTGTTCCAAACGGTGATGCAGGGACTGTGACAGGGCTGCT 421
                 |||||| ||||||| ||||||||| ||||||||
Db   87 GlyArgGlyHisSerLeuThrPheGluAsnIleArgThrSerThr--AsnGlyAlaAla 105

Qy   422 GTTAACAGCAGCGTGGTAGATAAATCTACCACGTTTATAGGGTTTCTTCGCTATCTTTT 481
                :::::::||| ||||| |||||||| |||||||||
Db   106 LeuSerAsnSerAlaAlaAspGlyLeuPheThrIleGluGlyPhePheLysGluLeuSerPhe 125

Qy   482 -------ATTGCGTCCTCCTGGAAGTTCGATAAACTACCGGCAAAAGGAGGCCGTT 526
                     ::: || :::||||||| ||||||||
Db   126 SerAsnCysAsnSerLeuLeuAlaValLeuProAlaAlaThrThrAsnLysGlySerGln 145

Qy   527 AGCTGCTCTCACGGGTAGC----------------------------TTGAGT 550
                :::|||| ||||||
Db   146 ThrProThrThrSerThrProSerAsnGlyThrIleTyrArgSerLysThrAspLeuLeu 165

Qy   551 TTGACAAAAAATGTCAGTTGCTCTTCAGCCAAAAACTTTTCAACGGATAATGGCGGTGCT 610
                ||| :::||||||||||| :::|||||:::
Db   166 LeuLeuAsnGluLysPheSerSerLeuValSerAsnLeuValSerPheGlyGlyGlyAla 185

Qy   611 ATCACCGCAAAAACTCTTTCATTAACAGGGACTACCAGGTCAGCTGTTTTCTGAAAAT 670
                ||| |||||||||||| ::||||| ||||||
Db   186 IleAspAlaLysSerLeuThrValGlnGlyIleLeuSerLysLeuCysValPheGlnGluAsn 205

Qy   671 ACCTCCTCAAAGAAAGGCCGAGCCATTCAGACTTCCGATGCCCTTACCATTACTGGAAAC 730
                |||::: ::||||||| ::: :::
Db   206 ThrAlaGlnAlaAspGlyGlyAlaCysGlnValThrSerPheSerAlaMetAlaAsn 225

Qy   731 CAAGGGGAAGTCTCTTTT---------------------------- 748
                ::: :::||||||
Db   226 GluAlaProIleAlaPheValAlaAlaAsnValAlaGlyValAlaArgGlyValAlaValAla 245

Qy   749 ---------------TCTGACAATACTTCTTCCGGATTCT----------- 772
                ::: ||||||
Db   246 ValGlnAspGlyGlnGlyValSerSerSerSerThrSerThrGluAspProValValSer 265

Qy   773 ------------------------------GGAGCTGCAATT 784
                ::: ::|||||:::||||| :||||||

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Db   601  AlaGlySerValThrIleSerGlyProIlePhePheGluPheAspLeuAspAspThrAlaTyr  620

Qy  1697  GAAAATCATAGT---TTAAGAAATCCTCAGTCCTACGACATCTTAGAGCTTCAAAGCTTCT  1753
               :::||||||::|||     ||    ||::  ||||   |||| ||::||
Db   621  AspArgTyrAspPheGlyTrpLeuGlySerAsnGlnLysIleAsnValLeuLysLeuLeu---  639

Qy  1754  GGAACGTAACAAGCACCGCAGTGACTCCAGATCCCATAATAGGGTGAGAAATTC---CAT  1810
               ||||||   :::|  | |||||||:::|||     ::|||
Db   640  GlyThrLysProAlaAsnAlaProSerAspLeuThrLeuGlyAsnGluMetProLys  659

Qy  1811  TACGGCTATCAGGGAACTGGGGCCCAATTGTTGGGGACAGGGGCTTCTACGACTGCA  1870
               ||||::|||:::||     ::   ||
Db   660  TyrGlyTyrGlnGlySerTrp---LysLeuAlaTrpAspProAsnThrAlaAsnAsnGly  678

Qy  1871  ACCTTC---------AACTGGACTAAAACTGGCTATATTCCTAATCCCGAGCGTATC  1918
               :::           |||||||||||    |||    :||   ||||  ||||
Db   679  ProTyrThrLeuLysAlaThrThrLysTrpThrGlyTyrAsnProGlyGluArgVal  698

Qy  1919  GGCTCCTTAGTCCCTAATAAGCTTATGGAATGCATTATAGATATTAGCTCTCCCATTAT  1978
               ||||||||||||||    ::  ||||||||| |||  | ||||:||
Db   699  AlaSerLeuValProAsnSerLeuTrpGlySerIleLeuAspIleArgSerAlaHisSer  718

Qy  1979  CTTATGGAGACTGCAAACGAAGGGTTGCAGGGAGACCGTGCTTTTTGGTGTCTGGATTA  2038
               ::::::  :::  :||  ||    |||    ::||||:
Db   719  AlaIleGlnAlaSerValAspGlyArgSerTyrCysArgGlyLeuTrpValSerGlyVal  738

Qy  2039  TCTAACTTCTTCCATAAGGATAGTACAAAAACCACGACGCGGGTTTCGCCATTGAGTGGC  2098
               :::||||||||||  ::  |||||:::||   |||  ::|||||
Db   739  SerAsnPhePheTyrHisAspArgAspAlaLeuGlyGlnGlyTyrArgTyrIleSerGly  758

Qy  2099  GGTATGTCATAGGAGGAAAACCTACATACTTGTTCAGATAAGAATTCTAGTGCTGCATTT  2158
               ||||||   |   ::  ||   ||
Db   759  GlyTyrSerLeuGlyAlaAsnSerTyrPheGlySer---SerMetPheGlyLeuAlaPhe  777

Qy  2159  TGTCAGCTCTTTGGAAGAGATAGAGACTACTTGTAGCTAAGAATCAAGGTACAGTCTAC  2218
               :::::|||||||||    ::::::
Db   778  ThrGluValPheGlyArgAspSerLysAspTyrValCysSerArgSerAsnHisHisAlaCys  797

Qy  2219  GGAGGAACTCTCTATTACCAGCACACACAAACCTATATCTCTTCCTTGCAAACTACGG  2278
               ||  ::
Db   798  IleGlySerValTyrLeuSerThrGlnGlnAlaLeu------------  809

Qy  2279  CCCTTGTTCGTTGTTCTTATGTTCCTACGAGATTCCTGTTCTCTTTTCAGGA--------  2329
               |||||     ||||
Db   810  ---CysGly---SerTyr--------------LeuPheGlyAspAlaPheIle  820

Qy  2330  AACCTTAGCTACACCCCATACGGATAACGATCTGAAAACCAAGTATACAACATATCCTACT  2389
               ||||||     |||| :::  ||||||||  |||||||
Db   821  ArgAlaSerTyrGlyPheGlyAsnGlnHisMetLysThrSerTyrThrProAlaGluGlu  840

Qy  2390  GTTAAAGGAAGCTGGGGGAATGATAGTTTCGCTTTAGAAATTCGGTGAAGAGCTCCGATT  2449
               :::  ||||||||||||||    ||||||||||| | ||||
Db   841  SerAspValArgTrpAspAsnAsnCysLeuAlaGlyGluIleGlyAlaGlyLeuProIle  860

Qy  2450  TGCTTAGGATGAAAAGTGCTCTATTT---GAGCAGTACATGCCCTTCATGAAATTGCAGTTT  2506
               :::     |||     :::::  |||||  ||   ||
Db   861  ValIleThrProSerLysTyrLeuAsnGluLeuArgProPheValGlnAlaGluPhe  880

Qy  2507  GTCTATGCACATCAGGAGAGGTTTAAGAACAGGGAACAGAGAGCTCGTGAATTTGGAAGT  2566
               |||||    :::  |||||| |||  ||||     ::|||||
Db   881  SerTyrAlaAspHisGlnGluSerPheThrGluGluGluSerGlnIleAlaArgGlyAlaPheLysSer  900

Qy  2567  AGCCGTCTTGTGAATCTTGCCTTACCTATCGGAAGGAATCAGATTGATAAGGAATCAGACTGC  2626
               |||  :::  :: ||    :::||  |||||  ::||||
Db   901  GlyHisLeuLeuAsnLeuSerValProValGlyValLysPheAspArgCysSerSerThr  920

Qy  2627  CAAGATGCAACCTACAACTAACTCTTGGTATACTCTGGATCTTGGTCTTGGTCTTGTTCGTAGTAACCCCC  2686
               :::|||    ||||||     :::||||   |||  ||||||||
Db   921  HisProThrThrTyrSerPheMetAlaAlaTyrIleCysAspAlaTyrArgThrIleSer  940

Qy  2687  GACTGTACGACAACACTGCGAATTAGCCGTGATTCTTGGAAAACCTTCGGTACGAATTTG  2746
               :::|||     ||||  |||    :::||||||:
Db   941  GlyThrGluThrThrLeuSerHisGlnGluThrTrpThrThrAspAlaPheHisLeu  960
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Qy  2747  GCAAGACAAGCTTTAGTCCTTCGTGCAGGAGAACCATTTTTGCTTAACTCAAATTTGAA  2806
               |||||||        :::||||:::||:::                ::  :::
Db   961  AlaArgHisGlyValValValAlaValArgGlyLysMetTyrAlaSerLeuThrSerAsnIleGlu  980

Qy  2807  GCCTTTAGCCAATTTTCTTTTGAATTGCGTGGTCATCTCCGAATTACAATGTAGACTTA  2866
               :::         ||  :::||||
Db   981  ValTyrGlyHisGlyArgTyrGluTyrArgAspAlaSerArgArgGlyTyrGlyLeuSerAla  1000

Qy  2867  GGAGCAAAATACCAATTC  2884
               |||::::|||:::  :::
Db  1001  GlySerLysValArgPhe  1006
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RESULT 13
US-09-598-419-190

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;  Sequence 190, Application US/09598419
;  Patent No. 6565856
;  GENERAL INFORMATION:
;  APPLICANT: Skeiky, Yasir A.W.
;  APPLICANT: Scholler, John
;  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
;  TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
;  FILE REFERENCE: 210121.469C6
;  CURRENT APPLICATION NUMBER: US/09/598,419
;  CURRENT FILING DATE: 2000-06-20
;  NUMBER OF SEQ ID NOS: 357
;  SOFTWARE: FastSEQ for Windows Version 3.0/4.0
;  SEQ ID NO 190
;    LENGTH: 1006
;    TYPE: PRT
;    ORGANISM: Chlamydia
US-09-598-419-190
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Alignment Scores:
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Pred. No.:                                  Length:        1006
Score:                   6.53e-91           Matches:        303
Percent Similarity:      1126.50            Conservative:   160
Best Local Similarity:   46.02%             Mismatches:     372
Query Match:             30.12%             Indels:         171
DB:                      20.83%             Gaps:            30
                         4
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US-09-428-122-1 (1-3000) x US-09-598-419-190 (1-1006)

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Qy   242  GAAGATGCTGGAACTACCTACCTATTTAAGGGAAATGTCACTCTAGAAAATATTCCTGA  301
               ::: :::|||:::|||  :::|||  ||| ||:::||  |||:::
Db    47  AspProSerGlyThrThrValPheSerAlaGlyLeuLeuThrLeuLysAsnLeuAspAsn  66

Qy   302  ACAGGCACAGCAATCACAAAAAGCTGTTTAACAACTAAGGCGATTTGACTTTCACA  361
               ||  ||:::| ::||     ||  ||||||| :::|  ::|||
Db    67  SerIleAlaAlaLeuProLeuSerPheGlyAsnLeuLeuGlySerPheThrValLeu  86

Qy   362  GGTAACGGGAACTCTCTATTGTTCCAAACGGTGGATGCGGGACTGTAGCAGGGGCTGCT  421
               ||||||||     :::|||||| ||||||||   |||||||||||||
Db    87  GlyArgGlyHisSerLeuThrPheGluAsnIleArgThrSerThr---AsnGlyAlaAla  105

Qy   422  GTTAACAGCAGCGTGGTAGATAAATCACCGTTTATAGGGTTTTCTTCGCTATCTTT  481
               :::::||||||     |||||||||  |||||||  :::||||||||||
Db   106  LeuSerAsnSerAlaAlaAspGlyLeuPheThrIleGluGluLysGluGluSerPhe  125

Qy   482  --------AATTGCGTCTCCTGGAAGTTCGATAACTACCGGCAAAGGAGGCCGTT  526
               |||||||||  ::|||||  :::||||
Db   126  SerAsnCysAsnSerLeuLeuAlaValLeuProAlaAlaLeuThrThrArgAsnLysGlySerGln  145

Qy   527  AGCCGTCTTACGGGTAGC--------------------------TTGAGT  550
               ::: :::|||
Db   146  ThrProThrThrSerThrProSerAsnGlyThrIleTyrArgLysThrAspLeuLeu  165

Qy   551  TTGACAAAAATGTCAGTTTGCTTCTTCAGCAAAAACTTTCAACGGATAATGGCGGTGCT  610
               |||   :::|||||||||  :::|||:::|||
Db   166  LeuLeuAsnAsnGlyLysPheSerPheTyrSerAsnLeuValSerGlyGlyAspGlyAla  185

Qy   611  ATCACCCGCAAAAACTCTTCATTAACAGGGACTACAATGTCAGCTCTGTTTTCTGAAAAT  670
               |||   ::::|||::|:::||  :::|||   |||     ||
Db   186  GlyThrGluThrThrLeuSerHisGlnGluThrTrpThrThrAspAlaPheHisLeu  (...)
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Db  186  IleAspAlaLysSerLeuThrValGlnGlyIleSerLysLeuCysValPheGlnGluAsn  205

Qy  671  ACCTCCTCAAAGAAGAAGGCGGAGCCATTCAGACTTCCGATGCCTTACCATTACTGAAAAC  730
              |||:::              |||         :::       :::
Db  206  ThrAlaGlnAlaAsnAspGlyGlyAlaCysGlnValValThrSerPheSerAlaMetAlaAsn  225

Qy  731  CAAGGGGAAGTCTCTTTT------------------------------------------  748
         :::::||
Db  226  GluAlaProIleAlaPheValAlaAsnValAlaLaGlyValAlaArgGlyGlyIleAlaAlaAla  245

Qy  749  ------------------TCTGACAATACTTCTTCGGATTCT----------------  772
                           |||  :::||||||||:::::::
Db  246  ValGlnAspGlyGlnGlnGlyValSerSerThrSerProValSer                  265

Qy  773  ---------------------------------GGAGCTGCAATT                  784
                                           |||||||
Db  266  PheSerArgAsnThrAlaValGluPheAspGlyAsnValAlaAargValAlaGlyGlyGlyIle  285

Qy  785  TTTACAGAAGCCTCGGTGACTATTTCTAATAATGCTAAAGTTTCCTTTATTGACAAT--  841
         ||||||         ::::|||
Db  286  TyrSerTyrGlyAsnValAlaPheLeuAsnAsnGlyLysThrLeuPheLeuAsnAsnVal  305

Qy  842  ------------------AAGGTCACGAGGACGAGCTCCTCAACACG                871
                           :::||         ||:::::|||:::
Db  306  AlaSerProValTyrIleAlaAlaLysLeuProThrSerGlyGlnAlaSerAsnThrSer   325

Qy  872  GGGGATATG---TCAGGAGGTGCTATCTGTCGTTATAAA--------------ACTAGT  913
              |||||||:::           |||||
Db  326  AsnAsnTyrGlyAspGlyGlyGlyAlaAlaIlePheCysLysAsnGlyAlaGlnAlaGlySerAsn  345

Qy  914  ACAGATACTAAGGTCACCCTCACTGGAAATCAGATGTTACTCTTCAGCAACAATACACG   973
         ||||||         :::::               ||:::
Db  346  AsnSerGlySerValSerPheAspGlyGluGlyValValPheSerSerAsnValAla     365

Qy  974  ACAACAGCGGGAGAGCTATCTATGTGAAAAGCTCGAACTGGCTTCCGGAGACTTACC   1033
         ||||||||||     :::||:::
Db  366  AlaGlyLysGlyGlyIleAlaIleTyrAlaLysIleLysLeuSerValIleAlaAsnCysGlyProVal  385

Qy  1034 CTATTCAGTAGAATAGTGTCAATGGAGGTACAGCTCTAAAGGTGGAGCCATAGCTATC  1093
         |||||||||                        :::
Db  386  GlnPheLeuArgAsnIleAlaAsn---------AspGlyGlyAlaIleTyrLeu      400

Qy  1094 GAAGATAGTGGGGAATTGAGTTTATCCGCGATAGTGGTGACATTGTCTTTAGGGAT   1153
         :::::|||||||         :::::
Db  401  GlyGlyGluSerGlySerGlyLeuSerLeuSerArgIleAspPheTyrArgGlyAspIleIlePheIleGluPheAspGlyAsn  420

Qy  1154 -----------ACAGTCACTTCTACTACTCCTGGACGAAT---------AGAAGT   1189
                   |||                        :::
Db  421  LeuLysArgThrAlaLysGluAsnAlaLaAspValAsnGlyValThrValSerSerGln  440

Qy  1190 AGTATCGACTTAGGAACAGAGTGCAAAGATGACAGCTTTCCGTTCGCTGGTAGAGCC  1249
              ||||||||:::
Db  441  AlaIleSerMetGlySerGlyLysGlyLysIleThrThrLeuArgAlaLysAlaGlyHisGln  460

Qy  1250 ATCTACTTCTGATGATGCCCATAACTACAGGATCATCCACACA----------GTTACA  1297
         |||:::||||||                               :::
Db  461  IleLeuPheAsnAspProIleGluMetAlaAsnGlyAsnGlnProAlaGlnSerSer     480

Qy  1298 GATGTCTTAAAGTTAATGAACACTCCGGCAGATTCTGCACTACAATATACAGGGAACATC  1357
               :::||:::
Db  481  LysLeuLeuLysIleIleAsnAspGlyGluGly---------TyrThrGlyIleAspIle  495

Qy  1358 ATCTTCACAGGAGAGAAAGTTATCAGAGACACAGAGGCCGCAGATTCTAAAAATCTTACTTCG  1417
         :::|||||||
Db  496  ValPheAla-------------------AsnGlySerSer                      502

Qy  1418 AAGCTACTACAGCCTGTAACTCTGACTACTTCTGAGGAGTACTTCTATCTTAAAACAATGGAAGTGACT  1477
                ||| :::        ||||||||::
Db  503  ThrLeuTyrGlnAsnValThrLeuGluGlnGlyArgIleValArgIleGlyArgLeuArgValLysAlaLys  522

Qy  1478 CTGCAGACTCAGGCATTCACTCAACAGACCAGAATTCGTCTGCAAATGGACGTAGGAACT  1537
         ||| :::                   :::|||
Db  523  LeuSerValAsnSerLeuSerGlnThrGlyGlySer---LeuTyrMetGluAlaGlySer  541
```

```
Qy  1538 ACTTCTAGAA-------------------------------------CCTGCTGATACTAGC------  1561
         |||||:::
Db  542  ThrLeuAspPheValThrProGlnProProGlnProProAlaAlaAsnGlnLeuLeu           561

Qy  1562 ACCATAAACAATTGGTCATTAACATCAGTTCTATA-------------------------------  1597
         ||||||||||||||||:::
Db  562  ThrLeuSerAsnLeuHisLeuSerLeuSerLeuAlaAsnAsnAlaValThrAsn             581

Qy  1598 ------------------GACGGTGCAAAGAAGGCAAAAATAGAAACCAAAGCTACG          1636
                        :::|||||||||||
Db  582  ProProThrAsnProProAlaGlnAsnAspSerHisProAlaValIleGlySer---ThrThr      600

Qy  1637 TCAAAAAATCTGACTTTATCTGGAACCATCACTTTATTGGACCCGACGGGCACGTTTTAT  1696
         :::              ||||||||||||
Db  601  AlaGlyLeuSerValThrLeuThrIleSerGlyProIlePhePheGluAspLeuAspThrAlaTyr    620

Qy  1697 GAAAATCATAGT---TTAAGAAATCCTCAGTCCTACGACATCTTAGAGCTCAAAGCTTCT  1753
         :::  |||                             :::
Db  621  AspArgTyrArgAspTrpLeuGlySerAsnGlnLysIleAsnValLeuLysLeuGlnLeu--  639

Qy  1754 GGAACTGTAACAGCAGGCACCGCAGTGACTCCAGATCCTATAATGGTGAGAAATTC---CAT  1810
         ||||||
Db  640  GlyThrLysProProAlaAsnAlaProSerAspLeuThrLeuGlyAsnGlyMetProLys    659

Qy  1811 TACGGCCATCAGGGAACTTGGGGCCCCAATTGTTGGGGACACAGGGGCTTCTACGACTGCA  1870
         ||||||||||||                          :::
Db  660  TyrGlyTyrGlnGlySerTrp---LysLeuAlaTrpAspAspProAsnThrAlaAsnGly   678

Qy  1871 ACCTTC-------------AACTGGACTAAAAACTGGCTATATTCCTAATCCCGAGCGTATC  1918
         ||||||:::                           :::
Db  679  ProTyrThrLeuLysAlaThrTrpThrLysThrGlyTyrTyrAsnProGlyProGluArgVal  698

Qy  1919 GGCTCTTTAGTCCCTAATAGCTTATGGAATGCATTTATAGATAATTAGCTCTCCATTAT  1978
         |||||||||                   :::
Db  699  AlaSerLeuValProAsnSerLeuTrpGlySerIleLeuAspIleArgSerAlaHisSer  718

Qy  1979 CTTATGGAGACTGCAAAACGAAGAGGTTGCAGGGAGACCGTGCTTTTTGGTGTGTGGATTA  2038
         |||||:::                   :::
Db  719  AlaIleGlnAlaSerValAlaSpGlyArgSerTyrCysArgGlyTyrLeuTrpValSerArgGlyVal  738

Qy  2039 TCTAACTTCTTCCATAAGGATAGTACAAAAAACACGACGGCCGGTTTCGCCATTGAGTGGC  2098
         |||||||||                :::::
Db  739  SerAsnPhePheTyrHisAspArgSerArgSerAsnHisAlaCys                  758

Qy  2099 GGTTATGTCATAGGAGGAGAAAACCTACATACTTGTTCAGATAAGATTCTTAGTGTGCTGCATTT  2158
         |||||||||                        :::
Db  759  GlyTyrSerLeuGlyValAlaAsnSerTyrPheGlySer---SerMetPheGlyLeuAlaPhe  777

Qy  2159 TGTCAGCTCCTTTGGAAGAAGATAGAGGACTACTTTGTAGCTAAGAATCAAGGTACAGTCTAC  2218
         |||||:::
Db  778  ThrGluValPheGlySerArgLysAspGlyTyrValValCysArgSerAsnHisAlaCys    797

Qy  2219 GGAGGAACCTCTATTACCAACGACAACGAAACCTATATCTCTTCCTTGCAAACTACACG  2278
         :::||||||                                :::
Db  798  IleGlySerValTyrLeuSerThrGlnGlnAlaLeu-----                      809

Qy  2279 CCCTTGTTCGTTGTGTCTTATGTTCCTACACAGAGATTCCTGTCTCTTTTCAGGA----------  2329
         |||||||:::
Db  810  ---CysGly---SerTyr---------------------LeuPheGlyAspAlaPheIle    820

Qy  2330 AACCTTAGCTACACCCATATAACGATCTGGAATAACGATCTGAAAACATCCACACATATCCTACT  2389
         |||||||||
Db  821  ArgAlaSerTyrGlyPheGlyAsnGlnHisMetLysPheSerTyrThrPheAlaGluGlu     840

Qy  2390 GTTAAAGGAAGCTGGGGAATGATAGTTTCGCTTTAGAATTCGGTGGAAGAGCTCCGATT  2449
         :::                      ||||||
Db  841  SerAspValArgTrpAspAsnCysLeuAlaGlyIleValLeuAlaGlyLeuProIle     860

Qy  2450 TGCTTAGATGAAAGTGCTCTATTT--GAGCAGTACATGCCCTTCATGAAATTGCAGTTT  2506
         ||||||                  :::                         :::
Db  861  ValIleThrProSerLeuTyrLeuAsnGluLeuAsnGlyAlaGlyProPheValGlnAlaGluPhe  880
```

```
Qy   2507 GTCTATGCACATCAGGAAGGTTTAAAGAACAGAGGAACAGAAGCTCGTGAATTTGGAAGT 2566
          ||||||         |||||||          :::||||||     ::|||||  |||
Db    881 SerTyrAlaAspHisGluSerPheThrGluGluValGlyAspGlnAlaArgAlaPheLysSer 900

Qy   2567 AGCCGTCTTGTGAATCTTGCCTACCTATCCGGATCCGATTTGATAAGAAATCAGACTGC 2626
          ::::|||||||||  :::||:|||||||||:::||||||||||:::          |||
Db    901 GlyHisLeuLeuAsnLeuSerValProValGlyValLysPheAspArgCysSerSerThr 920

Qy   2627 CAAGATGCAACGTACAATCTAACTCTTGGTTATACTGTGGATCTTGTTCGTAGTAACCCC 2686
          |||||         :::          |||          :::||||||||||||||||
Db    921 HisProAsnLysTyrSerPheMetAlaAlaTyrIleCysAspAlaTyrArgThrIleSer 940

Qy   2687 GACTGTACGACAACACTGCGAATTAGCGGTGATTCCTGGAAAACCTTCGGTACGAATTTG 2746
          |||||:::          :::::|||||          |||          :::|||:|
Db    941 GlyThrThrGluThrProLeuLeuSerHisGlnGluThrTrpPheThrAspAlaPheHisLeu 960

Qy   2747 GCAAGACAAGCTTTAGTCCTTCGTCGCAGGGAACCATTTTTCCTTTAACTCAAATTTTGAA 2806
          |||||         :::||||||||||||          |||          :::||||||
Db    961 AlaArgHisGlyValValValArgGlyGlySerMetTyrAlaSerLeuThrSerAsnIleGlu 980

Qy   2807 GCCTTTAGCCAATTTTCTTTGAATTGCGTGGGTCATCTCGCAATTACAATGTAGACTTA 2866
          |||          :::          :::||||||     |||     :::
Db    981 ValTyrGlyHisGlyArgTyrGluTyrArgAspAlaSerArgGlyTyrGlyLeuSerAla 1000

Qy   2867 GGAGCAAAATACCAATTC 2884
          ||||:::|||  :::|||
Db   1001 GlySerLysValArgPhe 1006
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RESULT 14
US-09-556-877-176
; Sequence 176, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
;   APPLICANT: Probst, Peter
;   APPLICANT: Bhatia, Ajay
;   APPLICANT: Skeiky, Yasir
;   APPLICANT: Fling, Steve
;   APPLICANT: Maisonneuve, Jeff
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
;   TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
;   FILE REFERENCE: 210121.469C5
;   CURRENT APPLICATION NUMBER: US/09/556,877
;   CURRENT FILING DATE: 2000-04-19
;   NUMBER OF SEQ ID NOS: 305
;   SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 176
;   LENGTH: 982
;   TYPE: PRT
;   ORGANISM: Chlamydia
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(982)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-556-877-176

Alignment Scores:
Pred. No.:   Length: 982
Score: 9.7e-91   Matches: 303
Percent Similarity: 45.92%   Conservative: 159
Best Local Similarity: 30.12%   Mismatches: 373
Query Match: 20.79%   Indels: 171
DB: Gaps: 30

US-09-428-122-1 (1-3000) x US-09-556-877-176 (1-982)

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Qy    242 GAAGATGCTGAACTACCTACCTATTAAGGGAAAATGTCACTCTAGAAAATATTCCTGGA 301
          :::          |||:::|||||||     |||     |||     :::|||||||||
Db     23 AspProSerGlyThrValPheSerAlaGlyGluLeuThrLeuLysAsnLeuAspAsn 42

Qy    302 ACAGGCAGCAGCAATCACAAAAAAGCTGTTTAACAACTAAGGGCCGATTTGACTTCACA 361
          :::|||||          ||||||          |||          :::|||:::|||
Db     43 SerIleAlaAlaLeuProLeuCysSerPheGlyAsnLeuLeuGlySerPheThrValLeu 62
```

```
Qy    362 GGTAACGGGAACTCCTCTATTGTTCCAAACGGTGGATGCAGGGACTGAGCAGGGGCTGCT 421
          |||||         :::||||||     :::|||||||          |||||||||||
Db     63 GlyArgAlaGlyHisSerLeuThrPheGluAsnIleArgThrSerThr---AsnGlyAlaAla 81

Qy    422 GTTAACAGCAGCGTGGTAGATAAATCCACACGTTTATAGGGTTTCTTCGTCATCTTT 481
          :::::|||||||||||     :::||||||          |||||||||:::  |||
Db     82 LeuSerAsnSerAlaAlaAspGlyLeuPheThrIleGluGlyPheLysGluLeuSerPhe 101

Qy    482 ----------ATTGCGTCCTCTGGAAGTTCGATAACTACCGGCAAAGGAGGAGCCGTT 526
                    :::          |||          :::||||||||||||||||||||
Db    102 SerAsnCysAsnSerLeuLeuAlaValLeuProAlaAlaThrThrAsnLysValGlySerGln 121

Qy    527 AGCTGCTCTACGGGTAGC---------------------------------------TTGAGT 550
          |||:::          |||                                      ||
Db    122 ThrProThrThrSerThrProSerAsnGlyThrIleTyrSerLysThrAspLeuLeu 141

Qy    551 TTGACAAAAATGTCAGTTGCTTCTTCAGCAAAACTTTTCAACGGATAATGGCGGTGCT 610
          |||          :::||||||||||     |||          :::   :::||||||
Db    142 LeuLeuAsnAsnGlyLysPheSerPheTyrSerAsnLeuValSerGlyAspGlyGlyAla 161

Qy    611 ATCACCGCAAAAACTCTTCATTAACAGGGACTCATCTCGCAATTACAATGTAGACTTA 670
          |||     :::||||||||||     |||          :::||||||:::|||||||
Db    162 IleAspAlaLysSerLeuThrValGlnGlyIleSerLysValCysValPheGlnGluAsn 181

Qy    671 ACCTCCTCAAAGAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTACCATTACTGGAAAC 730
          |||||                  :::          :::               :::|||
Db    182 ThrAlaGlnAlaAspGlyInValValThrSerPheSerAlaMetAlaMetAlaAsn 201

Qy    731 CAAGGGGAAGTCTCTTTT--------- 748
          |||||         ::::|||||||||
Db    202 GluAlaAProIleAlaPheValAlaAsnValAlaGlyvalArgGlyGlyIleAlaAla 221

Qy    749 ----------------------TCTGACAATACTTCTTCTGGATCT--------- 772
                                :::|||||||||:::||||||||||||||
Db    222 ValGlnAspGlyGlnGlyValSerSerSerThrSerThrGluAspProValValSer 241

Qy    773 ----------------------------------GGAGCTGCAATT 784
                                            :::||||||||
Db    242 PheSerArgAsnThrAlaValGluPheAspGlyAsnValAlaAlaArgValGlyGlyGlyIle 261

Qy    785 TTTAGAAGCCTCGGTGACTATTCTTAATAATGCTAAAGTTTCCTTTATTGACAAT-- 841
          |||||         :::          |||          ::::::|||:::|||||
Db    262 TyrSerTyrGlyAsnValAlaPheLeuAsnAsnGlyLysThrLeuPheLeuAsnAsnAsnVal 281

Qy    842 ----------------------AAGGTCACAGGAGCGAGCTCCTCAACAACG 871
                                :::||||||||||||||||||||||
Db    282 AlaSerProValTyrIleAlaAlaLysGlnProThrSerGlyGlnAlaSerAsnThrSer 301

Qy    872 GGGGATATG--TCAGGAGGTGCTATCTGTGCTTATAA------------------ACTAGT 913
          |||          :::               :::::||                :::|||
Db    302 AsnAsnTyrArgGlyGlyAlaIlePheCysLysAsnGlyAlaGlnAlaGlySerAsn 321

Qy    914 ACAGATACTAAGGTCACCCTCACTGAAATCAGATGTTACTCTTCAGCAACAATACATCG 973
          :::          |||          |||:::|||:::||||||||||||:::   :::
Db    322 AsnSerGlySerValSerPheAspGlyGluGlyValValPheSerSerAsnValAla 341

Qy    974 ACAACAGCGGAGGAGCTATCATGTGAAAAAGCTCGAACTGGCTTCCGGAGGACTTACC 1033
          |||||:::          |||||||||||          :::||||:::|||||||||
Db    342 AlaGlyLysGlyGlyAlaIleTyrArgAlaLysLeuSerValAlaAsnCysGlySerAsn 361

Qy   1034 CTATTCAGTAGAAAATAGTGTCAATGAAGTGACAGCTCCTAAAGGTGAGCCATAGCTATC 1093
          |||||          :::               :::|||               :::|||
Db    362 GlnPheLeuArgGluAsnIleAlaAsn------------------------------AspGlyGlyAlaIleTyrLeu 376

Qy   1094 GAAGATAGTGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGTCTTTTAGGGAAT 1153
          :::||||||     :::||||||:::||||||:::||||||||||:::||||:::|||
Db    377 GlyGluSerGlyLeuGluSerLeuSerAlaAspTyrGlyAspIleIlePheAspGlyAsn 396

Qy   1154 ----------ACAGTCACTTCTACTACTCCTCGGGACGAAT------------AGAAGT 1189
                    :::||||||               |||||||            :::|||
Db    397 LeuLysArgThrAlaLysGluAsnLeuLeuGlyAsnLeuGlySerPheThrValLeu 416

Qy   1190 AGTATCGACTTAGGAACGAGCGAGTGCAAAGATGCAAAGATGAGCAGCTTTGCGTTCTGCTGCTAGAGCC 1249
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Db 754 ThrGluValPheGlyArgSerLysAspTyrValValCysArgSerAsnHisAlaCys 773
Qy 2219 GGAGGAACTCTATTACCAGCACACAGCGAAACCTATATCTCTTCCTTGCAAACTACGG 2278
         |||:|||||| :::
Db 774 IleGlySerValTyrLeuSerThrGlnGlnAlaLeu--------------------- 785
Qy 2279 CCTTGTGTCGTTGTCTATGTTCCTACAGAGATTCCTGTTCTCTTTCAGGA-------- 2329
         ||| ||||| |||||
Db 786 ---CysGly---SerTyr---------------LeuPheGlyAspAlaPheIle 796
Qy 2330 AACCTTAGCTACCACCCATACGGATAACGATCTGAAAACCAAGTATACAACATATCCTACT 2389
                ||||||| :::   :::
Db 797 ArgAlaSerTyrGlyPheGlyLysAsnGlnHisMetLysThrSerTyrThrPheAlaGluGlu 816
Qy 2390 GTTAAAGGAAGCTGGGGAATGATAGTTCGCTTTAGAATTCGGTGGAGAGCTCCGATT 2449
         |||:::   :::
Db 817 SerAspValArgTrpAspAsnAsnCysLeuAlaGlyLeuIleGlyAlaGlyLeuProIle 836
Qy 2450 TGCTTAGATGAAAGTGCTCTATTT--GAGCAGTACATGCCCTTCATGAAATTGCAGTTT 2506
         ||||||| :::
Db 837 ValIleThrProSerLysTyrLeuAsnGluLeuArgProPheValGlnAlaGluPhe 856
Qy 2507 GTCTATGCACATCAGGAAGGTTTAAAGAACAGGAGAACCAGAGAGCTCCTGAATTTGAAGT 2566
                  :::
Db 857 SerTyrAlaAspHisGluSerPheThrGluGlnGlyLysAspGlnAlaArgAlaPheLysSer 876
Qy 2567 AGCCGTCTGTGAATCTTGCCTACCATGCGGATCCGATTGATAAGGAATCAGACTGC 2626
         |||:::   :::|||||||
Db 877 GlyHisLeuLeuAsnLeuSerValProValGlyValLysPheAspArgCysSerSerThr 896
Qy 2627 CAAGATGCAAGTCAACATACAACTCTTGGTTATACTGTGTATACTGTTCGTAGTAACCCC 2686
         |||||||
Db 897 HisProAsnLysTyrSerPheMetAlaAlaTyrIleCysAspAlaTyrArgThrIleSer 916
Qy 2687 GACTGTACGACAACACTGCGAATTAGCGGTGATTCTTGGAAACCTTCGGTACGAATTTG 2746
Db 917 GlyThrGluThrThrLeuLeuSerHisGlnGluThrTrpThrAspAlaPheHisLeu 936
Qy 2747 GCAAGACAAGCTTTAGTCCTTCGTGCGAGGAACCATTTTGCTTAACTCAAATTTTGAA 2806
         ||||||| :::|||
Db 937 AlaArgHisGlyValValValAlaArgGlySerMetTyrAlaSerLeuThrSerAsnIleGlu 956
Qy 2807 GCCTTAGCCAATTTCTTTGAATTGCGTGGGTCATCTCGCAATTACACATGTAGACTTA 2866
         :::||| :::|||
Db 957 ValTyrHisGlyArgTyrGluTyrGluThrValGlyArgArgAspAlaSerArgGlyTyrGlyLeuSerAla 976
Qy 2867 GGAGCAAAATACCAATTC 2884
         :::
Db 977 GlySerLysVal***Phe 982

417 AlaIleSerMetGlySerGlyGlyLysIleThrLeuThrArgAlaLysAlaGlyHisGln 436
1250 ATCTACTTCTATGATCCCATAACTACAGGATCATCCACAACA--------GTTACA 1297
437 IleLeuPheAsnAspProIleGluMetAlaAsnGlyAsnAsnGlnProAlaGlnSerSer 456
1298 GATGTCTTAAAAGTTAATGAGACTCCGCAGATTCTGCACTACAATATACAGGGAACATC 1357
457 LysLeuLeuLysIleLeuAsnAspGlyGluGly----------TyrThrGlyAspIle 471
1358 ATCTTCACAGAGACAAAAAGTTATCAGAGACAGAGGCCGCAGATTCTAAAAATCTTACTTCG 1417
472 ValPheAla----------AsnGlySerSer 478
1418 AAGCTACTACAGCCCTGTAACTCTTTCAGGAGGTACTCTATCTTTAAAAACTGGAGTGACT 1477
479 ThrLeuTyrGlnAsnValThrIleGlnGlyValLeuArgGlyLeuArgIleValAlaLeuArgGluValLeuArgIleValAlaLys 498
1478 CTGCAGACTCAGGCATTCACTCAACAGCAGATTCTGTCTGAAAATGGACGTAGGAACT 1537
499 LeuSerValAsnSerLeuSerGlnThrGlySerGly----------LeuTyrMetGluAlaGlySer 517
1538 ACTCTAGAA----------CCTGCTGATACTAGC--------- 1561
518 ThrLeuAspPheValThrProGlnProGlnProGlnProAlaAlaAlaAsnGlnLeuIle 537
1562 ACCATAAACAATTTGGTCATTAACATCATCTATA---------- 1597
538 ThrLeuSerAsnLeuHisLeuSerLeuSerLeuLeuAlaAsnAsnAlaValThrAsn 557
1598 ----------GACGGTGCAAAGAGGCAAAAATAGAAACCAAAGTACG 1636
558 ProProThrAsnProAlaGlnSerHisProAlaValIleGlySer---ThrThr 576
1637 TCAAAAATCTGACTTATCTGGAACCATCACTTATTGGACCCGACGGGCACGTTTTAT 1696
577 AlaGlySerValThrThrIleSerGlyTyrProIlePhePheGluAspTyrAlaTyr 596
1697 GAAAATCATAGT--TTAAGAAATCCTCAGTCTCAGTGACCATCATCTTAGAGCTCAAAGCTTCT 1753
597 AspArgTyrAspTrpLeuGlySerAsnGlnLysIleAsnValLeuLysLeuGlnLeu--- 615
1754 GGAACTGTAACAAGCACCGGACTCCCAGTGACTCCTATAATGGGTGAGAAATTC---CAT 1810
616 GlyThrLysProProAlaAlaAsnAlaProSerAspLeuThrLeuGlyLeuAsnGlyMetProLys 635
1811 TACGGCTATCAGGGAACTTGGGGCCCAATTGTTTGGGGGACAGGGGCTTCTACGACTGCA 1870
636 TyrGlyTyrGlnGlyGlySerTrp---LysLeuLeuAlaTrpAspProAsnThrAlaAsnAsnGly 654
1871 TACCTTC----------AACTGGACTAAAACTGGCTATATTCCTAATCCCGAGCGGTATC 1918
655 ProTyrThrLeuLysAlaThrTrpThrLysThrGlyTyrAsnProGlyProGluArgVal 674
1919 GGCTCTCTTTAGTCCCTAATAGCTTATGGAATGCATTATGAGATATTAGCTCTCTCCATTAT 1978
675 AlaSerLeuValProAsnSerLeuTrpGlyTrpGlySerIleLeuAspIleLeuArgSerAlaHisSer 694
1979 CTTATGGAGACTGCAAACGAAGGTTGCAGGGAGACCGTGCTTTTTGGTGTGCTGGATTA 2038
695 AlaIleGlnAlaSerValAspGlyArgSerTyrCysArgGlyTyrLeuTrpValSerGlyVal 714
2039 TCTAAACTTCTTCCATAAGGATAGTACAAAAAACACACGCCGGGTTCGCCATTGAGTGGGC 2098
715 SerAsnPheTyrHisAspArgAspAlaLeuGlyGlnGlyTyrArgTyrIleSerGlyGly 734
2099 GGTTATGTCATAGGAGGAGAAACCTACACTTGTTCAGATAAGATTCTTAGTGCTGCATTT 2158
735 GlyTyrSerLeuGlyAlaAsnSerTyrPheGlySer--------SerMetPheGlyLeuAlaPhe 753
2159 TGTCAGCTCTTTGGAAGAGAATAGAGACTACTTTGTAGCTAAGAATCAAGGTACAGTCTAC 2218

RESULT 15
US-09-620-412C-176
; Sequence 176, Application US/09620412C
; Patent No. 648234
; GENERAL INFORMATION:
,   APPLICANT: Steven P. Fling
,   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
,   TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
,   FILE REFERENCE: 210121.469C7
,   CURRENT APPLICATION NUMBER: US/09/620,412C
,   CURRENT FILING DATE: 2000-07-20
,   NUMBER OF SEQ ID NOS: 363
,   SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 176
,   LENGTH: 982
,   TYPE: PRT
,   ORGANISM: Chlamydia
,   FEATURE:
,   NAME/KEY: VARIANT
,   LOCATION: (1)...(982)
,   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-620-412C-176

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Alignment Scores:
Pred. No.:              9.7e-91
Score:                  1124.50
Percent Similarity:     45.92%
Best Local Similarity:  30.12%
Query Match:            20.79%
DB:

                    Length:         982
                    Matches:        303
                    Conservative:   159
                    Mismatches:     373
                    Indels:         171
                    Gaps:           30

US-09-428-122-1 (1-3000) x US-09-620-412C-176 (1-982)
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Qy    242  GAAGATGCTGGAACTACCTATTTAAGGGAAATGTCACTCAGAAAATATTCCTGGA  301
                ::: |||||||        |||    |||:::|||:::::|||::|||
Db     23  AspProSerGlyThrThrValPheSerAlaGlyLeuThrLeuLysAsnLeuAspAsn  42

Qy    974  ACAACGCGGGAGGAGCTATCTATGTGAAAAAGCTCGAACTGGCTCCGGAGGACTTACC  1033
                                                |||||||  :::|||:::|||
Db    342  AlaGlyLysGlyAlaIleTyrAlaLysLysLeuSerValAlaAsnCysGlyProVal  361

Qy   1034  CTATTCAGTAGAAAATAGTGTCAATGAGAGTACAGCTTCCTAAAGGTGGAGCCATAGCTATC  1093
                                                                     --------
Db    362  GlnPheLeuArgAsnIleAlaAsn-                        AspGlyGlyAlaIleTyrLeu  376

Qy   1094  GAAGTAGTGGGGAATTGAGTTTATCCGCCGATAGTGGTGACATTGCTCTTTTAGGGAAT  1153
                :::|||||||||                |||    |||:::|||::|||||::::|||
Db    377  GlyGluSerGlyGlyGluLeuSerLeuSerAlaAspTyrGlyAspIleIlePheAspGlyAsn  396

Qy   1154  ------------ACAGTCACTTCTACTACTCCTGGACGAAT                 AGAAGT  1189
           --------                                               ------
Db    397  LeuLysArgThrAlaLysGluAsnAlaAlaAspValAsnGlyValThrValSerSerGln  416

Qy   1190  AGTATCGACTTAGGAACGAGTGCAAAGATGACAGCTTTGCGTTCTGCTGGTAGAGCC  1249
                :::|||  :::|||      |||       :::|||       |||||||
Db    417  AlaIleSerMetGlySerGlyLysGlyIleThrThrLeuArgAlaLysAlaGlyHisGln  436

Qy   1250  ATCTACTTCTATGATCCCATAACTACAGGATCATCCACAACA--------------  GTTACA  1297
                                         :::                          :::
Db    437  IleLeuPheAsnAspProIleGluMetAlaAsnGlyAsnAsnGlnProAlaGlnSerSer  456

Qy   1298  GATGTCTTAAAAGTAATGAAGACTCCGGCAGATTCTGCACTACAATATACAGGGAACATC  1357
                :::|||  :::|||::::::|||                        TyrThrGlyAspIle  471
Db    457  LysLeuLeuLysIleLeuAsnAspGlyGluGly-

Qy   1358  ATCTTCACAGGAGAAAAGTTATCAGAACAGAGGCCGCAGATTCTAAAAATCTTACTTCG  1417
                :::|||                                            AsnGlySerSer  478
Db    472  ValPheAla-

Qy   1418  AAGCTACTACAGCCTGTAACTCTTCTCATCTTAAAACATGGAGTGACT  1477
                |||       :::|||:::||||
Db    479  ThrLeuTyrGlnAsnValThrIleGluGlnGlyArgIleValLeuArgLeuLysAlaLys  498

Qy   1478  CTGCAGACTCAGGCATTCACTCAACAGGCAGATTCTCGTCTCGAAATGGAGTAGGAGAACT  1537
                :::|||                |||||||        :::|||
Db    499  LeuSerValAsnSerLeuSerGlnThrThrGlyGlySer--LeuTyrMetGluArgGlySer  517

Qy   1538  ACTCTAGAA--------                        CCTGCTGATACTAGC-  1561
           |||                                     |||
Db    518  ThrLeuAspPheValThrProGlnProProGlnProProAlaLeuAlaAsnGlnLeuIle  537

Qy   1562  ACCATAAACAATTGGTCATTAACATCAGTTCTATA--------------  1597
                :::|||:::|||        ||||||
Db    538  ThrLeuSerAsnLeuHisLeuSerSerLeuLeuAlaAsnAsnAlaValThrAsn  557

Qy   1598  --------                GACGGTGCAAAGAAGGCAAAAAATAGAAAACCAAAGCTACG  1636
                                     :::          |||||||
Db    558  ProProThrAsnProProAlaGlnAsnAspSerHisProAlaValIleGlySer---ThrThr  576

Qy   1637  TCAAAAAATCTGACTTTATCTGAACCACACTTTATTGACCGGACACGTTTAT  1696
                :::|||||||        :::|||        ||||||
Db    577  AlaGlySerValThrIleSerGlyProIlePhePheGluArgLeuAspLeuAspThrAlaTyr  596

Qy   1697  GAAAATCATAGT---TTAAGAAATCCTCAGTCCTACGACATCTTAGAGCTCAAAGCTTCT  1753
                                     :::  :::          :::|||:::
Db    597  AspArgTyrAspTrpLeuGlySerAsnGlnIleSerAsnValLeuLysLeuGlnLeu---  615

Qy   1754  GGAACTGTAACAAGCACCGCAGTGACTCCAGATCCTATAATGGGTGAGAAATTC---CAT  1810
                :::||||||        :::          |||:::|||
Db    616  GlyThrLysProProAlaAsnAlaProSerAspLeuThrLeuGlyAsnGluMetProLys  635

Qy   1811  TACGGGCTATCAGGGAACTTGGGGCCCAATTGTTTGGGGACAGAGGGCTTCTACGACTGCA  1870
                |||||||:::                                  ||||||:::
Db    636  TyrGlyTyrGlnGlySerTrp---LysLeuLeuAlaTrpAspProAsnThrAlaAsnGlyAsnGly  654

Qy   1871  ACCTTC--------                AACTGACTAAAACTGGCTAATTCCTAATCCCAGCGTATC  1918
                :::                        |||||||
Db    655  ProTyrArgLeuLysAlaThrThrTrpThrLysThrGlyThrTyrAsnProGlyProGluArgVal  674
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```
Qy    302  ACAGGCACAGCAATCACAAAAAGCTGTTTAACACACTAAGGGCGATTTGACTTTCACA  361
               :::  |||        :::|||      |||||||
Db     43  SerIleAlaAlaLeuProLeuSerPheGlyAsnLeuLeuGlySerPheThrValLeu  62

Qy    362  GGTAACGGGGAACTCTCTATTGTTCCAAACGTGGGATGCAGGGACTGTAGGCAGGGGCTGCT  421
               |||                |||:::|||        :::
Db     63  GlyArgGlyHisSerLeuThrProGluAsnIleArgThrSerThr--AsnGlyAlaAla  81

Qy    422  GTTAACAGCAGCGGTGGTAGATAAATCTACCACGTTTATAGGGTTTTCTTCGCTATCTTTT  481
               ::::::::|||                        |||
Db     82  LeuSerAsnSerAlaAlaAspGlyLeuPheThrIleGluGlyPheLysGluLeuSerPhe  101

Qy    482  -----------ATTGGCTGCCTGGAAGTTCGATAACTACCGGCAAAGGAGAGCCGTT  526
                              :::  ||||||  :::|||
Db    102  SerAsnCysAsnSerLeuLeuAlaValLeuProAlaIleAlaThrThrAsnLysAsnLysSerGlySerGln  121

Qy    527  AGCTGCTCTACGGGTAGC---------------                TTGAGT  550
               :::||
Db    122  ThrProThrThrSerThrProSerAsnGlyThrIleTyrSerLysThrAspLeuLeu  141

Qy    551  TTGACAAAAATGTCAGTTGCTCTTGCACTTTCAGCAGAAAACTTTTCAACGGATAATGGCGGTGCT  610
               |||                :::          |||:::|||
Db    142  LeuLeuAsnAsnGluLysPheSerPheTyrSerValSerGlyAspTyrAspGlyAlaGlyAla  161

Qy    611  ATCACCCGCAAAAAACTCTTTCATTAACAGGGACTCAGCTCTGTTTCTGAAAAT  670
               |||||||        :::          :::|||        |||
Db    162  IleAspAlaLysSerArgLeuThrValGlnGlyTyrIleSerLeuLysCysSerValPheGluGlnGluAsn  181

Qy    671  ACCTCCTCAAAGAAAAGGCGGAGCCATTCAGACTTCCGATGCCCTTACCATTACTGAAAC  730
               ||||||                :::||  :::
Db    182  ThrAlaGlnAlaAspGlyAlaCysGlnValValThrSerSerAlaSerPheSerAlaMetAlaAsn  201

Qy    731  CAAGGGGAAGTCTCTTTT---------------                  748
               :::|||||||
Db    202  GluAlaProIleAlaPheValAlaAlaAsnValAlaAlaAlaGlyValValArgGlyValIleAlaAla  221

Qy    749  ---------------TCTGACATACTTCTTCGGATTCT                  772
                              ::||||||||:||||||||
Db    222  ValGlnAspGlyGlnGlnValSerSerGlnThrGluSerThrGluAspProValValSer  241

Qy    773  ---------------GGAGCTGCAATT                  784
                              ||||||
Db    242  PheSerArgAsnThrAlaValAlaValGluPheAspGlyAsnValAlaAlaArgValAlaLeuGlyGlyIle  261

Qy    785  TTTACAGAAGCCTCGGTGACTATTCTAATAATGCTAAAGTTCCTTTATTGACAAT---  841
               ||||||        :::  :::          ::::::|||
Db    262  ThrAlaGlnAlaAspGlyAlaCysGlnValValThrSerSerPheSerAlaMetAlaAsn  281

Qy    842  ---------------AAGGTCACAGACGGAGCGAGCTCCAACAACG  871
                              :::|||:::          |||||:::|||
Db    282  AlaSerProValTyrIleAlaAlaAlaAlaLysGlnProThrSerGlyGlnAlaSerAsnThrSer  301

Qy    872  GGGGATATG--TCAGGAGGTGCTATCTGTGTCTTATAAA---------------  ACTAGT  913
               :::                                        ::|||:::
Db    302  AsnAsnThryrGlyAspGlyGlyTyrAlaIleIlePheCysLysLysAsnGlyAlaGlnAlaGlySerAsn  321

Qy    914  ACAGATACTAAGGTCACCCTCACTGAAAATCAGATGTTACTCTTCAGCAACAATACATCG  973
               |||        :::||||||:::||||||        :::  :::
Db    322  AsnSerGlySerValSerPheAspGlyGluGlyValPheGlnValPheGlnAspSerSerAsnValAla  341
```